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Book of Abstracts

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TALKS

Distinguished Fellow talk

Abstract ID: 2475

40 years of speciation research

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I will give a rather personal overview of how speciation research has developed, one might even say progressed, in the last four decades. This period has seen many changes, obviously in the technology available but also in perceived priorities in speciation research. Coyne and Orr's landmark book in 2004 might be considered something of a watershed but many old questions are still with us, particularly about the relative contribution of different processes to the generation of biological diversity.

ESEB Presidential address

Abstract ID: 2474

ESEB Presidential address

Astrid T. Groot
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Research lines evolving
To understand the process of speciation, my research focus over the past 20 years has been to discover evolutionary causes and consequences of variation in sexual attraction, as my main hypothesis is that variation in sexual attraction is the main driver of speciation. Moths are ideal model organisms for this research, as sexual attraction in this species-rich group of animals is through well-defined and species-specific sex pheromones. This focus has led to surprising avenues, ranging from fundamental research on the origins and evolution of the genetic code and predicting evolution, to research on the effects of artificial light on food webs in which moths and their caterpillars play a central role. Since sexual attraction in moths is mainly through sex pheromones, we are now also developing an odor dictionary to increase awareness of the odor world in which we live. Chemical communication is the oldest form of communication in life, and discovering how chemical communication networks within and across species evolve give fundamental insights in the evolution of community networks.

Roberto Torres, Director of La Ciència Al Teu Món and Dissemination officer of the EuroScitizen COST Action

Abstract ID: 2473

Promoting scientific literacy in Evolution through citizen science practices in high schools

Roberto Torres
Director of La Ciència Al Teu Món and Dissemination officer of the EuroScitizen COST Action

Hands-on citizen science practices have already demonstrated its efficiency to establish a long-term relationship between evolutionary biologists and high school students, teachers, farmers and other interested parties from rural areas across Europe (and beyond), in order to expedite, and make more participative, cutting-edge scientific research in adaptation genomics. Citizen science practices, also contribute to generate the knowledge to build on citizens the capacities that are necessary to face societal challenges such as monitoring and analyzing the impact of climate change in global and local biodiversity. This evidences the relevance and the convenience of citizen science to involve society in all the different stages of the scientific process: from co-creation of research processes, development of fieldwork technological solutions, to data collection and analysis, and the dissemination of results. As such, citizen science practices allow citizens to become the enablers of a global change in the perception of the implications of basic science, and the correct understanding of evolutionary processes with implications for climate change, pest control and host pathogen interactions, all relevant for citizens daily lives. Moreover, we will share the compendium of citizen science recommendations gathered in the publication “Promoting scientific literacy in Evolution through citizen science”, developed by the citizen science working group of the EuroScitizen COST Action 17127 (euroscitizen.eu).

Talks by John Maynard Smith Prize winners

Abstract ID: 2477

Reproducibility of antibiotic resistance evolution

Camilo Barbosa, Andrew F. Read, Robert J. Woods
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Evolution is the root of the antibiotic resistance crisis. Clarifying the evolutionary processes leading to resistance, in particular the determinants of chance and repeatability, are thus pivotal to the goal of understanding how pathogens adapt to drugs. Two important open questions are how reproducible antibiotic resistance evolution is within human hosts and to what extent those evolutionary paths seen *in vivo* can be recapitulated *in vitro*. To address these two questions, we retrospectively identify changes in resistance against daptomycin and linezolid when these drugs are used as the main treatment in patients with blood stream infections with *Enterococcus*

faecium. *E. faecium* isolates from blood cultures of hospitalized patients are routinely stored in our lab. Twelve patients were identified with *in vivo* resistance evolution of *E. faecium* to daptomycin and 6 to linezolid, each obtained from independent patients. We fully sequenced and assembled the genomes of 18 initially sensitive isolates. We then performed whole genome sequencing of the subsequent isolates showing an increase in resistance against the corresponding drug within the same patient to identify the repeatability of genomic changes associated with resistance. Additionally, each of the 18 initially sensitive isolates was used to found 20 independent biological replicates from in vitro evolution against increasing concentrations of the corresponding drug to determine whether the same mechanisms identified *in vivo* emerge *in vitro*. This study cast light on the role of determinism and contingency in evolution, with implications for medical treatment.

Abstract ID: 2478

From patterns to processes: towards a mechanistic understanding of the human microbiome

Stefany Moreno Gamez
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The human body harbours trillions of bacterial cells that live in diverse communities. Much of what is known about the composition and dynamics of these communities comes from high-throughput metagenomic studies which have yielded a large inventory of bacterial species and genes that are correlated with health and disease. Although these catalogs underscore the
relevance of the microbiome for human health, they offer limited insights on how microbial communities in the human body assemble, what determines their functional properties and how they evolve. My long-term goal is to build a mechanistic understanding of the human microbiome by establishing how broader ecological and evolutionary patterns are linked to the
underlying physiology and interactions of individual microbes. In this talk, I will present two examples of the insights that can be gained by this comprehensive approach. First, I will show that in bacterial populations made of single species and even of single genotypes, variation in how individuals sense and respond to their environment is pervasive, and underlies the evolution
of phenomena like antibiotic tolerance and resistance. Second, I will shift the focus to multispecies communities, and show how bacterial physiology shapes the evolution of private and public resource utilization strategies in the gut microbiome, and how this process can be modulated by the human host.

Abstract ID: 2479

What does evolution have to say about ecosystem resilience?

Catalina Chaparro Pedraza
Eawag, -, Switzerland

Evolutionary and ecological processes influence one another. This realization has led the disciplines of ecology and evolutionary biology to become increasingly integrated. Yet, some problems in each discipline are still viewed through a mono-disciplinary lens. This

was until recently the case of ecological resilience theory. I will show how the introduction of evolutionary dynamics in the ecological resilience theory can fundamentally reshape our knowledge about resilience and tipping points in ecosystems. For example, it is traditionally established that an ecosystem tips to an alternative stable state when an environmental threshold is exceeded. On the contrary, we have shown that eco-evolutionary feedbacks can cause an ecosystem to tip without exceeding an environmental threshold. I will conclude highlighting the tight link between evolutionary mechanisms, and population and community process.

Symposium: S01. Tug of war between the sexes: The transcriptomic architecture of sex-linked traits (id: 6)

Abstract ID: 2481

Sexual conflict over gene expression? Insights from stick insects with different reproductive modes

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Males and females feature strikingly different phenotypes, which are thought to arise primarily from sex-biased gene expression during development. However, because different sexes and developmental stages are produced from a shared genome, genetic constraints can result in sub-optimal gene expression levels. We are examining how putative genome-sharing constraints affect transcriptome evolution by using comparative studies of sexual and asexual stick insect species. Because asexual species consist solely of females, selection can optimise female phenotypes independently of any correlated effects in males. I will present data on sex-biased gene expression and dosage compensation over development for sexual stick insects and show how gene expression changes upon the loss of selection on male traits.

Abstract ID: 1739

Sex-biased gene expression: cause versus consequence of sexual dimorphism

Iulia Darolti, Judith Mank
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Males and females within a species often exhibit dimorphism across a broad range of phenotypes despite sharing largely the same genome. Differential expression of genes that are present in both sexes is thus thought to be key to the development of sexually dimorphic traits, and sex-biased genes are increasingly used to study the footprint of sex-specific selection within the genome. However, studies of differential gene expression often measure expression from whole organs or even whole-body samples, which represent complex aggregates of different cell types. These approaches cannot determine if sex-biased gene expression results from regulatory differences between males and females within similar cell types, or if it is a consequence of differences in cell-

type abundance due to sex-specific developmental programs. To disentangle between these processes, we analyzed single-cell RNA-sequencing data from multiple somatic and reproductive tissues of male and female guppies, in order to distinguish sex-biased genes that show regulatory rewiring from those that arise from differences in cell-type abundance. By comparing rates of molecular evolution and polymorphism between sex-biased genes that are responsible for sexual dimorphism and those that are simply a consequence of it, we offer a powerful and unprecedented test of the relationship between sexually antagonistic selection and differential gene expression.

Abstract ID: 1642

Sex or sex role – unravelling the evolutionary route of sex-specific senescence

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Senescence, defined both as biological aging and cell deterioration, varies across the animal kingdom, from species to individuals and even between tissues. Sex differences in lifespan were identified in many species from longer-lived females and shorter-lived males to fewer cases where the opposite is true. The classic theoretical evolutionary model interprets aging as a cost of reproduction, where evolution has favoured sex-specific life history strategies (sex roles) and lifespans. However, research focusing on how sex role influences aging remains scarce. Making use of the enigmatic sex-role reversed model system, the broadnosed pipefish *Syngnathus typhle (Syngnathidae),* with its unique male pregnancy, we investigated the link between aging, sex and sex role. Syngnathids provide the unique opportunity of decoupling the role of the female sex (defined as contribution of eggs) and sex role due to its unique evolution of male pregnancy, allowing to investigate the complex relation between sex, sex role and aging. Using mRNA-Seq, we compared transcriptome expression of young and old female, male and pregnant pipefish. Sex-specific gene expression in the brain is more diverse in younger fish. Important senescence genes, such as igf3, were found to be upregulated in the ovaries of old females, but downregulated in the testis of old males. Whilst in the head-kidney age appears to have a stronger effect on females compared to males. Such results indicate that sex-specific senescence is not influenced by the biological sex but rather by the sex role and the incorporated differences in life-history strategy.

Abstract ID: 1509

Gene expression responses to selection for increased and reduced sexual dimorphism

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Sexually dimorphic phenotypes are some of the most striking in nature. However, there remain many unanswered questions about how evolution produces such phenotypes

given that the sexes share the vast majority of their genomes. The proximate mechanism by which it is thought sex differences can be achieved is regulation of gene expression. Here we combine artificial selection with RNA-seq to test how the evolution of sexual size dimorphism influences gene expression in *Callosobruchus maculatus* seed beetles. Our selection experiments, targeting shared and sex-specific genetic variation for adult body size across 10 generations of sex-limited and sexually antagonistic (SA) selection, successfully changed sexual size dimorphism by up to 50%. Results indicated a role for female-specific dominance variation, male-specific X-linked variation and, unexpectedly, Y-linked variation underlying the response to selection. Subsequent work showed that SA selection in particular maintained female-specific dominance variation for body size. A possible mechanism for this is sex-specific allele specific expression (SS-ASE). Testing this, we here investigated gene expression changes in heterozygous F1 offspring from isofemale line crosses created from the final generation of our selection lines. In addition to changes in sex-biased gene expression and sex-specific alternative splicing across our experimental selection lines, we investigated the novel possibility that SS-ASE might facilitate the evolution of sexual dimorphism. Combining a knowledge of selection history, phenotypic evolution and gene expression changes, our findings provide a comprehensive view of the resolution of sexual conflict over the shared genome, contributing to the growing literature on the genomics of sexual dimorphism.
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Abstract ID: 1134

On the genetic basis of sex differences in gene expression: sex-bias eQTLS

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Females and males are subject to contrasting selective pressures on traits that have a shared genetic basis between them, which leads to a sexual “conflict of interests” at the genetic level. The resolution of this conflict relies on the evolution of sexual dimorphism, i.e. of mechanisms that decouple the genotype-to-phenotype relationship among females and males. At the molecular level, such mechanisms involve sex linkage and various types of sex-specific expression of shared regions. Sex differences in regulatory architecture have been traditionally studied via sex-stratified eQTL analyses, which identify sex-specific associations between mutations and gene expression phenotypes. However, we argue that this strategy has statistical constraints and is not directly informative of the genetic basis underlying sex differences in expression.
Here we propose an alternative approach, exactly to this end: sex-bias eQTL analyses, whereby we characterize the genetic variation associated with expression differences across sexes explicitly, via eQTL analysis on sex bias in expression across *Drosophila melanogaster* lines, corresponding to F1s from crosses across DGRP inbred lines, separately for heads and gonads. We characterize its modus operandi (influencing gene expression in a sex-specific, sex-biased or sexually-antagonistic manner, acting in cis- or trans-), effect size distribution, genomic location and tissue-specificity.
This novel approach, in combination with the traditional sex-stratified analysis, can shed light on the molecular basis of sexual dimorphism as well as its evolutionary dynamics and constraints.

Abstract ID: 2455

Developmental architecture of sexual dimorphism and its evolution: insights through the study of horned dung beetles

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The developmental mechanisms allowing males and females to develop divergent phenotypes despite a shared genome are beginning to be uncovered. Here, we summarize recent findings in the study of the developmental genetic underpinnings of sexual dimorphism and its evolution in various species of horned dung beetles. Combining transcriptomics, comparative functional genetics, analyses of chromatin accessibility, and geometric morphometrics, we document that the conserved sex-determination gene *doublesex (dsx)* instructs sexual dimorphism in morphology, life history, and behavior via changes in gene expression patterns. Studying *Dsx*'s function in a range of traits and species suggests (i) that *dsx* is a key regulator of trait-specific sexual dimorphism, (ii) that *dsx* modulates sex differences in plastic responses to environmental conditions, and (iii) that the context-specificity of *Dsx*'s function diversifies rapidly across species. Because *Dsx* is a highly conserved transcription factor that undergoes sex-specific splicing, this suggest that the capacity of male- and female-specific isoforms to regulate independent ranges of target genes enables males and females to overcome between-sex genetic correlations. We discuss how the co-option of sex determination pathways into the development of secondary sexual traits contributes —at least partially— to the resolution of intralocus sexual conflict. More generally, we discuss how alternative splicing allows males and females to diverge in life history, morphology, and behavior on a molecular level. Similar mechanisms may contribute to the resolution of conflict arising from environment-dependent antagonistic selection among sexes and other contexts in a wide range of animals.

Abstract ID: 1634

What great big (and sex-specific) eyes you have: the turbanate eyes of mayflies

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Evolutionary innovations are biological revolutions: new organs are critically associated with the emergence of new species and their exploitation of new niches. One of the most striking examples of a sexually dimorphic novel structure occurs in males of the mayfly species *Cloeon dipterum. Cloeon* males develop, in addition to the compound eyes (shared by males and females), an extra pair of extremely large dorsal, turban-shaped eyes. How this morphological novelty appeared and evolved in males of the Baetidae family of Ephemeroptera? What adaptive advantages and new capabilities confer this novel sex-specific visual system? To answer these questions, we first describe the development of the eye and its integration with the optic lobes of male and female *C.*

dipterum nymphs. Second, we compare sex-specific gene expression in nymphal heads of male and female individuals at single cell resolution, to reveal which genes are expressed in the cell populations of the developing male-specific eye and to identify the gene regulatory network responsible for the origin of this sexually dimorphic visual system. Finally, we show male-specific opsins, expressed specifically in the turbanate eye, which may provide additional visual abilities to Baetidae males and advantages to detect mating partners while flying.

Abstract ID: 2072

Evolutionary sex-biased gene expression in Lake Tanganyika cichlid fishes

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Male and female individuals of the same species have mild differences in their genomes, although phenotypic variation may be more significant. Hence, sexual dimorphism is often explained by a set of genes differentially expressed between sexes, in which different evolutionary selective forces are exerted over a trait, promoting intralocus sexual conflict ascent. Sex-biased gene expression evolution has been proposed to resolve such types of sexual conflict. Within the diverse assemblage of Lake Tanganyika cichlid fishes, some species display pronounced sexually dimorphic traits presumably evolved under sexual conflict. However, the contribution of sex-biased gene expression evolution is still unknown. Here we show, how sex bias in gene expression in 15 Lake Tanganyika cichlid tribes has evolved in five body organs: brain, liver, gill, lower pharyngeal jaw, and gonads. Our main findings showed that gonads were the body organ with the highest number of sex-biased genes, with a greater number of male-biased genes than female-biased genes. And in gonads, male-biased genes are evolving faster than female-biased genes. Besides, genes with extreme expression are found to be under more positive selection than low and mid-expressed genes, and extremely expressed genes also showed more differentiation across sexes. Sex-biased gene turnovers correlate to sperm competition rank and coloration degree in livers. Our findings describe, for the first time, how evolution in sexual conflict is helping to shape one of the most extraordinary adaptive radiation processes on earth and open further questions on sexual conflict resolution across the whole assemblage of Lake Tanganyika cichlid fishes.

Abstract ID: 2258

Evolution of sex chromosomes and mechanisms of dosage compensation in squamate reptiles

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Squamate reptiles possess variability in sex determination, ranging from environmental to genotypic sex determination with differentiated sex chromosomes. Genotypic sex determination evolved within amniotes independently at least 40 times, resulting in systems varying from poorly to highly differentiated sex chromosomes under both female (ZZ/ZW) and male (XX/XY) heterogamety. Recently, it was demonstrated that the same parts of genome play the function of differentiated sex chromosomes in different amniote lineages. The independent co-option of the same regions for the role sex chromosomes in different lineages might be caused by limited multiple choices. Nevertheless, an intriguing possibility is that only particular regions can meet the requirements to become differentiated sex chromosomes such as low recombination rates, gene content involved in gonad differentiation, development of sex-linked traits and epigenetic regulation. Particularly, we will review how the amniote lineages cope with differences between males and females in copy numbers of genes linked to paired sex chromosomes (X or Z) missing on the degenerated unpaired sex chromosomes (Y or W). I will summarize the recent advances in transcriptomics and genomics and conceptual approaches allowing us to identify the sex-specific gene content in details and to shed light on the evolution of sex chromosomes and dosage compensation mechanisms in amniotes.

Symposium: S02. Sex chromosome evolution: the canonical model and so much beyond (id: 963)

Abstract ID: 976

Multiple evolutionary strata on mating-type chromosomes despite the lack of sexual antagonism

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Sex chromosomes can display successive steps of recombination suppression known as “evolutionary strata”, which are thought to result from the successive linkage of sexually antagonistic genes to sex-determining genes. However, there is little evidence to support this explanation. We show that evolutionary strata have evolved repeatedly without sexual antagonism in fungi that display suppressed recombination extending beyond loci determining mating compatibility despite lack of male/female roles associated with their mating types. By comparing genomes from anther-smut fungi with or without recombination suppression in their mating-type chromosomes, we inferred the ancestral gene order and derived chromosomal arrangements. This approach shed light on the chromosomal fusion underlying the linkage of mating-type loci in fungi and multiple independent cases of chromosomal rearrangements leading to regions of suppressed recombination linking these mating-type loci in closely related species. Such convergent transitions in genomic architecture of mating-type determination indicate strong selection favoring linkage of mating-type loci into cosegregating supergenes. We also find multiple independent evolutionary strata (stepwise recombination suppression) in several species over a range of ages in mating-type chromosomes. Several evolutionary strata did not include genes involved in mating-type determination. The existence of strata devoid of mating-type genes, despite the lack of sexual antagonism, calls for a unified theory of sex-related chromosome evolution. We developed a general model showing that evolutionary strata can evolve around permanently heterozygous alleles for sheltering recessive deleterious mutations that are pervasive in genomes, which can explain

stepwise recombination suppression around sex-determining but also mating-type loci and other supergenes.

Abstract ID: 1027

A deleterious mutation-sheltering model for the evolution of sex chromosomes and supergenes

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Many organisms have sex chromosomes with large non-recombining regions that have expanded stepwise, generating “evolutionary strata” of differentiation. The reasons for this remain poorly understood, but the principal hypotheses proposed to date are based on antagonistic selection due to differences between sexes. However, it has proved difficult to obtain empirical evidence for these hypotheses, and antagonistic selection has been shown to be unlikely to account for the evolutionary strata observed on fungal mating-type chromosomes. There may, therefore, be other mechanisms involved in the extension of non-recombining regions. We show, by mathematical modeling and stochastic simulation, that recombination suppression on sex chromosomes and other supergenes can expand in a stepwise manner under a wide range of parameter values simply because it shelters recessive deleterious mutations, which are ubiquitous in genomes. Permanently heterozygous alleles, such as the male-determining allele in XY systems, protect linked chromosomal inversions against the expression of their recessive mutation load, leading to the successive accumulation of inversions around these alleles without the need for antagonistic selection. Similar results were obtained with models assuming recombination-suppressing mechanisms other than chromosomal inversions, and for supergenes other than sex chromosomes, including those without XY-like asymmetry, such as fungal mating-type chromosomes. We explicitly state and model a simple and testable hypothesis explaining the stepwise extensions of recombination suppression on sex chromosomes, mating-type chromosomes and supergenes in general.

Abstract ID: 2422

Epigenetic conflict on a degenerating Y chromosome increases mutational burden in Drosophila males

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Large portions of eukaryotic genomes consist of transposable elements (TEs) replicating at the expense of host fitness. During early embryonic development, the establishment of transcription-repressing heterochromatin at the maternal-zygotic transition safeguards the genome from deleterious TE mobilization. However, prior to full heterochromatin establishment, TEs may exploit the ramp-up of zygotic expression for proliferation; repeat-rich Y chromosomes can further act as reservoirs for TEs taking advantage of this window of compromised defense. Here, we contrast the dynamics of early TE activation

in two Drosophila species, D.psueoobscura and D.miranda, with Y chromosomes of disparate sizes and ages. In both species, zygotic TE expression is elevated in male embryos relative to females, mostly due to Y-linked TEs. Interestingly, male-biased TE expression diminishes across development in D.pseudoobscura, but remains elevated in D.miranda, the species with the younger and larger Y. Using ChIP-seq against the heterochromatin mark H3K9me3 in sexed embryos, we find that heterochromatin formation is compromised on the D.miranda Y. This is because the younger Y still contains thousands of actively transcribed genes with open chromatin interspersed among high density of repeats. The close proximity of genes and repeats create an epigenetic conflict between activating and suppresive chromatin environments that TEs exploit. We further find that, surprisingly, elevated TE expression in males causes de novo insertions. These results reveal that the 'toxic' Y chromosome creates a mutational burden in males especially when genome defense is compromised, and suggest a previously unappreciated conflict on evolving Y chromosomes between genic transcription and TE suppression.

Abstract ID: 982

Y recombination arrest and degeneration in the absence of sexual dimorphism

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Current theory proposes degenerated sex chromosomes, such as the mammalian Y, evolve via three steps: recombination arrest, linking male-beneficial alleles to the Y chromosome; Y degeneration due to the inefficacy of selection in the absence of recombination; and dosage compensation correcting the resulting low expression of X-linked genes in males. Here we investigate a model of sex chromosome evolution incorporating the coevolution of cis- and trans-regulators of gene expression. We show that the early emergence of dosage compensation favors the maintenance of Y-linked inversions by creating sex-antagonistic regulatory effects. This is followed by degeneration of these non-recombining inversions caused by regulatory divergence between the X and Y chromosomes. In contrast to current theory, the whole process occurs without any selective pressure related to sexual dimorphism.

Abstract ID: 2275

Evolution of sex chromosomes in Leucadendron, the world's most sexually dimorphic flowering plants

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The question of how suppressed recombination evolves is a major gap in our knowledge about sex chromosomes and other supergenes. The diverse hypotheses regarding the

drivers of recombination suppression include sexually antagonistic selection, ancestral lack of recombination, as well as neutral evolution. Here, we present empirical results from comparative analyses of ancestrally shared but recently diverged sex chromosomes in an evolutionary radiation. The iconic South African plant genus Leucadendron is fully dioecious and includes some of the most sexually dimorphic of all flowering plants. Our chromosome-scale genome assembly of L. rubrum provided fully contiguous X and Y haplotypes (Nanopore long-reads and Hi-C), which reveal the mutational steps taken during their formation in unprecedented detail. Furthermore, we re-sequenced males and females of 25 Leucadendron species (short-reads), and delimited non-recombining sex-linked genomic regions in each species separately. This allows us to test the effects of genomic proximity, DNA sequence content, and species biology (extent of sexual dimorphism) on loss or (re-)gain of recombination.

Abstract ID: 1548

Y chromosome facilitates sexual size dimorphism in the seed beetle

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The male-limited Y chromosome should be important for mitigating sexual conflict by accumulating sexually antagonistic alleles that benefit males, but empirical support is limited. In the seed beetle *Callosobruchus maculatus* body size is sexually dimorphic and subject to sexually antagonistic selection. Here we present evidence that variation in sexual size dimorphism is linked to the heteromorphic Y chromosome. We confirmed the connection to Y by introgressing different Y chromosomes into a common genetic background, which identified two distinct Y haplotypes showing a major effect on male body size. We then sequenced and assembled the previously uncharacterized *C. maculatus* sex chromosomes and identified molecular differences between the two predicted Y haplotypes. The Y chromosome of *C. maculatus* shows typical hallmarks of degeneration: it is repeat-rich and approx. 80% smaller than the X. Nevertheless, the Y harbors over 400 genes and is enriched with metabolic and gene regulatory functions. Crucially, we find that besides an autosomal copy of the gene *Target of rapamycin* (TOR), males carry an additional *TOR* copy on the Y chromosome. *TOR* is known to regulate body size across organisms. A Y-linked copy of *TOR* thus provides a male specific opportunity to alter growth. Interestingly, the two identified Y haplotypes show copy number variation for *TOR*, where the Y haplotype that causes increased sexual dimorphism by lowering male growth rate, has two additional *TOR* copies. In line with the predictions, our findings provide both phenotypic and molecular empirical support for the accumulation of sexually antagonistic genes on the Y.

Abstract ID: 1074

Experimental evolution of a de novo sex chromosome system

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The evolution of gonochorism from hermaphroditism via the establishment of sex chromosomes is currently mainly studied using theoretical and comparative approaches. In order to attempt to study the evolution of a de novo sex chromosome system in real time, we developed an experimental evolution approach in the simultaneously hermaphroditic flatworm *Macrostomum lignano*. For this, we used a green fluorescent protein (GFP) marker as a dominant sterility mutation, which is inherited in a Mendelian fashion. In the male-limited selection lines, the GFP locus is only inherited through sperm (resembling the early stages in XY chromosome evolution), while in the female-limited selection lines the GFP locus is only inherited through eggs (resembling the early stages in ZW chromosome evolution). After tens of generations, we investigated how these lines have responded in terms of allele frequencies, gene expression, and mating behaviour. We found evidence of changes consistent with sexual specialization in the selection lines on all levels, with the male-limited selection lines showing most evidence of a response in mating behaviour, while the female-limited selection lines showed most evidence of a response in gene expression. Interestingly, we also found changes in structural variant frequency consistent with increased purifying selection in the male-selected lines but increased recombination rate in the female-selected lines. Overall, we can conclude that our worms have indeed responded to the sex-limited selection in a way that is generally consistent with our expectations from other young sex chromosome systems.

Abstract ID: 2225

Diverse sex chromosomes in Caribbean leaf-litter geckos (*Sphaerodactylus*)

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Geckos have diverse sex-determining mechanisms with repeated transitions among them over their long evolutionary history. However, detailed information about sex chromosomes is lacking for most gecko species, leaving large gaps in our understanding of the distribution of sex chromosomes in the group. To begin to address this, we assembled a chromosome-level genome for the gecko *Sphaerodactylus townsendi* and used this assembly to search for sex chromosomes among six closely related *Sphaerodactylus* species using several kinds of genomic data, including whole-genome re-sequencing, RADseq, and RNAseq. Two species of *Sphaerodactylus* geckos were previously shown to have XX/XY sex chromosomes but lacked information on sex chromosome synteny. Using this expanded dataset, we identified sex chromosomes in five of the six sampled species with between two and four sex chromosome cis-transitions (XX/XY to a new XX/XY) among them. Interestingly, we confirmed two different linkage groups as sex chromosome systems that were previously unknown to act as sex chromosomes in tetrapods (syntenic with chicken chromosome 3 and chicken chromosomes 18/30/33), highlighting a trend that many, if not most, amniote chromosome have the potential to act as sex chromosomes.

Abstract ID: 1662

Comparative genomics and gene editing evidence rapid evolution of sex determination in frogs

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The African clawed frog *Xenopus laevis* has a female-specific gene called *dmw* that drives feminization of the developing gonad by competing with a male-related partner called *dmrt1*. Scrutiny of *dmw* in an evolutionary context reveals dynamic functional evolution of this gene and its associated sex-determination pathway, including independent instances of empowerment, sidelining, and loss in different lineages. Gene editing of the small female-specific supergene of *X. laevis* points to recruitment of female-specific loci that are neither sufficient nor necessary for fertility. Gene editing and comparative genomic analyses of *dmrt1* evidences subfunctionalization and biased gene silencing of this duplicated, sex-related, but non-sex-linked locus. These findings illustrate how crucial components of sex determination pathways evolve rapidly, raising the question of whether rapid sex-related evolution is typical of many amphibians, catalyzed by the pervasive genome duplication in *Xenopus*, or both.

Abstract ID: 2053

The chromosome-scale genome of the European green toad reveals a sex-determination candidate region.

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Vertebrate sex determination repeatedly evolved environmentally or simple/complex genetically-triggered systems. Contrasting to mostly differentiated sex chromosomes of mammals, birds and some reptiles, other reptiles and most fish and amphibians retain

undifferentiated sex chromosomes. Palearctic green toads form a radiation with >15 (therein 3 allotriploid, 2 allotetraploid) taxa of Pleistocene origin. Undifferentiated sex chromosomes of diploids were shown by microsatellite and gene transmission, with linkage-group (LG)1 governing a male-heterogametic XY-system, in which male X/Y-recombination is drastically reduced but occasionally occurs on evolutionary timescales. To gain further insights, we first applied ddRADseq, confirming LG1 but failing identification of a sex-diagnostic region. To scrutinize undifferentiated sex chromosome evolution, in 2020/21 we *de novo* assembled a female 3.8 Gbp *Bufo*(*tes*) *viridis* reference genome. ONT-long-reads, paired-end short-read-correction and Arima-HiC-data yielded a chromosome-scale genome with 94% reads assigned to the 11 haploid chromosomes (final scaffold/chr.N50: 470 Mbp). Annotation involved published green toad, *Bufo* sp., and other anuran transcriptomes, modelling 21.605 protein-coding genes. Pool-sequencing of phenotypically-sexed male and female green toads from multiple European populations and mapping to the reference assembly allowed the identification of a ca. 70 kb X/Y diagnostic region adjacent to two candidate genes, including increased X/Y-heterozygosity and INDELs, enabling designing PCR-markers. This region is sex-diagnostic at least in multiple diploid species of the maternal ancestry of the polyploids. Long-PCRs and XY-phylogenies of multiple diploid species are underway. We are exploring the evolution of this system in the hybrid polyploids and try gaining mechanistic insights.

Abstract ID: 1061

A novel sex determination gene on a polymorphic XY sex chromosome system in fourspine stickleback

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Different sex determination systems, sex chromosomes, and sex determination genes have independently evolved in many species. Multiple turnovers and an independent evolutionary history of sex chromosomes have been characterized in stickleback (Gasterosteidae) species, making them an excellent system to study sex chromosome turnover and differentiation. Previous studies in fourspine stickleback (*Apeltes quadracus*) have suggested that there is variation among populations in the presence of heteromorphic sex chromosomes. Here, we collected samples from three populations of fourspine stickleback and used whole-genome DNA and RNA sequencing data to identify chromosome 23 as an XY sex chromosome system in all three populations. Unlike in the threespine stickleback (and other *Gasterosteus* species), which possess a highly degenerate Y chromosome, fourspine stickleback possess a pair of young and homomorphic chromosomes without extensive degeneration. The extent of differentiation between sexes varies among populations on the sex chromosome, which is likely due to a polymorphic inversion on the X chromosome. There is also region of divergence shared among all populations that contains a novel candidate sex-determination gene (ZAR1). We are currently using CRISPR knock-out and base-editing experiments to test the role of ZAR1 in sex determination. Our results thus identify a novel candidate sex determination gene in fish, as well as a polymorphic sex chromosome system that provides an opportunity for further investigation of the role of inversions in sex chromosome evolution.

Abstract ID: 1618

Turnover of sex chromosomes and male pregnancy related genes in seahorse species

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Unlike birds and mammals, many teleosts have homomorphic sex chromosomes that comprise a great paradigm for understanding the transition between different sex chromosome systems. Here we report the independently originated homomorphic XY chromosomes and putative sex-differentiation genes of the big-belly seahorse and lined seahorse, the ancestor of which evolved a brood pouch for unique male pregnancy. Most chromosomes of both species exhibit a much higher GC content at one chromosome end than other regions of the same chromosome, suggesting highly localized crossovers in male meiosis, though the average recombination rate is probably lower in males than in females. Part of the big-belly seahorse chromosome 6, and almost the entire lined seahorse chromosome 4 have become sex-linked, with however no signs of chromosome inversions that completely stop recombination. Instead, we find evidence of occasional recombination possibly mediated by sex reversals, which has likely prevented extensive genetic divergence of sex chromosomes of both species. In addition to the ancestral recombination landscape, evolution of seahorse sex chromosomes may have influenced or been influenced by their gene content. While chromosome 4 is enriched for testis genes in both species and is also a sex chromosome in numerous other teleosts; chromosome 6 became a sex chromosome recently and has subsequently acquired male pouch biased transcription in many genes. This may reflect adaptive changes in transcription of Y-linked and pouch-related genes, suggesting a role of male-specific selection.

Abstract ID: 2147

Disentangling the complex evolution of sex determination in snakes

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Despite that homologous ZZ/ZW sex determination was speculated for decades for all snakes, cytogenetic and genomic studies revealed variable sex determination systems in this group. A stable ZZ/ZW sex chromosomes are well documented for all caenophidian snakes, the group encompassing above 80% of all snake species. Recent studies revealed two distinct XX/XY systems in two species of boas (*Boa imperator, B. constrictor*) and a python (*Python bivittatus*). In addition, ZZ/ZW sex chromosomes were reported in the Madagascar boa *Acrantophis* sp. cf. *dumerilii* and in the blindsnake *Myriopholis macrorhyncha*, but the sex chromosome gene content and homology to other snake sex chromosomes remained unknown. We combined advanced molecular cytogenetic methods (*in situ* hybridization with probes for rDNA loci

and telomeric motifs), comparative genome coverage of Illumina DNAseq reads and a qPCR-based test of sex chromosome homology to uncover sex chromosomes in more lineages of non-caenophidian snakes. We detected lineage-specific XX/XY sex chromosomes in the family Tropidophidae, and ZZ/ZW sex chromosomes in the families Sanziiniidae and Calabariidae. The sex chromosomes of the families Sanziiniidae and Calabariidae share a gene content with the sex chromosomes of *Python bivittatus* and the caenophidian snakes, pointing to their putative homology. The emerging pattern suggests that snakes have ancestrally poorly differentiated sex chromosomes, which were quite prone to turnovers, while derived highly differentiated sex chromosomes became evolutionary very stable across a large diversity of caenophidian snakes.

Abstract ID: 1415

Devil is in the details: Meiotic sex chromosome dynamics in the Marsupial germ line

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During meiotic prophase I, homologous chromosomes pair, synapse and recombine in a tightly regulated process, which ensures the generation of genetically variable haploid gametes. The presence of partially or completely unsynapsed regions induces a transcriptional silencing checkpoint, including the meiotic sex chromosome inactivation (MSCI), to avoid the premature expression of genes that would induce meiotic arrest at pachytene. In marsupials, sex chromosomes lack a pseudo-autosomal region, so the association via a marsupial specific structure called the dense plate (DP) ensures faithful segregation of sex chromosomes in the absence of synapsis and recombination. Due to their key basal position in the mammalian evolutionary tree, marsupials offer a unique opportunity to explore previously uncharacterized meiotic features, from sex chromosome pairing strategies to X chromosome transcription dynamics. Here, we combine cytological analysis and single-cell RNA sequencing to study the sex chromosome dynamics during meiotic progression in the Australian marsupial tammar wallaby. Our results show that sex chromosomes pair forming the so-called dense plate following different sex chromosome pairing strategies in marsupial species, which correlates with differential sex chromosomes architecture and transcriptional patterns. Remarkably, we detected that the tammar X chromosome is partially transcribed during meiosis and escapes MSCI for much of pachytene, which has important implications for sex chromosome evolution.

Abstract ID: 1843

The role of toxic W chromosomes in Haldane's rule

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A common characteristic observed in the phenomenon of hybridisation is its asymmetric nature as described by the Haldane's rule: upon hybridisation, if one sex is sterile or unviable, the sex is the heterogametic one (female in ZW system; male in XY system). While the Haldane's rule is widely observed in nature, no single shared molecular mechanism has been found, rather a plethora of mechanisms with different prevalence and relevance throughout the organisms taken into consideration. This suggests that likely many factors concur to the same outcome.
Here, thanks to an avian study system, I investigated the possible role of the sex-limited chromosome (W) and its load of active transposable elements during hybridisation failure. To this aim, I used genomic and transcriptomic data of chicken, Japanese quail, and their hybrid embryos (that follow the Haldane's rule). I identified differences in transposable element activity between female and male hybrid embryos as well as differences between the embryos and their parental species at several embryonic stages.

Abstract ID: 985

Distribution, genomic structure and evolution of housefly male-determining loci

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The housefly (*Musca domestica*) has a polymorphic sex determination system in which dominant male-determining (*M*) loci can be either located on the Y chromosome, any of the five autosomes, and even the X-chromosome. Both geographically distant and nearby housefly populations can differ strongly in the chromosomal localisation and frequency of *M* loci. The various *M*-loci are partly homologous and contain the *Musca domestica male determiner* (*Mdmd*) gene, except for *M* on autosome I, but differ largely in size. The *M*-locus on autosome III is large (circa 591 kb) and contains one complete and 87 incomplete duplicates of *Mdmd* as well as truncated copies of a other genes, embedded in various repetitive sequences. Comparative sequence analysis indicate that the various *M* loci evolved by *cis*-duplication and interchromosomal translocation in line with the birth-decay-rebirth model of sex chromosome evolution. Our findings contribute to a better understanding of the evolution of sex determining loci and sex chromosomes.

Abstract ID: 1751

Assembly and characterization of W chromosome in monarch butterfly (*Danaus plexippus*)

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Here we report a novel genome assembly for the monarch butterfly (*Danaus plexippus*), focusing on the W chromosome. This species harbors a neo-Z chromosome, arising from the fusion of the ancestral Z with an autosome. Previous cytogenetic analyses indicated a similarly large and bipartite W chromosome, suggesting the possibility of a comparable neo-W, but much ambiguity remains concerning the sequence and history of monarch W. We generated PacBio HiFi reads with Hi-C data from females to support *de novo* assemblies of maternal and paternal haplotypes using Trio binning. Putative W contigs from the maternal genome were determined based on male to female coverage and sex specific kmers. The paternal assembly and W contigs were scaffolded using Hi-C data. This produced chromosomal level scaffolds for the Z and all autosomes, including three autosomes assembled from telomere to telomere. The W chromosome scaffold length was around 10Mbp, thus leaving about one third of this chromosome in unscaffolded contigs. While primarily composed of transposable elements (TEs), the W contains at least three protein coding genes that arose either through retroposition or ectopic recombination from other chromosomes. None of these W-linked copies appear pseudogenized and one appears to be evolving adaptively. The prevalent repetitive content of the W chromosome are elements from the LINE and LTR retrotransposon groups. Surprisingly, the TEs on W chromosome have lower divergence compared to rest of the genome, suggesting their ongoing accumulation. Finally, despite this novel W assembly, strong evidence for or against a neo-W chromosome origin remains elusive.

Abstract ID: 1192

Switching it up: algal insights into the genomic basis of transitions in sex determining systems

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Co-sexuality has evolved repeatedly from ancestors with separate sexes across a wide range of taxa. The switch to co-sexuality is expected to involve major molecular readjustments at the level of gene expression patterns, as modified males or females will express the opposite sexual function for which their phenotypes have been optimized. However, the molecular changes underpinning this important transition remain unknown, particularly in organisms with haploid sexual systems such as bryophytes, red and brown algae. I will present recent work in our lab focusing on apprehending the molecular and evolutionary processes involved in the transition from separate sexes to co-sexuality. We explored four pairs of closely related brown algal species representing four independent events of transition from sex chromosome-based sex determination to hermaphroditism. I will present how we are uncovering the fate of sex chromosomes whilst in a hermaphrodite context, and the nature, evolution and degree of convergence of the gene expression changes that accompany the breakdown of dioicy. More broadly, our results help to better understand the evolutionary trajectory of UV sex chromosomes, the molecular paths and genomic consequences of switches in sexual systems, and advance models on how UV sex chromosome evolve.

Symposium: S03. Diversity and evolution in sperm, ova, and other primary reproductive traits (id: 937)

Abstract ID: 1970

The scope for sexual selection during pollen-pistil interactions

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Sexual selection is generally thought to emerge in situations where males produce more numerous gametes than females, rendering ovules as a 'rare resource' for which males compete for. Sexual selection theory should thus be universally valid for all sexually reproducing anisogamous organisms, thus encompassing plants. Yet, most research on sexual selection in plants has remained disconnected from theoretical and empirical studies developed by animal biologists. Notably, research in plants provides scarce insight as to the evolutionary consequences of variation in the number of mates – the central parameter in sexual selection thinking. This presentation will review how knowledge accumulated by molecular biologists on pollen-pistil interactions offer several candidate macroscopic and molecular traits for the action of sexual selection. It will further highlight how classical models of the sexual selection theory, including those that explain the evolution of female choice through 'Fisherian runaway' or 'good-genes' processes, ultimately consists of generic processes that could apply to pollen-pistil interactions. The most central predictions of sexual selection theory have accordingly been tested by varying the strength of sexual selection through experimental evolution in both the hermaphroditic plant *Brassica rapa* and dioecious populations of *Mercurialis annua*. Both pollen competitive traits and/or candidate pistil traits for female choice processes have evolved rapidly in response to elevated levels of polygamy in both experimental evolution studies. Taken together, these results point to the postpollination phase of plant mating as a potentially important step for the action of sexual selection.

Abstract ID: 1421

Bateman gradients from first principles

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In 1948, Angus Bateman presented experiments and concepts that remain influential and debated in sexual selection. The Bateman gradient relates reproductive success to mate number, and this relationship was presented as the cause of intra-masculine selection. A deeper causal level was subsequently asserted: that the ultimate cause of sex differences in Bateman gradients is the sex difference in gamete numbers (e.g. fewer eggs than sperm), an argument that remains controversial and without mathematical backup. I will present models showing how asymmetry in gamete numbers alone can generate steeper Bateman gradients in males. This conclusion remains when the further asymmetry of internal fertilisation is added to the model and fertilisation is efficient. Strong gamete limitation can push Bateman gradients towards equality under external fertilisation and reverse them under internal fertilisation. Thus I provide a mathematical

formalisation of Bateman's brief verbal claim, while demonstrating that the link between gamete number and Bateman gradients is not inevitable nor trivial.

Abstract ID: 1445

Hermaphroditic origins of anisogamy

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Anisogamy – the size dimorphism of gametes – is the defining differences between the sexes. In animals, it is often presumed that anisogamy arose in sessile broadcast spawners, and that the earliest anisogamous animals had separate sexes. There is little empirical or theoretical evidence to support this picture. I briefly consider the phylogenetic contexts in which anisogamy has evolved and what we can say for certain about the first anisogamous animals. I then present a model of the origins of anisogamy that allows for both separate sexes and hermaphroditism to evolve directly. Which of these outcomes emerges depends crucially on the population structure during fertilisation. Lastly, I consider how the sex allocation of newly anisogamous hermaphrodites differs from their isogamous ancestors.

Abstract ID: 2074

The effect of male age on sperm traits in a sexually promiscuous passerine

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In many animal species, organismal performance declines with age in a process known as ageing or senescence. Ageing typically leads to a deterioration of physiological functionality and can impact the development of primary sexual phenotypes. Sperm production is a complex and costly process that is sensitive to changes in individual physiological state, yet remarkably little is known about age-related changes in sperm morphology and sperm performance. Here we use a non-linear GAMMs modelling to evaluate age-related changes in sperm morphology, sperm velocity and ejaculate size (estimated as cloacal protuberance sizes) in the European barn swallow (*Hirundo rustica rustica*), a relatively short lived sexually promiscuous passerine species. The data, based on 686 observations of 495 individual males followed over their lifetime, revealed a clear asynchrony in age-related changes among sperm morphology and sperm production traits, with sperm head and midpiece sizes showing a clear (non-linear or linear, respectively) reduction with age within males, sperm velocity showing a steady increase with male age, and ejaculate sizes showing no age-related pattern. Subsequent analysis indicated a breakpoint (no trend followed by a sharp shortening) for sperm head size to be at two years of age. We discuss the potential reproductive implications of age-related

changes in sperm phenotypes in this passerine species where male extra-pair fertilization success has been shown to increase with age.

Abstract ID: 1037

Evolution of novel female reproductive strategy in protein-restricted populations of *D. melanogaster*

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Availability of adequate nutrition is essential for reproduction. However, organisms frequently experience fluctuation in diet quality and/or quantity which has a profound impact on their reproductive traits. In several insects, including *Drosophila*, reproductive output is reliant on protein availability. While short-term protein restriction is known to be consequential to fitness, little is known about how reproductive traits evolve under prolonged protein deficiency. Long-term protein restriction, in fact, is expected to select for traits that maximize reproductive output despite such nutritional challenges. To test this theory, we subjected four replicate populations of *Drosophila melanogaster* to complete deprivation of live-yeast supplement, thereby mimicking protein-restricted ecology. Following >24 generations of experimental evolution, compared to their controls, females from experimentally evolved populations had an increased early-life reproductive output, both in the presence and absence of live-yeast. Investigation of juvenile traits suggested the observed increase in fitness to be independent of changes in the juvenile fitness traits. Further, we found no evidence of changes in lifespan, starvation resistance, and lifelong cumulative reproductive output in females. However, the reproductive output of the females in evolved lines declined faster with advancing age, indicating faster reproductive senescence. Thus, females adapted to protein restriction evolved a novel reproductive strategy wherein they attained higher early-life reproductive output followed by faster reproductive senescence. Such reproductive adaptation was found to be associated with physiological and behavioural modifications, including increased protein and lipid storage in the body, higher larval resource uptake and modifications in ovarian structure and function.

Abstract ID: 1166

Evolution of age dependent female care of male gametes

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Ageing is a biological process with profound consequences. The frequency of deleterious germline mutations increases with age, which reduces offspring quality and has implications for life-history evolution and sexual selection processes, such as optimal mate choice. Males typically transfer more de novo mutations to their offspring than females and show a faster age-related increase in mutation rate. Females have

developed DNA repair and maintenance mechanisms to counteract DNA damage in the oocyte and early zygote. There is evidence that the efficiency of these repair mechanisms is age-dependent, but how they coevolve with changes in life history traits, such as longevity and the age at first reproduction, remains unexplored. Here we used long-term experimental evolution lines of a seed beetle that have evolved under regimes manipulating the timing of reproduction since 1989 (>300 generations). We challenged females to repair ejaculates with artificially elevated levels of DNA damage, quantifying female repair efficiency through an assessment of offspring quality in the two subsequent generations. We find pronounced evolved differences in female repair and maintenance between the selection regimes, suggesting an optimization of repair mechanisms at the time of peak reproduction. Our study provides the first compelling experimental evidence for the coevolution of the timing of reproduction and female care of male gametes. Furthermore, our results imply that these mechanisms can evolve relatively rapidly but their evolution is constrained early in life.

Abstract ID: 1110

Synergistic impacts of hot exposure events on male and female fertility in a model insect

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Extreme weather events are becoming more frequent and severe due to anthropogenic climate change. These extreme weather events include hot exposure events (HEE) during heatwaves whereby very high temperatures may be experienced for a few hours, posing a potential threat to biodiversity. Little is understood about how these HEEs may impact reproductive function. In a model insect system, *Tribolium castaneum*, we are investigating how HEEs at the edge of a species' survival limits may cause sub-lethal reproductive damage through multiple avenues; male-driven fertility losses, female-driven fertility losses as well as potentially synergistic impacts when both experience HEEs. We exposed sexually mature unmated males or unmated females to either 30°C control conditions or experimental HEEs of temperatures that have occurred globally ranging from 42–50°C in 2°C intervals for 2, 5 or 10 hours. We then mated them to a standard-reared conspecific and assessed the impacts of HEEs over 20-day reproductive output (representing ~50% of lifetime reproductive output). To further understand the impacts of HEEs on reproductive fitness, we investigated potential synergistic impacts. We subjected females in receipt of an ejaculate (stored sperm) to a range of HEEs to study the vulnerabilities of stored sperm within females. Furthermore, we looked at the impact on reproductive output when both females and males experienced a HEE before being mated under standard conditions. These findings will help us better understand the extent to which HEEs may impact sex-specific reproductive function and impact biodiversity under climate change.

Abstract ID: 2166

Uncovering new roles for auxin in the evolution of seed plants

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The seed is a complex plant organ composed of tissues of different ploidy and parental contributions. The embryo represents the next generation, which in angiosperms is nourished by the endosperm. Both of these tissues are the product of fertilization. In contrast, the gymnosperm embryo is nourished by the haploid megagametophyte, which develops independently of fertilization. The evolutionary advent of angiosperms coincides with the sexualization of the embryo-nourishing structure and the appearance of the endosperm. The role of auxin as a critical factor for seed viability and endosperm development has been described in *Arabidopsis thaliana*: Ectopic auxin application leads to fertilization-independent endosperm development; and auxin biosynthesis genes are paternally imprinted in the endosperm, i.e. the maternal alleles are silenced by epigenetic mechanisms and thus auxin biosynthesis only takes place after fertilization. This leads us to hypothesize that sexualization of auxin biosynthesis is the factor that coincides with the evolution of the endosperm and thus angiosperm diversification. We revised and histologically described different seed conformations and its compartments in selected taxa with a basal placement on the angiosperm phylogeny. We will report the expression of auxin related-genes and detail patterns of differential expression, as determined by transcriptomic analyses of laser-captured seed compartments. We will quantitatively show that ectopic auxin application triggers fertilization-independent seed development in basal angiosperms. Overall, our results show that auxin's role in modulating seed development is an evolutionarily conserved trait of the angiosperm seed.

Abstract ID: 2213

Evolution of gonads, gametes and genital tracts

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Primary sexual traits, from gametes to reproductive tracts, are extraordinarily diverse across the animal kingdom, especially in species with internal fertilization where male and female reproductive traits are most likely to co-evolve. Much of this diversity is usually attributed to postmating sexual selection, but different forms of selection can operate simultaneously. I will consider experimental and comparative evidence to discuss the putative roles of different modes of selection in driving the evolution and co-evolution of primary sexual traits.

Abstract ID: 1067

Runaway selection in plants: myth or reality?

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Runaway selection predicts the coevolution between female preference and male traits. While long studied in animals, this process is underexplored in plants and is likely impacted by the diversity of mating strategies, including selfing, outcrossing, hermaphroditism etc. found in angiosperms. We thus tested whether male traits (pollen performance) and female choice (style length) evolve following this evolutionary scenario. Our mathematical predictions suggest that "good gene" selection may be a major driver of the coevolution between pollen performance and female choice. In addition, their coevolution depends on the intensity of male-male competition for mating and also on the mating system. Male trait and female choice indeed (co)evolve much more slowly in a selfing scenario compared to an outcrossing one. These mathematical predictions echo our experimental evidence in several Arabidopsis species showing that pollen performance is more exacerbated in outcrossing lineages compared to selfing ones, and this is accompanied by transcriptomic changes. These results therefore suggest that male-female coevolution may significantly drive the evolution of plant reproductive traits.

Abstract ID: 1780

From ejaculates to behaviour: how pre and post-copulatory sexual selection shape reproductive traits

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The evolution of reproductive traits depends on pre- and post-copulatory selective pressures and on underlying trait correlations. To improve our understanding of correlated evolution and/or constraints on adaptation (genetic trade-offs) we measured the evolutionary responses of key reproductive traits to experimentally manipulated pre- and post-copulatory selective pressures in the field cricket *Gryllus bimaculatus.* After 6 generations of experimental evolution, with animals evolving under i) intense pre-copulatory selection, through monogamous matings following male fights, courtship and female choice, ii) intense post-copulatory selection, through sequential polyandrous matings allowing for sperm competition and cryptic female choice, and iii) relaxed selection through enforced monogamy, we measured a number of key pre- and post-copulatory traits. These traits include behaviours (male song, aggressiveness, attractiveness), morphology (mandible and testes size), and ejaculate quality (sperm viability). We'll report findings on trait covariances and whether trait divergence has occurred within this evolutionary timeframe, providing insights into the evolutionary processes underlying complex reproductive phenotypes.

Abstract ID: 2360

The genetics of variation in sperm and female sperm storage organ morphology in Drosophila

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Sperm, the most rapidly evolving cell type, exhibits dramatic variation both within and across species. Several within-species and comparative studies have revealed that sperm length is a postcopulatory ornament that evolves due to cryptic female choice exercised in the form of female seminal receptacle (SR) length. Further, covariation of sperm and SRs have been suggested to function as an "engine of speciation" in *Drosophila*. However, there's a near-total lack of knowledge of genes underlying variation in sperm and female sperm-storage organ morphology. Resolving this genotype-phenotype relationship and identifying potential targets for post-copulatory sexual selection remains a fundamental challenge in understanding the evolution of reproductive systems that could ultimately result in reproductive isolation. Here, we have attempted to identify the genes and/or gene networks contributing to sperm and SR length variation in *Drosophila melanogaster* by performing genome-wide association (GWA) mapping analyses in 126 highly inbred populations from the Drosophila Genetic Reference Panel. First, we quantified mean sperm and SR lengths of each line under near-identical experimental conditions and showed the presence of significant genetic variation. Next, we tested if there's a genetic correlation between sperm and SR lengths. Finally, we performed independent GWA analyses to identify genomic variation and candidate genes contributing to the observed phenotypic variation in sperm and SR length. Functional validation of these genes will provide valuable insights into the genetic variation in sperm and SR morphology which could be fundamental to our understanding of reproductive biology.

Abstract ID: 1100

Exploring winner-loser effects on plastic male reproductive investment and telomere dynamics

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Fight outcomes can have dramatic consequences for contestants. When contestants are evenly matched, winners will often go on to win again, while losers will tend to lose. These so-called 'winner-loser effects' can influence male fitness by determining their future access to mates. If male mating success can depend on the outcome of a single contest, do males that consistently experience only winning or only losing change how they allocate resources towards pre-and post-copulatory sexually selected traits? And, if so, do these responses then influence male telomere length and, by extension, lifespan? First, we experimentally manipulated the duration of the winning/losing experiences of pairs of size-matched male *Gambusia holbrooki* (for 1 day, 1 week or 3 weeks). We then tested if winning versus losing affected male investment into mating effort (pre-copulatory traits) versus ejaculates (post-copulatory traits), and if this varied with the duration of the contest experience. In a second 2x2 factor experiment we then tested if winning/losing combined with either high or low reproductive investment (access to females), influenced the relative telomere lengths of males. We discuss the general importance of controlling for inherent male condition when comparing male investment into condition-dependent traits.

Abstract ID: 1274

The regulatory architecture and evolution of male avian reproductive traits

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Male reproductive traits evolve rapidly and exhibit substantial variability both within and across species. Changes in gene expression are predicted to play a key role in this morphological divergence, however, our understanding of how sexual selection acts on the transcriptome is limited. Here, we examine how variation in expression drives the evolution of testes and sperm traits across birds. First, we test the regulatory architecture of a sex-linked supergene responsible for differences in sperm shape and speed within zebra finches. By comparing gene expression between different haplotypes, we show that the supergene is enriched for allele-specific expression in the testes, likely as a product of divergent selection for sperm traits but also relaxed purifying selection arising from reduced recombination (Price et al. in prep). Second, extending across species, the accelerated rate of expression change observed in the avian testes is widely assumed to be a product of sperm competition and sexual selection. However, we show that comparative approaches used to study expression evolution are subject to biases that can lead to false signatures of selection (Price et al. in press *Nature Ecol Evol*), necessitating a critical reappraisal of the link between sexual selection, gene expression, and male reproductive traits. Together, our results elucidate the role of expression variation in complex phenotypes and how selection acts on the male transcriptome.

Abstract ID: 1850

Female remating frequencies influence male reproductive trait evolution in dung flies

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Divergence between populations of widespread species occupying separate continents are often due to differences in climate and habitat. Genetic differentiation may further result from sexual selection on mate preferences and courtship signals or even antagonistic sexual interactions, which can contribute to incipient speciation within continents, even with modest gene flow. *Sepsis punctum* is a dung fly with widespread distribution across Europe (EU) and North America (NA) and displays exceptional variation in sexual selection. Specifically, females in EU mate more frequently than females from NA populations. This significant variation in polyandry is accompanied by diversification in several traits that are well-established targets of sexual selection notably sexual size dimorphism, male testes size, sperm length and even with respect to accessory gland gene expression. Here, we use Riptide^{TM}, an ultra-rapid high throughput rapid library prep technology that has been recently developed by iGenomX. Riptide^{TM} provides fast, cost-effective, and efficient sampling of whole genomes even with low quantities of DNA from minute samples. We generated nearly 400,000 SNPs and employed a population genomic approach to test predictions about the evolution of polyandry and its influence on male reproductive trait diversification across four EU and five NA populations of *S. punctum*. We report strong isolation-by-distance within the continents, accompanied by variation in female remating frequencies as well as male reproductive traits. We suggest that when studied in a geographical framework, both

morphometric analyses and molecular information such as haplotype networks and SNP data can have great explanatory power in reconstructing mechanisms underlying diversification.

Abstract ID: 1424

High fraction of sperm in a globular springtail estimated from whole genome sequencing data

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The low cost of sperm led to great variation in sperm production among species, with some of them carrying more sperm cells than actual body cells. We have discovered a globular springtail *Allacma fusca* should be listed among these high sperm-generating species. In our study we found that the cellular proportion of the sperm in the body in *A. fusca* can range from 27.5% to 35.3%. The estimates are based on a whole-genome sequencing approach that exploits karyotype variation between soma and sperm of this species. This two-tissue model is general and can be used to estimate relative proportions of any two tissues with different karyotypes. This approach can be automatically deployed to scan for karyotypic heterogeneity in whole-genome sequencing data and therefore to help to discover more reproductive peculiarities across the tree of life.

Abstract ID: 1978

Role of premeiotic endoreplication in obligate parthenogenesis in geckos

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Obligate parthenogenesis evolved in reptiles convergently several times, mainly through interspecific hybridization. The obligate parthenogenetic complexes typically include both diploid and triploid lineages. Offspring of parthenogenetic hybrids are genetic copies of their mother; however, the cellular mechanism enabling the production of unreduced cells is largely unknown. Here, we show that oocytes go through meiosis in three widespread, or even strongly invasive, obligate parthenogenetic complexes of geckos, namely in diploid and triploid *Lepidodactylus lugubris*, and triploid *Hemiphyllodactylus typus* and *Heteronotia binoei*. In all four lineages, the majority of oocytes enter the pachytene at the original ploidy level, but their chromosomes cannot pair properly and instead form univalents, bivalents and multivalents. Unreduced eggs with clonally inherited genomes are formed from germ cells that had undergone premeiotic endoreplication, in which appropriate segregation is ensured by the formation of bivalents made from copies of identical chromosomes. We conclude that the induction of premeiotic endoreplication in reptiles was independently co-opted at least four times as an essential component of parthenogenetic reproduction and that this mechanism enables the emergence of fertile polyploid lineages within parthenogenetic complexes.

Abstract ID: 1314

Maternal investment as an adaptive trait in response to harsh environments in the Brassicaceae

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Plants colonized a wide range of habitats including challenging environments such as deserts or high mountains. The adaptation to these harsh environments is mediated by many traits, including the allocation of resources to sexual reproduction. As maternal resources are limited, especially in such harsh environments, reproductive investment strategies are likely under selection. Under harsh conditions, maternal plants may be selected to produce a large brood with low resource investment in each particular seed ("strength in numbers" strategy) or vice versa (“single child” strategy), and which of these strategies is adaptive in the face of challenging environments is unclear. In this study, we addressed this question. For this purpose, we measured the ovule number among 70 Brassicaceae species with a wide range of distribution and environmental habitats but cultivated in the same environment (greenhouse). We then tested the relationship between environment of origin and ovule number by assessing whether environmental harshness contributes to the variation in ovule production. While most of this variation could be explained by the taxonomy, we found that plants originating from environments with lower nutrient availability had significantly lower ovule number, consistent with a “single child” evolutionary strategy to cope with nutrient scarcity. On the contrary, the plants originating from environments with higher precipitation seasonality had significantly higher ovule production rather fitting a “strength in number” strategy in the face of highly fluctuating water availability. In summary, we elaborated an integrative view on the role of maternal investment as an adaptive strategy in response to harsh environments.

Abstract ID: 1111

Male alternative reproductive tactics and sperm investment: a meta-analysis

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Male animals may exhibit discrete, alternative ways of obtaining fertilisations, known as alternative reproductive tactics. Males exhibiting alternative reproductive tactics typically differ in the degree of sperm competition they face, and theory predicts that males facing a high sperm competition risk should invest more into traits that improve their competitiveness after mating, such as large ejaculates or high-quality sperm. However,

evidence for differences in sperm and ejaculate investment between high- and low-risk tactics is mixed, and there has been no quantitative summary of this field. We performed a meta-analysis examining how testes size, sperm number and sperm traits differ between male alternative reproductive tactics that face a high or low sperm competition risk. We obtained data from 92 studies and 67 species from across the animal kingdom. Our analyses showed that male fish showing high-risk tactics had significantly larger testes (after controlling for body size) than those exhibiting low-risk tactics. However, this effect appears to be due to the inappropriate use of the gonadosomatic index as a body-size corrected measure of testes investment. Additionally, we found no significant difference in sperm number or sperm traits between high- and low-risk male tactics. Overall, our results suggest that, despite clear theoretical predictions, there is little evidence that male alternative reproductive tactics differ substantially in investment into sperm and ejaculates across species.

Symposium: S04. The evolutionary ecology of mating systems (id: 29)

Abstract ID: 2456

Ecological and evolutionary drivers of range-wide variation in mating system

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Mating system evolution is driven by the balance of the reproductive assurance that comes from selfing, and the associated fitness reduction due to the increased homozygosity. These benefits and costs of inbreeding may vary among populations within a species leading to variation in mating system. Here I explore ecological and genetic factors underlying a range-wide pattern in mating system. We conducted genetic analyses and field and greenhouse experiments on 24 populations sampled across the range of *Campanula americana*, an insect pollinated herb. Field experiments demonstrated no association between mating system and pollinator abundance, population size or pollen limitation, indicating mating system is not due to selection by local ecological factors. However, mating system was strongly associated with post-glacial colonization distance inferred from genetic analyses, with populations further from glacial refugia having greater selfing potential. This result supports the hypothesis that plants that can self are better colonizers, known as Baker's Law. Baker's Law may commonly shape mating systems as the ranges of many taxa are determined by postglacial expansion. In total, these results highlight the importance of considering historic factors when exploring contemporary patterns.

Abstract ID: 1412

Timing and genomic consequences of intraspecific transitions to homostyly in *Primula vulgaris*

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Heterostyly, a floral polymorphism that favors outcrossing, has attracted evolutionary biologists' attention since Darwin's classical work on this subject. Reported in 28 angiosperm families, heterostyly has been lost multiple times within and between species and is often replaced by homostyly, a floral monomorphism that enables selfing. Although the genetic basis of transitions from heterostyly to homostyly has been elucidated in *Primula*, estimates of the timing of such transitions are scarce, limiting our ability to propose likely evolutionary scenarios favoring the shift to homostyly. Here, we analyze whole-genome resequencing data in reference to a chromosome-scale genome assembly of *Primula veris* to investigate the timing and genomic consequences of transitions to homostyly in the common primrose (*Primula vulgaris*). Our demographic analyses show that homostyly likely evolved in Somerset, England, after the Last Glacial Maximum, around < 10,000 ybp. Despite its recent origin in *P. vulgaris*, homostyly has already triggered detectable genomic consequences, including reduced genetic diversity, increased linkage disequilibrium, and less efficient purifying selection. Furthermore, we corroborate previous results suggesting multiple transitions to homostyly within *P. vulgaris*. Finally, our results empirically confirm, for the first time, classic theoretical models for the expected frequencies of different S-locus genotypes in populations during early transitions to homostyly. Overall, our findings suggest that transitions from heterostyly to homostyly in *P. vulgaris* may be associated with recent events of human-driven habitat fragmentation in southern England, leading to genomic consequences conformant with those expected for transitions from outcrossing to selfing mating systems.

Abstract ID: 1141

Rescue through an increased selfing rate under pollen limitation: plasticity vs. genetic evolution

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Increased selfing rates are widely found in populations experiencing environmental changes, and a common explanation is that selfing offers reproductive assurance under pollen limitation because it relies less on extrinsic factors compared to outcrossing. However, an increase of the selfing rate may impose an initial fitness cost due to exposure of deleterious mutations. An increase of the selfing rate can be either through plasticity or/and genetic evolution at loci that modify the selfing rate. Specifically, under plasticity, the increase of the selfing rate is often instant, but the initial fitness cost can be severe. In contrast, under genetic evolution, the increase of the selfing rate, thus the benefit of reproductive assurance, is gradual, but the initial fitness cost is weaker. By building eco-evolutionary models, I compare the changes of fitness over time and the population survival probability under pollen limitation when the increase of the selfing rate is through plasticity vs. genetic evolution. Results show that under either plasticity or genetic evolution, the survival probability is highest under an intermediate increase of the selfing rate. Generally, rescue is more likely through plasticity than through genetic evolution, although a combination of both may sometimes confer the highest survival probability. The results also suggest rescue by enhanced self-fertilization may not be mainly due to reproductive assurance, but by purging of the genetic load.

Abstract ID: 1440

Dispersal and polyandry evolve as competing inbreeding avoidance strategies

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Understanding evolution of complex life-histories requires explicitly considering their multiple interactions, feedbacks, and shared drivers. Inbreeding depression is hypothesized to drive evolution of two life-histories which have far-reaching ecological and evolutionary consequence: dispersal and polyandry. Yet, the role of inbreeding depression in the separate evolution of these key life-histories is still debated, while the possibility for their joint evolution and consequent covariation has not been considered. I propose that dispersal and polyandry might be competing means of inbreeding avoidance which negatively feedback on each other's evolution. Using a genetically explicit individual-based model, I first demonstrate that inbreeding depression can drive the separate evolution of dispersal and polyandry. Although this is largely known for dispersal, it is not as well established for polyandry evolution, which generally remains an evolutionary puzzle. I show that polyandry can indeed evolve as means of indirect inbreeding avoidance in spatially structured populations. Second, when dispersal and polyandry can evolve jointly, a negative feedback emerges, such that they evolve as alternative inbreeding avoidance strategies across replicate systems, especially if there are fitness costs associated. Finally, although both dispersal and polyandry might be expected to shape the level of inbreeding depression, this is mainly affected by dispersal, while polyandry has a much more limited effect. These results emphasize the need to consider the potential joint evolution of dispersal and mating system in general, together with their genetic effects, to further our understanding of life-history evolution in spatially structured systems, and provide theoretical expectations for new empirical testing.

Abstract ID: 1465

Evolution of female multiple mating in spatially-structured populations

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Female multiple mating (FMM) is a component of the mating system that is widespread across taxa. Yet, explaining its evolution and persistence is an ongoing challenge in evolutionary biology, especially when it is costly to females. One main hypothesis is that the occurrence of inbreeding and inbreeding depression can drive the evolution of FMM as a mechanism of inbreeding avoidance, thereby accruing indirect benefits to females remating. Despite some experimental evidence supporting this hypothesis, theoretical models so far have generally concluded that the strength of indirect selection on FMM through inbreeding avoidance might be very small, thereby suggesting a minor role of inbreeding depression in FMM evolution. However, existing models and experiments do not fully consider the complex relatedness structure emerging from spatially structured populations, how it is consistently changing through time thus how it could affect the selective advantage of FMM. We present results from an experimental evolution study

designed to assess evolution of female multiple mating in spatially-structured populations. Using the cowpea weevil, *Callosobruchus maculatus*, as biological model, we implemented four experimental treatments where populations each consist of 10 sub-populations connected by different fixed dispersal rates (5%, 2% or no dispersal) or consist in a single panmictic population (panmictic populations), thus creating four different levels of spatial population structure. We present the impact of these different dispersal rates on the populations' resulting inbreeding levels, inbreeding depression in female fecundity, male fertility and offspring survival, and on the level of female multiple mating, after 20 generations of experimental evolution.

Abstract ID: 2396

DNA repair during non-reductional meiosis in the asexual rotifer Adineta vaga

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Bdelloid rotifers are microscopic animals notorious for their long-term persistence in the absence of canonical sexual reproduction. This evolutionary paradox is often counterbalanced by invoking their ability to repair high levels of genome breakage caused by desiccation and other genotoxic stresses. How bdelloid rotifers persist despite the expected negative consequences of asexuality and how they survive extreme conditions has been the focus of my research group. We have been employing population and comparative genomic analyses to study evolutionary processes. We also explore the molecular mechanisms making bdelloid rotifers unique in terms of hyper-resistance to desiccation and radiation. I will present here the chromosome-scale genome of the bdelloid rotifer *Adineta vaga*, having homologous chromosomes with signatures of recombination (Simion et al, 2021). Genomes from clonal lines maintained in the laboratory have been sequenced at different timepoints in a mutation accumulation experiment, also following exposure to desiccation and radiation, and the genome dynamics will be presented. Finally, by studying spatiotemporal dynamics of DNA damage response in *A. vaga*, we found that repair of germ line genomic lesions is delayed to a specific time window of oogenesis during which homologous chromosomes adopt a meiotic-like juxtaposed configuration. This data shows that *A.vaga* undergoes a non-canonical meiosis allowing homologous chromosomes to pair and recombine without segregating into haploid gametes, as in automictic parthenogens. It also results in a complete and faithful reconstitution of the genome in the offspring (Terwagne et al., 2022). All these results have started to resolve the evolutionary paradox of bdelloid rotifers.

Abstract ID: 1261

The origins of reproductive isolation in diverging zooplakter populations

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The emergence of reproductive isolation within species stabilizes the differences arising among populations, hence being one of the factors in maintaining local adaptation and promoting speciation. Different processes and mechanisms are involved in isolation, and the isolation itself can influence other steps in the journey of evolutionary divergence. This contribution aims to present an overview of the emergence of reproductive isolation in the facultatively sexual rotifer *Brachionus plicatilis*, with special accent on pre-mating reproductive isolation and its genetic background. We studied different populations in the Iberian Peninsula diverging either due to restriction of gene flow associated with large geographical distances, or in geographical proximity as a consequence of adaptation to local environmental conditions. We quantified the degree of behavioural isolation both in geographically distant, as well as neighbouring, but environmentally diverging groups of populations. We also studied differentiation in genes involved in mate recognition. Despite the high dispersal capacity described in zooplankton species and stabilizing selection acting on mate recognition traits, we found clear evidence for incipient behavioural reproductive isolation in most of the mating assays. We also found relatively high diversity in genes for mating traits. Findings from both sets of experiments were more notable in populations diverging under different environmental conditions with ongoing migration than in geographically distant ones. We then examined whether these divergences map onto overall reproductive isolation, including the post-mating steps.

Abstract ID: 2457

An introduction to the evolution and consequences of self-fertilisation, and the role of ecological and demographic processes

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Self-fertilisation frequently evolves from outcrossing and there is little indication that transitions back to outcrossing are a common occurrence. Fisher's ``automatic advantage'' coupled with short-term advantages linked to selection for beneficial and against deleterious mutations explain the ubiquity of this reproductive strategy, despite obvious long-term disadvantages linked to inbreeding. Theoretical approaches have greatly contributed to our understanding of the genetic processes involved in the evolution of self-fertilisation and the potential consequences of this strategy on species evolution. However, some empirical observations remain difficult to explain, notably the existence of mixed mating systems. Could accounting for ecological and demographic processes shed a light on these?

Abstract ID: 2132

Ecological drivers and genomic consequences of repeated evolution of inbreeding mating systems

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Transitions from outcrossing to inbreeding mating systems occur repeatedly in the animal kingdom, and are frequently associated with benefits of group living or

cooperation. Such transitions are hypothesized to be driven by ecological constraints, e.g. on dispersal or nest foundation, and benefits such as reproductive assurance and cooperation. The transition to an inbreeding mating system is associated with severe reduction in effective population size and elevated genetic drift. Over evolutionary time, these effects are expected to incur major costs: 1) to negatively impact genome function by reduced efficacy of selection and fixation of deleterious variants (genome integrity decay); 2) to accelerate loss of population genetic diversity and thereby adaptive potential. These substantial costs threaten lineage persistence, implying that evolution of inbreeding mating systems may be evolutionary dead ends. Evolutionary responses of changes in mutation rate or increased recombination rate may counteract genome decay; and elevated phenotypic plasticity could buffer populations with low genetic diversity against environmental challenges. I will present data on the ecological drivers of repeated transitions from outcrossing to inbreeding mating systems in a genus of spiders, *Stegodyphu*s, which contains three independent sister-species pairs of outcrossing and inbreeding species. We use comparative genomics to test the evolutionary consequences for genome integrity and for population and species-level genetic diversity, and to assess changes in mutation and recombination rate between outcrossing and inbreeding species. This system presents an ideal phylogenetic framework for testing of the generality of evolutionary processes that ultimately define speciation and extinction events.

Abstract ID: 1082

The evolution of recombination in self-fertilizing organisms

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Understanding the evolutionary advantage of sex and the associated process of meiotic recombination remains a major challenge in evolutionary biology. Useful insights on this question may possibly be gained from exploring the causes of genetic variation for recombination rates within and between species. In particular, a remarkable pattern observed in flowering plants is that self-fertilizing species tend to have higher rates of meiotic crossovers than their outcrossing relatives. We use analytical and simulation methods to investigate how selfing affects the sign and magnitude of stochastic and deterministic components of selection for recombination in hermaphroditic organisms. The results show that, while selection for recombination vanishes under complete selfing (as recombination has no genetic effect in fully homozygous individuals), it is often maximized for selfing rates slightly below one. This is primarily due to the fact that selfing increases the strength of selective interference among loci in finite populations, and may explain the higher crossover rates observed in inbred plant species.

Abstract ID: 1702

Pollinators of the sea: a discovery of animal mediated fertilization in seaweed

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Plants-insects relationship have a long co-evolution history that has been going on for at least 140 millions of years. Insect-pollination is the most widely distributed mode of fertilization in flowering plants. While it has been extensively studied on land, animal-pollination was only demonstrated recently in the marine environment, in a seagrass where the role of invertebrates species in pollen transport was highlighted. This finding contradicts the paradigm that animal mediated pollination is absent in the sea, opening up new avenues of inquiry in other phylums of the tree of life. This is particularly relevant in Rhodophyta since male gametes are non-motile and fertilization takes place onto a remote female organ. The non-flagellated sperms cannot swim to reach the receptive area of the female reproductive organ and depend entirely on passive transport in the water column, unless an additional active mechanism is involved in sperm transfer. Here, we studied biotic interactions between the red alga *Gracilaria gracilis* and the isopod *Idotea balthica*, often found in association in nature. Our results reveal that the presence of idotea under experimental conditions significantly increased the fertilization success of the algae. Moreover, confocal microscopy analysis shows that idoteas transported spermatia that adhere to their bodies. The discovery of animal mediated fertilization in seaweed bring a new vision on how the mating system evolves in algae, in which the role of animal interactions has never been questioned.

Abstract ID: 1586

Contagious asexuality reveals selection acting during evolutionary transitions to parthenogenesis

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Evolutionary transitions to asexuality are often studied by comparing asexuals found in nature with closely related sexuals. However, asexuals sampled in nature may represent only a small subset of the most successful lineages and may therefore contain limited information on the average properties of newly arising asexuals. Here, we generate new asexual lineages of two small crustaceans, *Daphnia pulex* and *Artemia parthenogenetica*, by contagious asexuality, where rare males from obligate asexual lineages transmit asexuality to new lineages by cross-mating with sexual females. In both species, we find that the newly created asexual lineages strongly differ from those sampled in nature, regarding their mode of asexual reproduction, loss of heterozygosity, recombination, and fitness. Together, these findings suggest that the creation of new asexual lineages through contagion may not be as straightforward as previously thought and may result in diverse, non-clonal offspring, on which subsequent selection may act. Our results also show the strength of laboratory-based experiments in complementing field-based studies, as the direction and degree of selection acting on novel asexual lineages can be inferred from the contrast between asexuals generated in the laboratory and older asexuals sampled in the field.

Abstract ID: 2160

Self-compatibility for reproductive assurance not population level compatibility

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Sexual reproduction by intra-haploid selfing lacks the common benefits from recombination and is at genetic level indistinguishable from asexual reproduction. Nevertheless, the evolution of self-compatibility, known as homothallism in organisms with mating types, has occurred many times over. There are two main hypotheses for the evolution of homothallism. First, it offers reproductive assurance, which is especially important when species have an obligatory sexual phase in their lifecycle. Second, loss of self-incompatibility generally leads to universal compatibility, potentially increasing the chance of outbreeding. Here, we test these hypotheses using the fission yeast *Schizosaccharomyces pombe*, which is homothallic by mating-type switching. We measured natural variation in the ratios of mating types analyzing genomic resequencing data. These ratios were used as a proxy for the strength of homothallism, after which mating efficiency and outcrossing ability were assessed for each strain. These measurements, supplemented with results from cellular automaton simulations, show that homothallism increases mating success, specifically when switching maintains balanced ratios. In contrast, outcrossing is reduced under homothallism, because gametes that mated through intra-clonal selfing are no longer available for outcrossing. Our results suggest that the recurrent evolution of haploid self-compatibility is driven by selection for mating assurance, not to increase the potential for outcrossing.

Abstract ID: 1844

Ancient mating alleles maintained by balancing selection in basidiomycete fungi

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In the fungal kingdom, different mating systems exist. In Basidiomycota, a tetrapolar multi-allelic mating system controlled by two unlinked loci has evolved. Different alleles at both loci are needed for a successful mating event. These loci are usually highly diverse with many alleles present in each species – a diversity maintained by balancing selection. We used an integrative approach where we combined genomic data with mating experiments to understand how mating is controlled in basidiomycete wood decay species. A total of 179 individuals of the sister species *Trichaptum abietinum* and *T. fuscoviolaceum*, and one individual of *T. biforme* were genome sequenced. The mating type alleles were molecularly characterized and *in vitro* crosses were performed to support our classification of mating alleles. A total of 17,550 mating

types were predicted based on the quantified number of mating alleles at the two mating loci. Phylogenetic analyses supported that the genetic diversity of mating alleles in *Trichaptum* is due to long-term balancing selection, with limited recombination and duplication activity. The alleles were ancient and had mainly evolved before the split of these species. We could further provide evidence for the level of divergence needed between the mating alleles for the fungi to successfully mate. The high number of sequenced strains highlighted the importance of sequencing multiple individuals from each species to detect the mating-related genes, the mechanisms generating the diversity and the evolutionary forces maintaining them.

Abstract ID: 1799

Pollinator abundance effects on sexual selection in plants

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Sexual selection should apply to all anisogamous sexually reproducing organisms with males producing greater numbers of gametes compared to females, thus encompassing plants. Yet, few predictions from the theory of sexual selection have been tested so far in the plant kingdom, and the effect of a third-party player, the pollinator, on a plant's number of mates remains to be evaluated. Here, we explore the effect of pollinator abundance on a central prediction of sexual selection thinking, that male reproduction relies on access to sexual partners more so than female reproduction. Specifically, we manipulated the abundance of bumblebees (*Bombus terrestris*) in experimental populations of the hermaphroditic plant *Brassica rapa*, and estimated its effect on mating systems regarding: (1) the number of sexual partners reached by pollen dispersal during the prepollination phase by tracking pollinator movements, and (2) the number of sexual partners which ovules have effectively been fertilized during the postpollination phase through paternity analyses. We test whether variation in pollinator abundance affects the balance between sexual selection occurring at the pre- and postpollination phases: (1) low abundances of pollinators may strengthen selection for attracting pollinators and for both exporting and capturing pollen, while (2) high abundances of pollinators may intensify competition for accessing ovules within pistils by augmenting pollen loads on pistils. By evaluating the evolutionary consequences of an ecological factor on mating systems both temporally and spatially variable in nature, our results extend the test of sexual selection predictions to plants with potential implication for plant fitness.

Abstract ID: 1443

Shifts to selfing during range expansion cannot overcome the accumulation of genetic load

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Mating system and demography shape genetic diversity within a population. Self-fertilization tends to occur more frequently towards species' range edges since mate reassurance that comes with selfing is a favorable trait for colonization. The

accumulation of genetic load during range expansions may be combated in selfers due to increased homozygosity resulting in purging. While the effect of range expansions on genetic load is well described, the combined consequences of complex demography and mating system shifts are less clear. We investigate this question by integrating forward-time simulations of range expansions with empirical data collected from more than 500 genomes across a post-glacial expansion of Arabis alpina, a mixed mating plant. Simulation results indicate differences in genetic load based on mating system during expansion, with more extreme selfers accumulating less load than mixed mating or outcrossing populations. Extreme selfers also expand their range more quickly, indicating fewer generations subject to genetic drift during repeated founder events characteristic of a range expansion. Empirical results show substantial load still accumulated in selfing range-edge populations, independent of the assumed dominance coefficient, as compared to outcrossing, range-core populations. This implies that despite the advantage to colonization and purging provided by selfing, the benefit of increased recombination from some level of outcrossing is still advantageous at range edges for adapting to novel environments. Complicated factors such as local adaptation at the range edge may force slower expansion and therefore limit the benefit of selfing and subsequent escape from accumulating genetic load.

Abstract ID: 1686

Using runs of homozygosity to distinguish mating system from inbreeding and demographic history

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Long stretches of homozygosity within the genome, known as runs of homozygosity (ROHs) are generated by self-fertilization, or more generally, increased inbreeding. Many studies have used ROHs to understand inbreeding in agricultural and breeding contexts, demographic history of human populations from ancient samples, or autozygosity in the context of recessive disease variants. Expectations for characteristics of ROHs depending on demographic history and mating system, however, have been little explored. ROHs may prove useful to infer the degree of self-fertilization in natural plant populations from genomic data. Yet there are many confounding factors in terms of demography that may leave similar signatures to selfing. We use simulations to understand which scenarios can be distinguished with ROHs, in terms of combinations of demography and varying degrees of selfing. We examine our results in comparison to natural populations of the alpine plant, Arabis alpina, which has undergone a historic range expansion from Italy into Switzerland, as well as a concurrent transition from outcrossing to selfing. We find that outcrossing populations should be distinguishable from selfing populations, when the lengths and counts of ROHs can be compared among populations. This largely holds even when population sizes become drastically reduced. Bottlenecks generate similar signatures to low rates of selfing, while more complex histories that include admixture among populations make differentiating selfing from outcrossing nearly impossible due to increased mixing of more haplotypes. This may also explain why some known, highly selfing populations of A. alpina resemble more outcrossed populations in terms of ROH characteristics.

Abstract ID: 1504

The selection and genomic architecture of hermaphroditism and dioecy under experimental evolution

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Abstract: Dioecy has evolved repeatedly from hermaphroditism in flowering plants. Modelling has long pointed to gynodioecy as a likely intermediate step in these transitions, with the invasion of females and a subsequent shift in the remaining hermaphrodites towards greater male allocation. Similar models indicate that the opposite path, involving the initial invasion of males into a hermaphroditic population, is much less likely, especially if the hermaphrodites are partially self-fertilizing. Here, we document the invasion and genomic architecture of males into experimental monoecious populations of the wind-pollinated plant *Mercurialis annua*. This case is peculiar because: the monoecious populations are the result of the rapid breakdown of dioecy under experimental evolution following the removal of XY males; and the evolved males are quite different from those that were originally removed at the start of the experiment, having different morphology and lacking a Y chromosome. We detail the evolution of the distribution of sex allocation among individuals in the experimental populations over the course of eight generations in terms of several measures of reproductive allocation and quantitative gender. On the basis of quantitative trait locus (QTL) analysis, we also show that variation in sex allocation in *M. annua* involves both trade-off loci, with different alleles favouring either male or female function, and loci that affect only one of the sexual functions but not the other. We discuss the implications of our results for understanding the interaction between sex allocation and the mating system in plants.

Symposium: S05. A combinatorial view on rapid speciation - the role of ancient genetic variants and hybridisation (id: 38)

Abstract ID: 2368

The role of ancient inversions in repeated dune adaptation and speciation

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The reuse of ancient genetic variation is known to facilitate rapid adaptation and speciation. Here, we explore this phenomenon in the sunflower species, *Helianthus petiolaris*, which has colonized sand dune habitats in multiple locations across North America. We find that dune habitats are associated with seven chromosomal inversions, four of which are shared between dune habitats in Colorado and Texas. We further show that these inversions are linked to ecologically relevant traits and fitness variation that underlies reproductive isolation. Overall, we suggest that ancient inversions contribute disproportionately to parallel genetic evolution and speciation in this system.

Abstract ID: 1517

Prevalence and influence of ancient hybridization in an african primate radiation

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The guenons (tribe Cercopithecini) are a species-rich group of African primates. Despite an extraordinary morphological, ecological and karyotypic diversity they frequently hybridize, even across genera. We sequenced whole genomes of 22 guenon representing all genera and species groups, and identified at least seven ancestral gene flow events throughout the radiation. We found that the two major clades, the arboreal and terrestrial guenons, experienced bidirectional geneflow some 10 million years ago. More recently, the *Cephus* and *Mona* group ancestors exchanged a substantial amount of genetic material, which may have contributed to the extensive diversification of these lineages. We assessed the genomic landscape of introgression, and found low levels of parallelism across independent admixture events. Introgressed genomic regions contained genes involved in chromosome pairing and segregation during meiosis, e.g., *RAD21L1*, *ASPM* and *PRDM9*, potentially facilitating gene flow across divergent lineages with different karyotypes. Furthermore, we uncover multiple occurrences of mito-nuclear discordances, shaped by complex patterns of ancestral mitochondrial introgression followed by differential retention of introgressed haplotypes in descendant lineages. However, even though mitochondrial transfers have occurred across deep evolutionary lineages, we find no indications of specific co-introgression of nuclear genes known to interact with the mitochondrion. Although hybridization is an increasingly acknowledged evolutionary force, mammals remain understudied likely as a result of their large and complex genomes. The remarkable diversity of guenons makes them an excellent system to further our understanding about the processes of, and interactions between, introgression and speciation.

Abstract ID: 2259

Alternative associations between ecological and spatial components of divergence in seahorses

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Understanding how adaptive structural variants combine with spatial genetic structure to generate new evolutionary lineages has garnered increasing attention. The long-snouted seahorse *Hippocampus guttulatus* is subdivided into partially reproductively isolated evolutionary units, consisting of geographical lineages in the northeastern Atlantic and of marine and lagoon ecotypes in the Mediterranean Sea. This situation might result either from rapid evolution or recent spatial re-assortment of existing variation, given that the current habitats of the North Atlantic lineage and the Mediterranean lagoon ecotype did not exist during the last glaciation. Furthermore, the divergence between geographical lineages partly shares a common genomic architecture with that between ecotypes, and may suggest combinatorial evolution of lineages involving both ecological and spatial components. To study the mechanism that gave rise to these lineages, we sequenced and analysed variation of contemporary genomes as well as a historical time series of samples from the present day to ~150 yr. We describe an original combinatorial assortment between genomic backgrounds structured by geography and large chromosomal inversions mainly structured by ecology. We observe differences in ancestry proportions among lagoons as well as within one lagoon sampled through time, suggesting a possible ongoing erosion of the background divergence against which inversions maintain. We also investigate the possibility of ancient hybridisation events with a closely related species, since coalescent times in inverted regions are greater than the genome-wide average. Our work may help to better understand to which extent gene flow and recombination take place between newly combined variants in divergent lineages.

Abstract ID: 1592

The reshuffling of pigmentation genes leads to rapid phenotypic evolution in a finch radiation

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Organisms in the early stages of speciation con be leveraged to study the nature of species boundaries. The capuchino seedeaters, a species-complex of South American finches in the genus *Sporophila*, have undergone an explosive and recent radiation. These predominantly sympatric seedeaters differ in male plumage and song, two sexually selected traits, but are otherwise morphologically and genetically very similar, and different species can still produce viable hybrid offspring in aviaries. Field experiments suggest that these divergent male traits govern species recognition and territorial defense. Various whole genome sequencing approaches have identified a few areas of the genome that are diverged among these otherwise genetically similar (average $F_{ST} < 0.01$), yet phenotypically variable, taxa. These narrow genomic regions are predominantly located in non-coding areas in the vicinity of melanogenesis genes, and presumably contain variants which contribute to regulating gene expression. I explore the processes that have shaped these outlier genomic regions using new methods for inferring the full ancestral recombination graph and machine learning methods for identifying selective sweeps. Different combinations of the same outlier regions are associated with differences in coloration among the multiple members of this radiation. Most outliers show signatures of relatively recent soft sweeps acting on standing genetic variation. These results suggest that coloration traits are generated by novel combinations of variants which are segregating in the species-complex. Plumage

patterning has likely originated through this process of reshuffling, rapidly generating novel sexual signal which contribute to establishing and maintaining prezygotic reproductive isolation.

Abstract ID: 1689

Shedding light on the early stages of a combinatorial event using whole-genomes from resting eggs

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The evolution of reproductive isolation and adaptive traits has often been considered as a slow process that happens over many generations. However, selection on slowly accumulating *de novo* mutations alone seems insufficient to explain numerous cases of rapid adaptation and speciation. Recently, it has been proposed that a combinatorial mechanism reorganizing ancient genetic variants via hybridization can facilitate rapid adaptation to new environments and speciation. With a few exceptions, most studies have focused on combinatorial events that occurred more than 1-500 kya and little is known about the early stages of a combinatorial event. Here, we make use of whole-genome time series obtained from *Daphnia* resting eggs deposited in lake sediments to reconstruct the early stages of a combinatorial event at high temporal resolution. The microcrustacean genus *Daphnia* comprises several hybridising complexes and well-studied examples for rapid adaptation. Recent anthropogenic change has sparked secondary contact events of different intensities in European peri-Alpine lakes, which have been recorded in the sediment archive. We take advantage of this unique system to study combinatorial events and their putative consequences for ecological adaptation and speciation. Finally, we discuss the implications of cyclical parthenogenesis, a feature of *Daphnia* life history, on the outcome of combinatorial events.

Abstract ID: 1479

Hybrid speciation and population extinction

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Hybridization is of growing interest both as a unique window for observing speciation mechanisms and a potential engine of speciation. One interesting and controversially discussed outcome of hybridization is hybrid speciation, where the hybrid population maintains a mixed combination of the parental genetic incompatibilities, preventing further gene exchange between the newly formed population and the two parental sources. We have previously demonstrated that, for specific linkage architecture (location and order of hybrid incompatibilities along the genome), their reciprocal sorting

could result almost always in hybrid speciation. Yet, the sorting of the incompatibilities creates a risk of population extinction. To understand how the demographic consequences of this purging interact with the formation of a hybrid species, we model an isolated hybrid population resulting from a single admixture event. We study how the population size, linkage architecture and strength of the incompatibility affect both the survival of the hybrid population, the resolution/purging of the genetic incompatibilities and the probability of observing hybrid speciation. We demonstrate that the sorting of the genetic incompatibilities is associated with a risk of extinction. This risk is highest for intermediately strong hybrid incompatibilities. In addition, the linkage architecture displaying the highest hybrid speciation probabilities changes drastically with the population size. Overall, this indicates that the population dynamics can strongly affect the outcome of hybridization and the probability of hybrid speciation.

Abstract ID: 1849

Predictable sorting of genetic variants in hybrid genomes driven by selection

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Hybridization combines genetic variants from two divergent lineages and instantantly increases genetic variation within a population. This increased variation can serve as a raw material for natural selection and fuel rapid adaptation or speciation. However, both deleterious and beneficial allele combinations are likely to be generated simultaneously in hybrid genomes. Consequently, it is unclear to what extent hybrid genome evolution, and so rapid speciation and adaptation via hybridization, is driven by deterministic selective pressures instead of random sorting of alleles. Using whole genomes and three replicate hybrid populations we show that selection led to correlated sorting of genetic variation in less than 50 generations in *Formica aquilonia* × *F. polyctena* wood ant populations. Removal of ancestry from the species with the lowest effective population size happened repeatedly in all populations, consistent with purging of deleterious load. This process was modulated by recombination rate variation and the density of functional sites. Moreover, haplotypes with signatures of positive selection in either species were more likely to fix in hybrids, suggesting hybrids might combine adaptive alleles from both species. These mechanisms led to predictable evolution of hybrid genomes over short timescales in nature, highlighting potential mechanisms of rapid adaptation at the genomic level.

Abstract ID: 2318

I get by with a little help from my friends: hybrid origins of a rare pupfish radiation

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The ability to hybridize, or the persistence of incomplete reproductive isolation, could allow lineages to rapidly acquire the awe-inspiring amount of genotypic, phenotypic, and ecological diversity we observe in adaptive radiations. Indeed, extensive histories of hybridization have been documented in many classic examples of adaptive radiations, making it a leading additional mechanism beyond ecological opportunity. Despite a growing appreciation for the generative role hybridization can play in adaptive radiation, we do not know how extensively radiating lineages differ from their non-radiating counterparts in their history and capacity for hybridizing. We leveraged a rare and young radiation of Caribbean pupfishes that occurs only on a single island and is nested within a large network of single species lineages on similar islands, to test out origin hypotheses against. Using 250 genomes from across *Cyprinodon*'s range, we characterized the distribution of genetic variation across the Caribbean. Most of the genetic variation involved in the radiation is widespread across Caribbean populations. Some was brought in through hybridization and introgression from these events may have modified the fitness landscape and increased craniofacial trait diversity on the island. The radiation contains stronger signatures of adaptive introgression than found in populations on other islands that did not radiate, lending support to the hybrid origins hypothesis. However, these other populations experienced introgression from some of the same sources and in some cases share 100% of the same genetic variation, highlighting that there is still much to learn about why introgressed variation aids adaptive radiation in only certain cases.

Abstract ID: 1603

Rapid radiation characterised by prevalent hybridization in the Neotropical genus *Tillandsia*

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Hybridization is often regarded as a key evolutionary process that can stimulate speciation, but excessive gene flow has also been reported to dissolve species boundaries, hampering diversification. The recent rapid radiation of *Tillandsia* subgenus *Tillandsia* (family Bromeliaceae) is a highly diverse Neotropical Monocot group which provides an attractive system for studying the drivers and constraints of species diversification. This group, which consists of predominantly epiphytic plants, is thought to have diversified within the last 3 million years during its expansion from South into Central America, following the closing of the Isthmus of Panama. We inferred phylogenomic relationships among 32 species of *Tillandsia* using whole-genome data and employed a tree-based approach to explore the evolutionary history of the clade. We report a lack of monophyly and deviations from a tree-like structure coupled with rampant gene tree discordance. Focusing on hybridization, Patterson's D (ABBA-BABA) and related statistics were used to describe the rates and timing of introgression events and to assign introgression events to internal tree branches rather than species. In contrast to previously formulated hypotheses, high rates of hybridization within and between clades suggest that the expansion of the subgenus into Central America proceeded in several migration events, followed by episodes of diversification and gene flow. Finally, we discuss the possible contribution of interspecific

gene flow to adaptive trait shifts. Our results underline the creative contribution that hybridization and introgression can play in evolution and document their driving roles during adaptive radiation.

Abstract ID: 1033

Signatures of introgression implicate a regucalcin in the evolution of mate preference behaviours.

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Hybridisation has been suggested to play an important role in behavioural evolution, but to our knowledge a direct link between behavioral phenotypes and specific introgressed loci has not previously been made. More broadly, the genetic mechanisms underlying behavioural evolution remain largely unknown. Here, we study the molecular underpinnings of convergent visual behaviours in *Heliconius* butterflies. These tropical butterflies have mimetic colour patterns, which are also used as mating cues. Across the *melpomene-cydno* group, warning patterns have evolved via adaptive introgression of red patterning alleles. In this study, we show that introgressed alleles are also strongly associated with the evolution of visual preference behaviours. Using behavioural data collected from hundreds of interspecific hybrids, we first show that divergent visual mate preferences across this butterfly group are associated with the same genomic location. We then demonstrate signatures of adaptive introgression between red-preferring butterflies at this genomic location, at the level of previously identified candidate behavioural genes. Patterns of gene and allele specific expression of one of our candidate genes within this QTL region, a *regucalcin,* is strongly associated with variation in preference behaviours across the *cydno-melpomene* clade. Finally, we present preliminary results on the behavioural effects of a CRISPR/Cas9 mediated knock out of this candidate gene. Overall, we find evidence that behavioural alleles crossed the species barriers to facilitate adaptation and speciation.

Abstract ID: 2179

Ancient and ongoing hybridisation in the adaptive radiation of silversides in the Malili lakes

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Hybridisation before or early in an adaptive radiation can fuel speciation as new combinations of DNA can produce new phenotypes, and thus new targets for selection. But what happens if hybridisation does not cease after species formation? Intuitively, we expect species which continually hybridise to eventually collapse into a single species. Yet there are species which occasionally hybridise and remain distinct. We propose that hybridisation may, in some cases, promote ecological divergence, when new combinations facilitate niche adaptation. To shed light on these mechanisms, we will characterise the genomic substrate for rapid ecological adaptation and species formation in the adaptive radiation of sailfin silverside fishes (genus *Thelmaterina*) from the Malili lake system in Sulawesi (Indonesia). The Malili silverside radiation consists of ~20 species covering a variety of ecological niches. Besides presumed hybridisation in their early divergence, sailfin silversides also show strong signs of ongoing genetic introgression. This makes the silverside radiation ideally suited as a study system to obtain an integrated picture of the effects of ancient and ongoing hybridisation in adaptive radiation. Using whole-genome sequences, we detected signals of hybridisation at the root of the species tree and identified introgression between (morpho)species. Two species of silversides, which occasionally interbreed, are known to both hybridise with the same riverine species. We will investigate whether, by incorporating different or similar parts of DNA from the riverine species, similarity between these two species of silversides could increase or decrease, respectively, and thus whether this ongoing hybridisation promotes or inhibits speciation.

Abstract ID: 1891

All roads lead to Rome: Complex histories of diversification and hybridization in wheatears

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Genomic studies suggest that rapid evolution is often underpinned by standing genetic variation or hybridization, rather than novel mutations. However, insights into the prevalence of each of these trajectories to adaptation and speciation are still limited, though highly relevant to the prospects that biodiversity has to adapt to ever faster changing environments. Here, we introduce a study system – wheatears (genus Oenanthe) – that is characterized by pervasive phenotypic parallelism and promises diverse insights into the roles of ancestral variation, hybridization, and novel mutations in phenotypic and species evolution. First, deploying a phylogenomic approach we show that phenotypic parallelism in wheatears likely involved all three trajectories. Second, we confirm this conclusion by leveraging a colour polymorphism and recombined colour phenotypes in hybrids in the O. hispanica-complex to identify the genetic variation underpinning within- and between-species colour variation and tracing its evolutionary history across wheatears. Finally, we show that the histories of diversification and hybridization in the O. hispanica-complex are substantially more complex than previously assumed, including cryptic diversity and idiosyncratic patterns of ancestries and reproductive isolation across multiple hybrid zones. Our results suggest that the

phenotypic and species diversity in wheatears evolved through combinations of genetic variation from diverse origins, including ancestral, introgressed, and novel variants.

Abstract ID: 1802

Evolution of assortative mating following experimental color introgression in *Drosophila*

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Adaptive introgression is ubiquitous in animals but experimental support for its role in driving speciation remains scarce. In the absence of conscious selection, admixed laboratory strains of *Drosophila* asymmetrically and progressively lose alleles from one parental species and reproductive isolation against the predominant parent ceases after 10 generations. Here, we selectively introgressed during one year light pigmentation genes of *D. santomea* into the genome of its dark sibling *D. yakuba*, and vice versa. We found that the pace of phenotypic change differed between the species and the sexes, and identified through genome sequencing common as well as distinct introgressed loci in each species. Mating assays showed that assortative mating between introgressed flies and both parental species persisted even after four years (~ 60 generations) from the end of selection. Our results indicate that selective introgression of as low as 0.5% of the genome can beget morphologically-distinct and reproductively-isolated strains, two prerequisites for the delimitation of new species. Those findings hence represent a significant step towards understanding the genome-wide dynamics of rapid speciation-through-introgression.

Abstract ID: 1425

The role of ancestral hybridization in clownfish adaptive radiation

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The contribution of hybridization in the generation of global species diversity has long been a subject of controversy among evolutionary biologists. However it is now increasingly accepted that hybridization has many impacts on the process of speciation. Especially, it is an important mechanism fostering adaptive radiation, because it can generate new phenotypic combinations enabling the occupancy of new niches. Here, we focused on clownfish (Pomacentridae), a clade of 28 coral reef fishes displaying a mutualistic interaction with sea anemones. This behavior is the key innovation that triggered adaptive radiation of clownfishes, as each species is able to occupy a different combination of host anemone species and habitat. Previous work suggested that hybridization might be responsible for the extant diversity of clownfish species. To test this hypothesis, we analyzed whole-genome datasets for each clownfish species. First, we reconstructed the phylogeny of the clade based on topology weighting method, which enables the visualization of the relationships between taxa across the genome. Then, we highlighted possible ancient hybridization events based on comparative genomic framework for detecting introgression in genomes. The resulting phylogeny is consistent

with previous works based on few mitochondrial and nuclear genes and shallow nodes are now well supported, in contrast to past studies. Furthermore, our results suggest that ancient hybridization events are associated with a burst of diversification, emphasizing the role of hybridization in the adaptive radiation of clownfish.

Abstract ID: 1026

Rate variation produces false signals of introgression

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The role of hybridization in the context of diversification dynamics has recently seen increasing attention as genomic studies enabled the identification of species produced through homoploid hybridization, and hybridization has been implicated as a driver of explosive adaptive radiations. Moreover, recent research has made it abundantly clear that even highly divergent species are sometimes still able to hybridize and backcross. These findings raise the question whether the methods developed for detecting hybridizations are still appropriate and applicable for suchlike scenarios, due to the fact that they were originally aimed for analyses at the level of populations and recent divergences. The reliability of these methods has been questioned when being applied to more divergent systems where the assumption of constant evolutionary rates, which is implicit in the most commonly used methods, is more likely to be violated. To test the limitations of these methods when being applied to highly divergent species, genomic data were simulated. These simulations included different settings with varying degrees of rate variation, introgression, and population size. We were able to show that commonly applied statistical methods, e.g. D-statistics and tests based on tree topologies, are producing false-positive signals of gene flow between highly divergent taxa. In addition, our results indicated that the presence and effects of long branch attraction biases must be taken into account when identifying the appropriate methodology for the detection of gene flow. For scenarios with rate variation we found a reliable statistic based on clustering of ABBA sites, that we implemented in Dsuite.

Abstract ID: 1113

A role for regulation of gene expression in hybridization derived novelty?

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Hybridization has been documented to the extent where its importance for generating evolutionary novelty can no longer be questioned. In spite of this, we lack an understanding of the evolution of regulation of gene expression in hybrid lineages and species, and its role in hybridization derived novelty. Gene expression evolves in a stabilizing manner where cis(local)- and trans(distal) regulatory elements co-evolve.

Interestingly, as hybridization breaks up co-inheritance of regulatory elements *transgressive* hybrid gene expression, outside the ranges of both parent species, may arise in spite of intermediate genome composition. While some recent studies show variable patterns of sub-genome dominance in allopolyploids, less is known about the evolution of gene expression in homoploid hybrids. I will present pilot findings of *transgressive* gene expression in the testes of the wild homoploid hybrid species Italian sparrow (*Passer italiae*), and outline a research program investigating how hybridization can result in *transgressive* gene expression. I propose that gene expression may be key to understanding how hybridization can contribute novel variation that selection can act on.

Abstract ID: 1038

Exploring hybridization in *Flaveria* (Asteraceae), the prime model of C_4 photosynthesis evolution

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Flaveria (Asteraceae) is the prime model for the study of C_4 photosynthesis evolution and seems to support a stepwise acquisition of the pathway through C_3-C_4 intermediate phenotypes, still existing in *Flaveria* today. Molecular phylogenies of *Flaveria* based on concatenated data matrices are currently used to reconstruct the complex sequence of trait shifts during C_4 evolution. To assess the possible role of hybridization in C_4 evolution in *Flaveria*, we re-analyzed transcriptome data of 17 *Flaveria* species to infer the extent of gene tree discordance and possible reticulation events. We found massive gene tree discordance as well as reticulation along the backbone and within clades containing C_3-C_4 intermediate and C_4-like species. An early hybridization event between two C_3 species might have triggered C_4 evolution in the genus. The clade containing all C_4 species plus the C_4-like species *F. vaginata* and *F. palmeri* is robust but of hybrid origin involving *F. angustifolia* and *F. sonorensis* (both C_3-C_4 intermediate) as parental lineages. Hybridization seems to be a driver of C_4 evolution in *Flaveria* and likely promoted the fast acquisition of C_4 traits. This new insight can be used in further exploring C_4 evolution and can inform C_4 bioengineering efforts.

Abstract ID: 2169

Does hybridization facilitate explosive speciation of Lake Baikal amphipods?

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The adaptive radiation of amphipods in Lake Baikal has brought forward more than 340 species (20% of the world's freshwater amphipods), making it one of the largest species flocks after the famous African cichlid radiations, and one of the only large radiations in temperate climates. Despite this iconic status the radiation has not yet been subject to detailed genomic investigation. During my PhD I was able to demonstrate excessive amounts of parallel adaptation among the transcriptomes of species of this adaptive

radiation. I our new project we test whether the previous results could be explained by hybridisation and adaptive introgression. These processes have been shown to occur in other adaptive radiations, but their functional role in rapid diversification is still debated. Our results, based on transcriptomic dataset, indicate that hybridization between two independent lineages of Baikalian amphipods emerged in the period when fast speciation started. Furthermore, we found intriguing signals of Dobzhansky-Muller incompatibilities as well as positive selection on introgressed loci. These findings provide evidence that hybridization likely facilitated adaptive radiation of Lake Baikal amphipods.

Symposium: S06. Revisiting chromosomal speciation in the genomic era (id: 8)

Abstract ID: 1163

Holocentric chromosomal evolution and diversification patterns: from macro to microevolution

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Carex, with ca. 2000 spp., is a megadiverse genus in the also large sedge plant family (Cyperaceae, ca. 5600 spp.). Cyperaceae species possess holocentric chromosomes, leading to a very large dysploid chromosome number variation, 2n = 12 to 2n = 124, sometimes even within species (i.e. *Carex laevigata* 2n = 69-84, *Carex helodes* 2n = 68-75). We constructed a graphical model of chromosome number evolution linked to diversification rates (chomoSSE) in genus *Carex*. This model includes parameters that differentiates between anagenetic and cladogenetic dysploidy, and allows for variation in diversification rate not due to chromosome number change (hidden states). We also performed phylogeographic and chromosome variation studies in several species of genus *Carex* to infer patterns of chromosomal differentiation at population level. We compared the macroevolutionary patterns with those found at microevolutionary scale. We report very fast rates of dysplidy across *Carex*. However, when we add diversification rate variation not linked to dysploid change, we find that these dysploid chromosomal transitions are mostly anagenetic changes. At microevolutionary scales, chromosome number variation seems to be geographically sorted in latitudinal and longitudinal gradients, and different cytotypes could be locally adapted. Within species, gene flow between divergent cytotypes, but not similar ones, produces hybrid dysfunction. Despite fast rates of dysploidy, single chromosome changes do not appear to cause reproductive barriers leading to speciation at macroevolutionary scales, although at microevolutionary scale chromosomal changes seem to have a crucial role on the patterns of genetic differentiation and local adaptation.

Abstract ID: 2217

Chromosomal speciation: Lessons learned from karyotype evolution in Lepidoptera

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Moths and butterflies (Lepidoptera) represent the most prominent lineage of exclusively phytophagous insects, which comprises about 10 % of described animal diversity. Their chromosomes lack localized centromeres, i.e., they are holocentric and spindle microtubules can attach along their entire length. Holocentricity supposedly facilitates chromosome rearrangements as it alleviates fitness cost of fusions and fissions due to loss or missegregation of acentric fragments or dicentric bridges. Lepidoptera have indeed the widest variation in chromosome numbers. Yet deviations from their modal and ancestral chromosome number 2n=62 are not that common as this genome organization has been conserved for at least 140 My. Karyotype evolution is biased towards chromosome fusions, but it was hypothesized that both fissions and fusions promote lepidopteran diversification. Recent studies paid particular attention to sex chromosomes as Lepidoptera represent the most species rich group with female heterogamety, i.e., WZ/ZZ sex chromosome system. Studies in species with high chromosome numbers resulting from fragmentation revealed that sex chromosomes resist fissions. Yet, unlike in other female heterogametic taxa, lepidopteran sex chromosomes are often involved in sex chromosome-autosome fusions giving rise to so-called neo-sex chromosomes. Formation of the neo-sex chromosomes and their differentiation could promote lepidopteran speciation. Main contributing factors to consider are: (i) changes in recombination landscape, (ii) increased number of sex-linked genes potentially causing genetic incompatibilities, (iii) repetitive content, and (iv) meiotic modifications due to holocentricity.

Abstract ID: 1240

The evolution of Merian Elements in Lepidoptera

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Chromosomes are a major unit of genome organisation and of inheritance. While chromosomes and their contents are usually evolutionarily stable, major karyotypic changes sometimes occur that have consequences for speciation, population divergence, and adaptation. Lepidoptera, butterflies and moths, are a diverse order of insects, with a largely conserved karyotype of 31 chromosomes. However, a subset of species display dramatic variation in patterns of genome and chromosome organisation. The growing number of high-quality, chromosomal assemblies means that we can begin to ask fundamental questions surrounding the processes that drive chromosome structure in Lepidoptera. Here, we draw upon 150 chromosomally-resolved lepidopteran genomes, generated as part of the Darwin Tree of Life Project, to analyse patterns of chromosome organisation across the group. By clustering genes by co-occurrence, we defined sets of genes that mark ancestral lepidopteran linkage groups, known as Merian elements, and used these to identify chromosomes that have undergone fusions or splits and place these events within a phylogenetic context. We inferred over 100 fusion and fission events, including dramatic karyotypic changes in Pieridae, Lycaenidae and Tortricidae. Moreover, we found that some chromosomes, including the Z, are more likely to fuse than others. I will discuss features that correlate with the distribution of rearrangements, such as transposable element density, and explore the possible mechanisms that could explain this relationship. Together, these analyses demonstrate how chromosomally-contiguous genomes across Lepidoptera offer an unprecedented

opportunity to explore the role of selective constraint in the evolution of genome structure.

Abstract ID: 1423

Multiple chromosomal inversions associated with strong reproductive isolation between ecotypes

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Reproductive barriers can cluster in the genome notably due to the presence of chromosomal rearrangements, but we still lack general insight on whether and how the accumulation of such chromosomal rearrangements results in the completion of speciation. The marine snails from the genus *Littorina* have been recently developed as a useful system to study these questions. This genus encompasses multiple species subdivided into ecotypes that are distinguished genetically by multiple chromosomal inversions. Here, I will present work on the evolution of a large and a dwarf ecotype of *L. fabalis.* These ecotypes are repeatedly found to overlap on wave exposure gradients in Europe, where they are known to hybridise. By analyzing whole genome polymorphism data, we found 13 inversions, located on 10 different chromosomes, that reach near differential fixation along two transects covering a hybrid zone between the two ecotypes. These inversions cover around 35% of the genome but carry more than 95% of SNPs with clinal variation along the transect, i.e. SNPs that are directly or indirectly affected by divergent selection. Interestingly, some of these inversions appear to be shared with the sister species *L. saxatilis*, where they also contribute to ecotype size differences. However, in *L. fabalis*, the inversions on different chromosomes are in strong linkage disequilibrium despite extensive gene flow elsewhere in the genome, suggesting that *L. fabalis* ecotypes are at a later stage of speciation than ecotypes of *L. saxatilis*. Overall, these results suggest that associations between multiple chromosomal inversions can facilitate speciation.

Symposium: S07. Chromosome rearrangements in evolution (id: 949)

Abstract ID: 1208

Chromosomal rearrangements and neo-sex chromosomes evolution in grasshoppers

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How the orthopteran sex chromosomes first evolved from autosomes and their levels of divergence and degeneration remains obscure for more than a century. The morabine

grasshoppers, Vandiemenella viatica species group (divergence time <3 my), is uniquely suitable for studying the early stages of newly evolved sex chromosomes divergence because neo-XY sex chromosome races have evolved independently through X-autosome fusions. Using chromosome-level assemblies of four chromosomal races representing two pairs of karyotypes with and without neo-sex chromosomes (P24X0/XY, P45bX0/XY), I show that the non-recombining region of the neo-Y chromosome in the races P24XY and P25XY is a unique fragment of ~60 Mb containing male-specific alleles. The fragments comprise hundreds of genes and stretches of DNA that duplicated and inverted from regions found at the same as well as different chromosomes. The P24XY neo-Y non-recombining region contains functional sex-determining genes (including a duplicate of the key sexual differentiation regulatory gene doublesex), genes involved in spermatogenesis, fertility and reproduction, which illustrates their integrated role as a masculinizing supergene. Contrary to what is expected following recombination suppression, the neo-Y show no signs of degeneration and genes loss and is less prone to repeat accumulation comparing to other genome regions. The findings demonstrate how large fusion events, inversions and duplications of regulatory genes may contribute to the evolution of co-adapted gene clusters, sex-limited chromosomes and the enigmatic evolution of the orthopteran neo-sex chromosomes in general.

Abstract ID: 1427

Evolutionary implications of 3D chromatin remodeling in the germ line

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The spatial folding of chromosomes and their organization in the nucleus has profound regulatory impacts on gene expression and genome architecture, whose evolutionary consequences are far from being understood. Here we explore the evolutionary plasticity of the 3D chromatin remodelling in the germ line given its pivotal role in the transmission of genetic information. Using a comprehensive integrative computational analysis, we (i) reconstruct ancestral rodent genomes analyzing whole-genome sequences of 14 rodent species representatives of the major phylogroups, (ii) detect lineage-specific chromosome rearrangements and (iii) identify the dynamics of the structural and epigenetic properties of evolutionary breakpoint regions throughout mouse spermatogenesis by applying integrative computational analyses. Our results show that evolutionary breakpoint regions are devoid of programmed meiotic DSBs and meiotic cohesins in primary spermatocytes but associated with functional long-range interaction

regions and sites of DNA damage in post-meiotic cells. Moreover, we detect the presence of long-range interactions in spermatids that recapitulate ancestral chromosomal configurations. Overall, we propose a model, which integrates evolutionary genome reshuffling with DNA damage response mechanisms and the dynamic spatial genome organization of germ cells.

Abstract ID: 1565

Chromosomal rearrangement drives genomic disequilibrium in falcons

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Falcons are diverse birds of cultural and economic importance. They have undergone major lineage-specific chromosomal rearrangements, resulting in greatly-reduced chromosome counts relative to other birds. We use 10X Genomics linked reads to provide new high-contiguity genomes for two gyrfalcons, a saker falcon, a lanner falcon, three subspecies of peregrine falcons, and the common kestrel. Assisted by a transcriptome sequenced from 22 gyrfalcon tissues, we annotate these genomes for a variety of genomic features, estimate historical demography, and then investigate genomic equilibrium in the context of falcon-specific chromosomal rearrangements. We find that falcon genomes are not in AT-GC equilibrium with a bias in mutations towards higher AT content; this bias is predominantly but not exclusively driven by hypermutability of CpG sites. Small indels and large structural variants were also biased towards insertions rather than deletions. Patterns of disequilibrium were linked to chromosomal rearrangements: falcons have lost GC content in regions that have fused to larger chromosomes from microchromosomes and gained GC content in regions of macrochromosomes that have translocated to microchromosomes. Inserted bases have accumulated on regions ancestrally belonging to microchromosomes, consistent with insertion-biased gene conversion. We also find an excess of interspersed repeats on regions of microchromosomes that have fused to macrochromosomes. Our results reveal that falcon genomes are in a state of flux. They further suggest that many of the key differences between microchromosomes and macrochromosomes are driven by differences in chromosome size, and indicate a clear role for recombination and biased-gene-conversion in determining genomic equilibrium.

Abstract ID: 2284

Introgression of a large rearrangement associated with dimorphic social organization in fire ants

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Rearrangements that restrict recombination can give rise to supergenes. Supergenes typically have multiple variants, each contributing to the phenotype of a different morph that co-exists in the population. Hybridization could allow such rearrangements - and their associated phenotypes - to spread between species. Here, we study the dimorphism in social organisation and life history found in many species of *Solenopsis* fire ants: some colonies have the ancestral single-queen form of social organisation and others the derived multiple-queen form. This dimorphism is determined by two variants of a “social chromosome” supergene, where three large inversions lead to joint inheritance of alleles of hundreds of genes. To understand how the social chromosome evolved, we sequenced the genomes of haploid males carrying alternate versions of the supergene, collected from colonies from across South America. We built phylogenies from these genomes using a coalescent-based approach. We show that the supergene variant responsible for multiple-queen colonies evolved in one species and repeatedly spread to other species through introgressive hybridization. The retention of the supergene variant after introgression suggests that the costs of hybridization are outweighed by the adaptive benefits of the multiple-queen social form and by the green beard behaviour of the variant-carrying workers. This finding highlights how supergene architecture enabled a new social form to evolve in one species and recurrently permeate species boundaries.

Abstract ID: 1374

Patterns of 3D chromatin folding and their impact on evolutionary genome reshuffling

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Exploring the evolution of chromatin conformation and DNA-protein interactions is fundamental for understanding the mechanism(s) responsible for the origin and plasticity of genome architecture. Distant loci within the genome interact non-randomly during the cell cycle to affect their function (i.e. gene expression). The study of the similarities and differences of these genomic interactions between species provides fertile grounds for determining the evolutionary dynamics of genome function and, ultimately, speciation. Here I will discuss principles of 3D genome folding dynamics and evolution in basal mammals. The combination of integrative computational analyses including genome-wide chromosome conformation capture analysis (*in situ* Hi-C) in representative therian species, coupled with comparative genomics, transcriptome sequencing (RNA-seq) and chromatin immunoprecipitation sequencing (ChIP-seq) of CCCTC-binding factor (CTCF) and histone modifications is providing new interpretative hypothesis to understand genome evolution.

Abstract ID: 1136

Genome evolution in crucifers: the role of chromosomal rearrangements (?)

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The ever-increasing number of complete genome sequences, combined with a series of methodological advances in comparative genomics and cytogenomics, are providing unprecedented insights into the patterns and mechanisms driving chromosomal evolution in land plants. Improved large-scale phylogenies coupled with paleogenomic reconstructions allow us to infer ancestral genomes and the direction of chromosome and karyotype evolution. In addition, genome analyzes have revealed numerous lineage-specific whole-genome duplications (WGDs) that have had a major impact on genome complexity and chromosome evolution in plants. **Due to the sequenced Arabidopsis genome, the economic importance of *Brassica* crops and the feasibility of comparative chromosome painting, the mustard family (Crucifers, Brassicaceae) has become a plant family with the most extensive knowledge of karyotype evolution. Crucifers provide a unique insight into the general mechanisms and evolutionary trends of chromosome evolution in plants**. The evolution of crucifer genomes family-wide was characterized by more than a dozen clade-specific WGDs, followed by many descending dysploidy events that diploidized polyploid genomes. Do we know to what extent the post-polyploid chromosomal rearrangements impacted speciation? Some (ancestral) crucifer genomes remained remarkably conserved in a number of present-day species, while in some other taxa they were altered by inversions, Robertsonian-like and end-to-end translocations, nested chromosome insertions, and centromere repositioning. I will address the fact that while we have made great progress in describing the patterns and mechanisms of chromosomal evolution, we are less clear about the importance of chromosomal rearrangements in plant speciation. This work was supported by a Czech Science Foundation research grant (21-07748L).

Abstract ID: 1273

The evolutionary history and adaptive role of chromosomal inversions in Atlantic herring

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Chromosomal inversions have been increasingly linked to local adaptation in natural populations. However, it is often unclear what selective forces maintain inversions in correlation with environmental gradients or what genes within inversions contribute to local adaptation. We study four chromosomal inversions in Atlantic herring (*Clupea harengus*) that are associated with a gradient of sea water temperature. We use long-read data from homozygotes for each inversion type to accurately characterize inversion

breakpoints. With short-read whole-genome data from individuals spanning the gradient of sea water temperature, we further show that the inversions originated after the split from the sister species, Pacific herring. Despite the expectation that mutational load accumulation should govern the maintenance of inversions as balanced polymorphisms due to suppressed recombination and impaired purifying selection, we find no evidence of accumulation of deleterious mutations or strong loss of genetic diversity in either derived or ancestral haplotypes. This suggests that purifying selection has been effective throughout the evolution of these herring inversions, perhaps linked to the large effective size of herring populations. Using gene expression data from larvae reared at different temperatures and segregating alternative alleles of the longest inversion, we find the differential expression of genes in the inversion important for energy metabolism and morphological development, in line with warmer temperature promoting faster growth in herring. Our results suggest that inversion haplotypes in Atlantic herring contain alternative alleles important for temperature adaptation, resulting in the maintenance of inversion polymorphisms by divergent selection across a gradient of sea water temperature.

Abstract ID: 1464

Programmed chromosome breakage delineated by precise scission sites are rearrangement hotspots

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Programmed DNA elimination refers to the developmentally-regulated removal of DNA from somatic cells. This phenomenon has been found sparsely across distantly related eukaryotes. We previously found programmed DNA elimination in *Oscheius tipulae*, a free living nematode closely related to *Caenorhabditis elegans*. In *O. tipulae*, between 4 and 134 kilobases of germline-restricted DNA is eliminated from each end of every chromosome. New telomeres are added at the break sites. To better understand this process, we generated chromosome level assemblies of four additional *Oscheius* species. While all species eliminate DNA from all their chromosome ends, as in *O. tipulae,* some also eliminate DNA from chromosome-internal sites. These internal breaks are healed by the addition of neo-telomeres, and result in different chromosome numbers in somatic and germline cells with up to 5 somatic chromosomes derived from a single germline chromosome. The sites of cleavage and addition of new telomeric repeats are distinguished by the same short palindromic sequence motif in all five species. Some sites of chromosome cleavage have a single copy of the motif and thus only a few bases are eliminated. Other internal cleavage sites are paired and hence exclude large segments of the genome from the somatic lineage. Multiple sites of cleavage correlate with chromosomal inversions and a translocation between species showing they are rearrangement hot spots. Our work sheds light on the chromosome level consequences of programmed DNA elimination which will help understand its evolution and help disentangle its underlying mechanism.

Abstract ID: 2354

A sex chromosome inversion impacts gene expression in testes and liver in the zebra finch

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In the zebra finch, an inversion on the Z-chromosome has a significant effect on sperm traits and fitness. Males heterozygous for the inversion have the longest sperm midpieces, the highest sperm velocity, the highest fertility and the highest siring success. To understand how the inversion can affect reproductive traits, we performed transcriptomics on testis tissue at various stages of testis development for three inversion genotypes (the two homozygotes and the heterozygote). Males were sampled between 45 and 65 days after hatch and both testes and liver were sampled. Developmental stage was assessed with histology of one testis and the other was used for RNAseq. Testes were grouped into 4 stages based on histology. Across the four stages there were clear clustering patterns of differential expression, with genes involved in biosynthesis showing a decreasing trend and genes involved in sperm assembly increasing across stages. When inversion genotype was considered, 404 genes had at least one significant expression difference relating to inversion genotype, and there was an overrepresentation of genes on the Z chromosome near the predicted breakpoint. For liver tissue, there were over 400 genes with significantly different expression due to genotype. However, only eight genes were in common between liver and testes, and none of these common genes were on the Z chromosome. Thus, differences in expression due to inversion genotype for both tissues suggests that the inversion impacts a pleiotropic regulatory mechanism that likely affects other traits in addition to reproductive traits.

Abstract ID: 1039

Detecting inversions across the species range of *Littorina saxatilis* using whole genome data

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Inversions are thought to play a key role in speciation by supressing recombination between diverging populations. Several examples have shown that adaptive traits cluster on inversions, or that inversion frequencies associate with environmental differences. However, in many organisms it is unclear if inversions are geographically and taxonomically widespread. The sea snail, *Littorina saxatilis*, is one such example. Extensive study has shown a strong association between putative inversions and phenotypic differences between two ecotypes of *L. saxatilis*, but most research has focused on a single district in Sweden. Previous research has also identified these associations in Spain and the UK, but no direct evidence for these inversions exists

outside of Sweden. Using whole genome data from 106 individuals, we found most inversions to be widely dispersed with many also identified in a sister species, *L. arcana*. Some inversion arrangement frequencies were significantly different between ecotypes across the species range. Hence, these inversions may have a parallel adaptive role in *L. saxatilis*. Many inversions were also polymorphic in *L. arcana*, hinting at a possible ancient role of these inversions in local adaptation.

Abstract ID: 1175

Genetic architecture and evolution of the distyly supergene in Linum

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Supergenes are found in a wide variety of systems, yet our understanding of their origins and evolution remains incomplete. The reciprocal placement of stigmas and anthers in pin and thrum floral morphs of distylous species constitutes an iconic example of a balanced polymorphism governed by a supergene. Recent studies have shown that the *Primula* distyly *S*-locus supergene is hemizygous in thrum individuals, due to structural variation at the supergene. If hemizygosity is common to other distyly supergenes, it could have major implications for the evolution of distyly. To shed further light on this question we characterized the genetic architecture and evolution of the distyly supergene in *Linum,* a system where Darwin described distyly. We generated a chromosome-level genome assembly of the distylous species *Linum tenue* and leveraged population genomic data to identify the distyly *S*-locus supergene and describe its genetic architecture and gene content. We combined this with differential expression analyses and analyses of molecular evolutionat the *S*-locus. We show that structural variation resulting in hemizygosity and thrum-specific expression of *S*-linked genes is a major feature of the *L. tenue S*-locus, and that the dominant haplotype exhibits a signature of relaxed purifying selection. Our study demonstrates remarkable convergence in the genetic architecture of the distyly supergene across widely diverged taxa with independently derived distyly. Our chromosome-level genome assembly and detailed characterization of the distyly *S*-locus in *L. tenue* will facilitate further elucidation of convergence in molecular mechanisms and pathways underlying the different forms of flowers described by Darwin.

Abstract ID: 1742

Tracing genome evolution: from ancestral karyotypes to current genomes in three mammalian clades

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Mammals show a wide range of chromosomic diversity. Their karyotypes range from 2n=6/7 in the Indian muntjac (Ruminantia) to 2n=102 in the Viscacha rat (Rodentia). Although the mammalian genome size is round 3.5Gb, the average chromosome size is highly variable, including species with a high number of small chromosomes such as cattle (a ruminant with 2n=60 and an average chromosome size of 87Mb), and species with a low number of big chromosomes such as Tasmanian devil (a marsupial with 2n=14 and an average chromosome size of 440Mb). Identifying and timing when and where gross genomic rearrangements occurred during evolution will help to explain changes in genome structure with functional consequences that might eventually lead to speciation. Here we used DESCHRAMBLER to reconstruct eight ancestral genomes of three different lineages: Ruminantia, Marsupialia and Afrotheria. We classified the rearrangement events occurring in each lineage and identified the Evolutionary Breakpoints regions (EBRs). Cattle and elephant showed the same number of well-defined EBRs, 32, while Tasmanian devil only showed 19. Marsupials and ruminants genomes are characterised by inversions, while interchromosomal rearrangements are also important in ruminants and are the main rearrangement force in the afrotherians. Our results significantly expand knowledge of mammal genome evolution and will facilitate greater understanding of the role of chromosome rearrangements in adaptation and speciation.

Abstract ID: 1808

The effect of chromosomal inversions on gene expression

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Chromosomal inversions have often been found to have strong phenotypic effects, for example in determining life histories, in many organisms. However the quantitative importance of chromosomal rearrangements, which include inversions and translocations, is not known, because only rearrangements of known effects have been historically studied. Here we investigate the role of chromosomal rearrangements in genomewide gene expression in 10 intrapopulation crosses segregating known and de novo identified inversions. We assembled the genomes of all parental lines from long reads, identified inversions, obtained full transcriptome data from about 2000 plants (parents and F2s) and constructed genetic maps. We estimate the relative importance of chromosomal rearrangements to gene expression variation relative to other kinds of mutation, and frequently inversions are cis- as opposed to trans-acting.

Abstract ID: 1885

Weak purifying selection and recombination shape the evolution of the fire ant *Social* supergene

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Supergenes are clusters of tightly linked genes that jointly produce complex phenotypes. Although widespread in nature, how such genomic elements control complex phenotypes is in most cases unclear. In the fire ant *Solenopsis invicta* and closely related species, a '*Social'* supergene controls whether a colony maintains one or multiple queens. The *Sb* haplotype of the *Social* supergene recently evolved by sequential incorporation of three inversions, which restrict its recombination with the ancestral *SB* haplotype. Here, we show that purifying selection is extremely weak on the *Sb* haplotype, leading to an ongoing molecular degeneracy. Despite the three inversions, gene flux (recombination) between haplotypes is not entirely suppressed, potentially mitigating the expected evolutionary degeneration. We also identified some genes that are not showing traces of degeneracy, nor traces of recombination with *SB* haplotypes. These genes show strong conservation across *Sb* haplotypes, with low diversity and fixed *Sb*-restricted alleles. Such genes could be essential for the complex phenotypes associated with the *Sb* haplotype. Overall, these results provide a detailed picture of the genomic innovations involved in the formation of a supergene controlling a complex social phenotype.

Abstract ID: 2077

Investigating the role of structural variants in rapid diversification of Lake Malawi cichlids

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The cichlid fishes in the African Great Lakes are well known for their explosive speciation events resulting in a wide range of trophic adaptations and rapidly evolving radiations. Recent research has identified a hybridisation event in an ancestral species of the Lake Malawi cichlids which has promoted their adaptive radiation. It has also been shown that gene flow between the early diverging species have enabled cross species transfer of the variations assisting in adaptation and aided in the diversification. To understand further about the underlying mechanisms behind the diversification processes we focused on structural variants. They are of particular interest as these types of genomic rearrangements can affect species fitness and phenotype by rearranging regulatory regions in the genome. Chromosomal inversions are a type of structural variant which arise when a part of the chromosome breaks and re-joins in a flipped orientation with respect to the original conformation. This kind of rearrangements are thus capable of linking adaptive alleles and making the species more suitable for novel ecological niches. Utilising short and long read sequencing data we have identified several inversions across the lake Malawi radiation. The roles played by these inversion haplotypes differ among the species, where some are being selected for specific ecomorphological clades while others function as sex determining regions in some species and not in

others. Hence, analysing the genomic data allows us to identify the fundamental processes governing the evolutionary dynamics of these inversions and their contribution to the rapid diversification in Lake Malawi cichlids.

Symposium: S08. Integrative biogeography: Past, present, future (id: 25)

Abstract ID: 2482

The dispersal and diversification events to explain spatial biodiversity patterns

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Abstract: The current occurrence of species is seldom consistent with where species are formed or where they will die, this poses a major challenge to understand temporal variation of the spatial distribution of diversity. In this talk, I show how the elevational diversity gradient arises by the interaction of key processes: colonization, extirpation, speciation and extinction. I will discuss the theoretical expectations from a simulation approach and present the results of a dynamic model fitted to empirical data. Unsurprisingly, I find that removing any of those four processes limits our power to describe evolutionary patterns. I, therefore, highlight that historical biogeography methods neglect lineage extinction which compromises our accuracy in reconstruction. I will introduce a potential solution to this problem and demonstrate that by including extinction into the analysis, we can reconciliate biogeographic stories that we could previously not.

Abstract ID: 2135

A new biogeographical model to reconstruct ancestral ranges: the spatially dependent walk model

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Ancestral ranges of species are essential to understand major evolutionary processes. Hence, following evolutionary biologists' quest to understand the origin of life and the role of the biotic and abiotic factors in shaping the evolution of life, we are developing a novel framework for explicitly reconstructing ancestral distribution ranges of species. Our new Spatially Dependent Walk (SDEW) model, inspired by the previous Landscape Based Geographical (LBG) model (Bouckaert et al. 2012), assumes that range evolution is a diffusion process evolving along a phylogeny and across the geographical landscape. SDEW models the diffusion as a continuous time Markov chain (CTMC). The simplest possible SDEW model assumes that the dispersal rate is constant over time and geographical landscape. Other flavors of SDEW can relax the constant-rate assumption by allowing rates to vary across geographical landscape and time. This flexibility enables testing different hypotheses for how spatial barriers and niche dependence affect range

evolution over spatio-temporal scales. We will demonstrate the functionality of SDEW by reconstructing range evolution of Madagascan beetles.

Abstract ID: 1580

Legacy of past geo-environmental dynamic on insular phylogeny

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Species diversification is strongly influenced by the geographical and environmental contexts and how they vary through time, and this may determine how species diversity builds up at various temporal and spatial scales. Recent theoretical studies showed that simple changes in geo-environmental dynamics may leave distinct signatures in the species phylogenies. Here, we expand this approach and investigated the consequences on diversification patterns of complex geographical histories continuously affecting evolutionary processes using simulations. Specifically, we developed a model in which we focus on a dynamic oceanic archipelago, where several islands vary in size and connectivity between their emergence and submergence. Using a neutral individual-based approach, we simulated microevolutionary processes from which speciation and extinction are emergent processes, and studied corresponding phylogenies. We showed that the shape of phylogenies vary consistently with the archipelago's geo-environmental dynamics. Tree imbalance and lineage accumulation are strengthened by increasing archipelago size. We demonstrated that this is due to: (i) gene flow between islands, which varies according to the islands size, and (ii) the possibility of colonising new spaces that gives rise to evolutionary radiations. Consistently, we observed that archipelagos with larger inter-island distances generate more balanced trees and that closer archipelago decreases the speed of lineage accumulation. These results document how complex environmental changes may explain contrasted diversification patterns throughout their influence on microevolutionary processes and how this may reflect into phylogenies.

Abstract ID: 2055

"In to the tropics", coping with warm climates gave rise to the near global expansion of shrews

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Adaptation to novel environmental conditions allows species to colonize new areas. Identifying how such expansions and colonizations evolved eventually explains current distribution patterns. One of the largest mammalian families with more than 440 species, the shrews (Soricidae), while originating in Eurasia, are distributed across Africa as well as North and Central America after multiple expansion events. Recent work suggested that this wide distribution was at least partly driven by competition for resources.

However, we now document, and corroborate, a strong effect of adaptation to novel climatic conditions by the different clades of shrews. Combining information on species distribution with environmental and especially climate data on the backdrop of the current phylogeny of shrews, we retrace their biogeographic history. Our results indicate that originally cold adapted Eurasian clades were the ones to colonize the African continent during the Miocene by becoming able to cope with the warmer climate. Later, convergent warm adaptations in North American clades allowed other ancestral clades to disperse into Central America. Clearly the family of Shrews represents a prime exception to one of the major evolutionary dynamics behind the global pattern of biodiversity, the "out of the tropics" hypothesis.

Abstract ID: 1438

The drivers of global plant diversity

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Species richness varies immensely around the world. Variation in the rate of diversification (speciation minus extinction) is often hypothesized to explain this pattern, while alternative explanations invoke time or ecological carrying capacities as drivers. Focusing on seed plants, the world's most important engineers of terrestrial ecosystems, we investigated the role of diversification rate as a link between the environment and global species richness patterns. Applying structural equation modeling to a comprehensive distribution dataset and phylogenetic tree covering all ca. 332,000 seed plant species and 99.9% of the world's terrestrial surface (excluding Antarctica), we test five broad hypotheses postulating that diversification serves as a mechanistic link between species richness and climate, climatic stability, seasonality, environmental heterogeneity and the distribution of biomes, respectively. Our results show that the global patterns of species richness and diversification rate are entirely independent. Diversification rates were not highest in warm and wet climates, running counter to the Metabolic Theory of Ecology, one of the dominant explanations for global gradients in species richness. Instead, diversification rates were highest in edaphically diverse, dry areas that have experienced climate change during the Neogene. Meanwhile, we confirmed climate and environmental heterogeneity as the main drivers of species richness, but these effects did not involve diversification rates as a mechanistic link, calling for alternative explanations. We conclude that high species richness is likely driven by the antiquity of wet-tropical areas (supporting the "tropical conservatism hypothesis") or the high ecological carrying capacity of warm, wet and/or environmentally heterogeneous environments.

Abstract ID: 2265

Diversity dynamics in birds of New World

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Three prominent explanations have been proposed to explain the dramatic differences in species richness across regions and elevations, (1) time for speciation, (2) diversification rates, and (3) ecological limits. But the relative importance of these explanations and, especially, their interplay and possible synthesis remain largely elusive. Integrating diversification analyses, null models, and GIS, I study avian richness across regions and elevations of the New World. My results reveal that even though the three explanations are differentially important (with ecological limits playing the dominant role), each contributes uniquely to the formation of richness gradients. Further, my results reveal the likely interplay between the explanations. They indicate that ecological limits hinder the diversification process, such that the accumulation of species within a region gradually slows down over time. Yet, it does not seem to converge toward a hard ceiling on regional richness. Instead, species-rich regions show suppressed, but continued, diversification, coupled with signatures of possible competition (esp. Neotropical lowlands). Conversely, species-poor, newly-colonized regions show fast diversification and weak to no signs of competition (esp. Nearctic highlands). These results held across five families of birds, across grid cells, biomes, and elevations. Together, my findings begin to illuminate the rich, yet highly consistent, interplay of the mechanisms that together shape richness gradients in the New World, including the most species-rich biodiversity hotspots on the planet, the Andes and the Amazon.

Abstract ID: 1930

Evaluating parameter impact on temporal calibration of Macroscelidea phylogenies

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To infer a taxon's biogeographic past, accurate temporal estimates are pivotal. For this, fossils are utilized to date multiple nodes across a phylogeny and thereby infer a timeline of evolution. However, due to the usually incomplete, ambiguous or absent fossil record and limitations of available data, parameters to time-calibrate phylogenies vary across different taxa and/or publications. These parameters are, among others, the type of DNA, the number of outgroups included and the number of fossil calibration points. We here generate a full-species phylogeny of sengis (order Macroscelidea) from nuclear and mitochondrial data and evaluate the impact of those parameters on the temporal estimates of sengi evolution. We show that, even after correcting for substitution saturation, the utilization of mitochondrial DNA results in much older ages than using only nuclear DNA. If outgroups and thus multiple fossil calibration points are included, the age of the sengi crown-fossil prior has basically no impact on the estimated time frame of evolution. Specific branch lengths mainly depend on the type of DNA (nuclear/mitochondrial) used. The number of outgroups included and the

outgroup/ingroup ratio has a major effect on the outcome of time-calibration. Although working on a specific group of mammals, this study demonstrates how commonly varied parameters in temporal calibration of phylogenies impact the outcome of the respective dating and thus the biogeographic interpretation of a taxon's past. Dated phylogenies (and subsequent biogeographic inferences) should be therefore seen in the context of the data set which was used to produce them.

Abstract ID: 1557

Do the species with large geographic range diversify faster?

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Range size is a universal characteristic of every biological species, and is often assumed to determine diversification rate. However, the relationship between range size and past and future diversification of species remains elusive. On one hand, there are strong theoretical arguments that large-ranged species should have higher rates of diversification. This theoretical view is challenged by observations that small-ranged species are often phylogenetically clustered and form spatially localized hotspots, claimed to be the cradles of biodiversity. The research of range-size evolution is a notoriously complex task, because the range sizes evolve not only anagenetically (range expansion or contraction), but also cladogenenetically (range size change between mother and daughter species during speciation). Here use a state-dependent diversification model covering both anagenetic and cladogenetic changes in range size, and apply it to the phylogeny and range size data of mammals. We show that in general, large-ranged species diversify faster, as theoretically expected, and that the phylogenetic clusters of small-ranged species reflect past fragmentation of large-ranged species, rather than ongoing radiations. However, the analysis of residual (concealed) variability of our models suggests that there are multiple mammalian taxa where this general pattern is reverted and small-ranged species indeed diversify faster. According to the ancestral state reconstructions, these ongoing radiations of small-ranged species typically take place in constantly insular landscapes, such as oceanic archipelagos. Our results suggest that, while range size is an important factor influencing species diversification, its effect in real-world systems is often locally modified or even inverted by idiosyncratic geographic setups.

Abstract ID: 2269

Can species trait-based models of contemporary range shifts be rescued?

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As the climate changes rapidly over contemporary timescales, many species are undergoing shifts in geographic range and distribution. Although there is a general trend toward poleward and upslope shifts in terrestrial systems, there is still considerable

variation in the magnitude and even direction of these range shifts. Because the consequences of these range shifts for biodiversity conservation, ecosystem function, and impacts on human society have outsized importance, much research effort has been devoted to understanding and forecasting range shift responses to climate change and other anthropogenic stressors. Trait-based approaches have received an especially large amount of attention, yet a number of recent syntheses have concluded that species traits are only modest predictors of range shifts. As trait values can vary over space and time, the incorporation of trait variation into analyses of range shifts could provide a route to improved explanatory power of trait-based models. We address this possibility using data from a long-term monitoring scheme of butterflies in North America in conjunction with a newly developed dataset of butterfly thermal physiological traits. We explore how physiological trait means, trait plasticity, and evolutionary potential are related to the magnitude and direction of butterfly range shifts, with a particular focus on how these traits might shape responses at leading versus lagging range edges. Our results suggest that integrating such population-level processes into trait-based analyses of range shifts might improve the explanatory power of these models.

Abstract ID: 1185

Range shifts of birds and moths, but not butterflies, are driven by width the of their thermal niche

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Species are altering their ranges as a response to climate change. However, the magnitude and direction of observed range shifts vary considerably between species. An ability to disperse and colonize new areas plays a crucial role in determining which species will thrive and which decline as climate change progresses. Recent studies have indicated that species' attributes describing their climatic niches and flexibility could provide a key for understanding responses to climate change. Long-term evolution to past conditions in climate may have shaped the scale of conditions suitable to specific species which could thus shape how they respond today. Species with broader niches could more readily *adapt in place* while species with narrow tolerances can only survive if they are able to *shift in space*. Based on the realized changes in northern range edges of 312 bird, butterfly, and moth species across a boreal latitudinal gradient over 20 years, we examined whether species range shifts are explained by their niche plasticity and find that moths and birds, but not butterflies, occupying a narrower thermal niche across their European distribution show stronger shifts towards the north. This pattern was especially prevalent among species occurring in warmer conditions on average. As this was largely

consistent among both moths and birds it points to similar drivers among various taxa, which are likely connected to thermal niche mean and breadth.

Abstract ID: 1649

The role of traits in biogeographic long-distance dispersal

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Species' traits are assumed to determine the success of dispersal and establishment to far-away locations. Yet we still know little about which traits facilitate species' biogeographic movements, and whether their importance varies between clades. Here, we tackle these questions by investigating the role of traits (body size and life-history strategy) in the biogeographic history of 55 tetrapod clades (covering reptiles, birds, amphibians and mammals). For each clade, we first identify independent body size and life-history trait axes across species, with phylogenetic factor analyses. Then we test how these traits relate to past dispersal success using trait-dependent biogeographic models. We find that for most clades (75%), traits are related to past dispersal success. In general, biogeographic movements were favored by big-bodied species (in ca. 50% of all clades), but for some clades, movement was favoured by small or intermediate body sizes. Interestingly, life histories affected dispersal in different ways between clades; in some clades fast life histories were related to biogeographic dispersal, while it was slow or extreme life histories in other clades. We show how body size and life history strategies have influenced the biogeographic history of many tetrapods, which invites new key questions: Why are some traits more important in some clades than in others? What is the role of clade geography (oceanic vs. continental dispersal), functional diversity, or ecological niche? Better understanding the role of traits in long-distance dispersal is essential to improve our knowledge of historical biogeography, community assembly processes, and predictions of species' future movements.

Abstract ID: 1325

Historical biogeography of personality traits in an amphibian

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We investigated for the first time whether the biogeographic history of populations, a major driver of eco-evolutionary processes, could influence spatial patterns in personality traits. We hypothesized that, if individual variation in personality reflects variation in the capacity to cope with the new demographic and/or environmental conditions encountered during a range expansion, a spatial structure in personality traits might emerge along the range of a historically expanded population. These questions were addressed using the

Tyrrhenian tree frog, *Hyla sarda*, as study species. This species underwent a range expansion from northern Sardinia (source) up to Corsica (newly founded) during the Late Pleistocene, and then the two populations became geographically isolated, thus preventing gene flow between the two islands. We sampled in two geographic areas per island along the expansion route, controlling for altitude, local habitat effects, demographic factors and bioclimatic differences between geographic areas and across time epochs. Then, we studied the spatial differentiation of two personality traits, measuring at the same time also two performance traits likely involved in the dispersal process, jumping acceleration at take-off and stickiness. Individuals from Corsica were overall more prudent (longer latency to exit from a shelter) and less active in a novel environment, and also displayed a stronger take-off and adhesion force compared to individuals from Sardinia. These results suggest that population differentiation in multiple traits associations including personality and performance might be an overlooked legacy of past biogeographic processes, opening intriguing evolutionary scenarios on the genetic and phenotypic architecture of animal populations.

Abstract ID: 2156

Better models for understanding patterns of range size across latitude

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The relationship between latitude and geographic range size is a central part of some theories of global biodiversity: for example, proponents of Rapoport's rule have explained high tropical diversity as a consequence of narrow ranges in the tropics. However, the linear models commonly used to study latitudinal trends in range size are inappropriate: regressing range size against latitudinal midpoint violates basic assumptions of regression, is demonstrably vulnerable to false positives, and frequently yields counterintuitive results. Here I develop a family of models specifying the probability of range sizes given latitudinal midpoints, where probability depends on the placement of species ranges relative to a set of latitudinal barriers. This family of models includes both reasonable null models and substantive biological hypotheses about barriers to dispersal, and can be directly compared with linear models using likelihoods. Using public occurrence databases and published datasets of the latitudinal ranges of marine organisms, I find these new models consistently yield higher likelihood than linear models. Moreover, data simulated with these models replicate two other features seen in empirical datasets: mid-latitude clustering of range limits, and plateau-shaped latitudinal diversity gradients. The success of models based on barriers to dispersal suggests the importance of continental configurations in explaining global trends in diversity and range size. Future insights into the processes governing these trends will likely come from modeling range evolution on empirical geographies and from using fossil data to test predictions at times in earth history when continental configurations have been different.

Abstract ID: 2458

Adaptive evolution reduces population-level resilience to climate change and generates geographic mosaics of climatic stress far from species' range limits

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Studies in birds and trees have shown climatic stresses distributed across species' ranges, not only at range limits. The butterfly Euphydryas editha reveals mechanisms that generate this type of pattern: geographic mosaics of natural selection, acting on tradeoffs between climate adaptation and fitness traits, cause some range-central populations to evolve to limits of climatic tolerance, while others remain resilient to changing climate. In one metapopulation, natural selection for avoidance of incidental mortality from grazers drove past evolution of positive geotaxis, with eggs placed near the hot ground where they risked exceeding their thermal tolerances. Oviposition behavior has evolved rapidly since the 1980s to increase egg heights above the ground, mitigating effects of warming at the cost of additional mortality from grazers. However, density-dependence from intraspecific competition is stabilizing and in 2022 the metapopulation persists at high density. In a second metapopulation of a different, endangered ecotype, past natural selection on fecundity drove evolution to the climate-sensitive phenological limit of ability to complete development within the lifespans of ephemeral hosts, causing routinely high density-independent mortality from insect/host phenological asynchrony. This evolutionary response to the trade-off between maternal fecundity and offspring mortality rendered climatic variability the main driver of dynamics, and increases in this variability, associated with climate change, were a key factor behind permanent extinction of a protected metapopulation.

Abstract ID: 1721

The case for prioritizing ecology/behavior over genomics/taxonomy in conservation assessments

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Climate change is driving species' losses both locally and globally as shifts in geographic placement of climate space interacts with land-use change. Climate change also increases potential for hybridization when climate-driven range shifts bring about partial sympatry between formerly allopatric species, subspecies or ecotypes. These impacts of climate change breathe new life into longstanding debates about species concepts and use of genetic or phenetic critieria to identify and prioritize entities for conservation. Adaptation options include habitat restoration, reintroductions and assisted colonization, but these are costly and time consuming, necessitating careful prioritization. Here we use the extensive ecotypic variation within an ecologically complex species, the butterfly *Euphydryas editha,* to illustrate a case in which sourcing individuals for reintroduction *to extinct sites* or translocation *to novel sites* should not rely on subspecies identity or genomic similarity to historic reference populations. In *E. editha,* host and habitat preferences evolve so rapidly that even genetically-close populations may differ sufficiently to doom restoration efforts. Conversely, introductions from distantly-related, ecologically similar populations may succeed. In addition, past work on this species also shows how hidden variation can emerge in

novel environments, thereby facilitating rapid evolution to altered conditions. Finally, we conclude that climate-change caused hybridizations among populations classified as different subspecies, far from being problemaic, may be essential for retaining necessary within-species genetic diversity to allow natural re-emergence of extinct ecotypes if climate change were eventually reversed and stabilized.

Abstract ID: 1952

A global database of genetic diversity (GenDivRange) and a test of the central-marginal hypothesis

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The distribution of genetic diversity across species range provides key insights to ecological, evolutionary, demographic, and biogeographic processes. Based on population genetic theory, one of the simplest predictions about the spatial distribution of genetic diversity is that populations at the center of their distribution range, where population size is large, harbor more diversity than populations at the edge, where population size is small and populations are isolated. This expectation is also commonly known as the central-marginal hypothesis (CMH). However, empirical research has been lacking consensus about the generality of the CMH. Here we develop a novel database, GenDivRange, that integrates some of the essential data to empirically test predictions of evolutionary theory. GenDivRange contains geo-referenced genetic diversity data for >13,000 populations and species distributions for >800 species across taxa and habitats around the globe. GenDivRange is presented as an R Shiny application, which allows for efficient search and visualization. In this talk, we will present the database as well as a test of the CMH. Although we found that more species had a negative relationship between genetic diversity and distance from the center of their distribution, the evidence for the validity of the CMH is not overwhelming. We explore the effect of data quality and sampling strategy, as well as organisms' dispersal capacity on the validity of the CMH. Beyond evolutionary research, GenDivRange could become a tool to inform natural conservation and management decisions in the times of biodiversity loss and changing climate.

Abstract ID: 1934

Demography, selection and polyploidization shape geographic mosaics of plant-pollinator coevolution

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The diversity of interacting species is shaped by coevolution. The strength of a coevolutionary relationship is rarely homogenous across the distribution of species interaction. Such geographic mosaics of coevolution are generated through variation in the degree of gene-flow among populations, the strength of local adaptation, and genomic events such as polyploidization that remix the distribution of traits across populations. Among the most diverse forms of species interaction are those between plants and pollinators. Here, we aim at disentangling the relative role of demography, selection and polyploidization in creating geographic mosaics of coevolution in the interaction between *Lithophragma* plants and *Greya* moths. This interaction has persisted for millions of years as the plants and moths have diversified. Using whole genome resequencing of seven diploid, six tetraploid and four hexaploid populations of *L. bolanderi*, we observed patterns consistent with isolation by distance model of population genetic structure. Analysis of demographic history allowed us to investigate regions of the genome that are significantly differentiated against a neutral background, thereby detecting potential candidate regions of selection underlying population divergence due to interaction with the pollinator. We finally analyzed mix-ploidy populations and the role of genome-wide duplications in creating geographic mosaics of coevolution. We used whole genome sequencing of four individuals of *L. glabrum*, a species previously suggested as contributing to polyploidization in *L. bolanderi*. The genetic clustering showed a complex population history for these polyploid populations which have likely arisen through a set of independent events of autopolyploidizations in *L. bolanderi* rather than allopolyploidization.

Abstract ID: 1211

Climate-mediated demographic changes and range shifts in a cold-adapted butterfly

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Cold-adapted species escape climate warming by latitudinal and/or altitudinal range shifts, especially along ‘sky islands’ in isolated mountain ranges of Southern Europe. The Apollo butterfly typically occurs in such sky island refuges, but the lack of information on population genetic features and climatic niche makes it difficult to predict the response of this species to climate change. We studied the genetic structure and demographic history of populations in France using single nucleotide polymorphisms and reveal six main genetic groups: two in Massif Central (Auvergne, Ardeche/Cevennes), one in the Pyrenees, and three in the Alps (Jura/North Alps, Chartreuse, South-Alps). Paleogeographic distribution based on species distribution models (SDMs), and effective population size, show that the last interglacial (LIG) was highly unfavorable for Apollo that probably survived in small refuges on the highest summits of Massif Central. The population shifted downslope and expanded south and eastward between LIG and LGM throughout the large climatically suitable Rhône valley between glaciated summits. The Massif Central, Pyrenees and Alps populations started diverging before the LGM but

remained largely connected until mid-Holocene. Population decline in Massif Central and Pyrenees was more gradual but stronger than in the Alps, where weak genetic structure suggests a non-equilibrium metapopulation functioning. The core Apollo population experienced contraction-expansion cycles in response to late Pleistocene climate fluctuations with inter-connected populations overtime according to a 'metapopulation-pulsar' functioning. This study demonstrates the powerful combination of population genomics and SDMs to determine past and future evolutionary trajectories of endangered species under climate change.

Abstract ID: 1263

New insights into Madagascar biogeography through a Hyb-Seq phylogeny of *Helichrysum* (Compositae)

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Madagascar's biota shows a distinct pattern of evolution in long-term isolation. It is widely agreed that both vicariance and long-distance dispersal contributed to today's Malagasy flora, renowned for its exceptionally high level of species endemism. However, the relative contribution of *in situ* diversification vs colonization and vicariance is yet unknown. Unraveling the historical biogeography of the Malagasy biota requires integrating phylogenetic and geographical data with highly resolved phylogenies including an extensive taxon sampling. Previous studies suggest that most Malagasy plant endemics originated during the Cenozoic through long-distance dispersal from Africa. To test this hypothesis, the genus *Helichrysum* is a promising group, since it represents one fifth of the Compositae species of the island with a high proportion of endemism occupying diverse habitats. We obtained a comprehensive dataset of 344 species (~ 50% of genus diversity) and applied a HybSeq approach (which targets 1061 nuclear loci and also yields full plastome sequences). Our ancestral range estimations confirm that *Helichrysum* originated in the arid Southern Africa and reveal several dispersal events to Madagascar, other African regions and Eurasia. Colonization of Madagascar from different African regions and climates occurred multiple times.

Dispersal events during the Miocene and Pliocene might be favored by the emergence of a land connection between Africa and Madagascar, Quaternary/Pleistocene glacial cycles, and changes in direction of wind currents. This multifactorial scenario laid the grounds for the evolution of the current extraordinary Malagasy biodiversity.

Abstract ID: 1196

Population genomics reconstruct complex histories of colonization across archipelagos by lizards

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Quaternary climatic fluctuations have shaped biogeographical patterns across species ranges. There is increasing evidence for glaciation-induced expansion in Mediterranean species, including the colonization of islands during major drops of the sea level. However, our understanding of the origin of island populations is repeatedly challenged by human-aided introductions. Here we aim at disentangling the native *versus* non-native status of island populations of the Italian wall lizard, *Podarcis siculus*, across four Mediterranean archipelagos: Tuscan (Central Italy), Dalmatian (Croatia), and Aegadian and Aeolian (Sicily) islands. We combine demographic reconstructions to infer divergence time and introduction modalities using genome-wide SNPs, and landscape resistance maps to estimate the probability of natural colonization of islands based on seal level at the times of introduction and the cost of land and overseas dispersal. The four geographical areas are highly differentiated and most islands show geographic structuring. Divergence dates between islands and their source relatives showed strong variation, ranging between 1 and 220 kya. Old splitting events are generally accompanied by lower genetic diversities in islands as compared to mainland and a high probability of natural colonization. On the contrary, recent introductions are often associated with ongoing gene flow that influences current genetic diversity. The current distribution of *P. siculus* across Mediterranean islands is the result of both natural range expansion due to higher availability of habitats during glacial periods and human-aided introductions in islands isolated by large sea channels. Our results highlight the powerful combination of population genetics and landscape ecology approaches to better understand biogeographic patterns.

Abstract ID: 1174

Pleistocene glaciations facilitate genetic divergence and evolution of Himalayan Ibex in India.

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Siberian Ibex is widely distributed across the highlands of the Central Asia, and in India, the distribution is restricted to trans-Himalayan region. Study on Himalayan ibex especially on genetic make-up is very finite. Pleistocene glaciations had a complex impact on the spatial distribution and genetic constitution of species in temperate ecosystems and a few studies exhibited the impact of large geo-climatic events on the species distribution, genetic makeup and structure in Asian highlands. We integrated phylogenomics and paleo-geoclimatic modelling to understand the evolution and origin of Himalayan Ibex in the Indian Himalayan region. Briefly, we analysed genomes from each ibex species i.e. Alpine ibex (*Capra ibex*), Siberian ibex (*Capra sibirica*), Iberian ibex (*Capra pyrenaica*), Nubian ibex (*Capra nubiana*) and bezoar (*Capra aegagrus*) along with genomes of Siberian ibex collected from Indian trans-Himalayan Region. We observed divergence of Himalayan ibex from the main range around 0.1mya following Pleistocene species pump concept, and its independent evolution as an allopatric refugium that coincides to the mid-late Pleistocene transitions. Further, the comparison of paleo-geoclimatic model with the present model suggests that the north and south of Pamir Mountains which support contiguous distribution of Siberian Ibex have experienced significant topographic metamorphosis over time which likely caused disjunction of Himalayan ibex. We suggest revision of taxonomic status of Himalayan Ibex as an evolutionary distinct phylogenetic species for prioritization in synchronised conservation and management.

Abstract ID: 1806

Using phylogenetic and geographic information to predict future *Agrilus* host ranges

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Vicariance events have separated insect species and their tree hosts into distinct co-evolving ecosystems across the globe. Now human translocations (e.g., through the transport of timber) can move pests between these ecosystems, as an inadvertent eco-evolutionary experiment. We have modelled the influence of evolutionary history and geographic proximity in an attempt to predict the vulnerability of plants to an invasive insect group, *Agrilus* (Coleoptera: Buprestidae). *Agrilus* is an extremely species-rich genus of plant-feeding jewel beetles, distributed all around the world. Unfortunately, some of these beetles have been accidentally introduced to new areas where they have proved devastating to novel hosts. Most notoriously, the Asian-native Emerald Ash Borer has now killed millions of ash trees in North America after its arrival over two decades ago. Here, we aim to assess the susceptibility of oaks (*Quercus* spp.), the most common host genus of *Agrilus* beetles and a taxon of great ecological, cultural and economic importance. We have evidence that there is a significant effect of both phylogenetics and spatial proximity in determining which oak species are known *Agrilus* hosts, and can use this information to predict the consequences of potential future introductions of *Agrilus* species into novel geographical ranges.

Abstract ID: 1790

Evaluating the past, present and future effects of climate change on a steppe-specialist raptor

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Climate change is rapidly altering local environmental conditions. To mitigate climate change effects, we need to understand how species have coped with past environmental changes, and incorporate knowledge on the neutral and adaptive forces governing present population dynamics. Assessing the potential impacts of climate change is especially important for species expected to be most affected by rapid environmental changes, such as habitat specialists and rare or endangered species. We integrated

landscape genomics, demographic analyses and ecological modelling to evaluate the effects of environmental change on past, present and future population dynamics of a migratory steppe-specialist raptor, the lesser kestrel (*Falco naumanni*). Despite low genetic differentiation, we identified two main genetic clusters, corresponding to European and Asian populations. These lineages diverged during the Last Glacial Period (LGP), coinciding with the onset of a four-fold population decline and an overall decrease in suitable breeding areas. Using genotype-environment association (GEA) analyses, we identified 65 variants associated with bioclimatic variables in candidate genes for local adaptation. These variants were used to derive metrics of potential maladaptation with and without considering dispersal. Combining this approach with species distribution models projected into the future, we show that Asian populations, and in particular populations at the contact zone, are at higher risk of maladaptation, suitable area reduction, increased migratory distance and hence extinction. Integrating assessments of maladaptation with demographic analysis and species distribution models improves our understanding of species responses to climate change and informs conservation efforts.

Abstract ID: 2267

Bucking the trend of pollinator decline? The genomic signatures of a bumblebee range expansion.

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World-wide, declines in many taxa are well documented. Insect pollinators are a particularly high profile group where decreases in abundance are the cause of significant concern. However, there are notable counter examples of pollinator species that are not declining but instead either shifting, or even expanding, from their original ranges. Understanding the factors underpinning the resilience of some lineages in comparison to others is important as it can inform us of the selective factors that may be driving changes in abundance and distribution. We here discuss data from recently published studies of *Bombus hypnorum*, a bumblebee pollinator species that has recently significantly and rapidly expanded west and north of its existing European range. While useful, these studies considered the genetic signatures, and from there inferred the potential patterns of this expansion, from samples covering a limited geographic distribution and/or with restricted genetic data-sets. A subsequent study that we have very recently completed includes a much wider geographic sampling distribution and whole genome population data. Collectively, our results give insights into the characteristics of this range expansion and the genomic signatures that may have been important in enabling this expansion.

Abstract ID: 1316

Evidence of serial depletion within the Baltic herring industry since the Viking Age

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Marine resource consumption has been a key component in European diet and culture since the Middle Ages, when fish consumption increased dramatically. Yet, the early origins of marine industries and the long-term ecological consequences of historical and contemporary fisheries remain debated. The Baltic Sea was home to the first “industrial” fishery ~800 years ago targeting the Baltic herring, a commercial species that is still economically and culturally important in the region today. We use ancient DNA to identify the first known long-distance trade in the region, illustrating that long-distance marine resource trade in the Baltic began during the Viking Age, much earlier than previously believed. We model past demography for four herring stocks within the Baltic to address impacts from fisheries in the region over time, illustrating demographic independence of Baltic herring stocks. Moreover, we associate these divergent demographic histories with changing patterns of exploitation, climatic impacts and interspecies dynamics, finding a pattern that is most consistent with serial depletion of Baltic herring stocks over the course of the last 1200 years. Our observations indicate that herring exploitation at both historical and recent intensities has not been and is not sustainable in the long term.

Abstract ID: 1451

History of introduction and adaptation of a malaria parasite in South America

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Plasmodium falciparum, malaria most virulent agent, is spread across Africa, Asia, Oceania, and South America. Native to Africa, it followed humans during their migrations. It was introduced twice independently into South America during transatlantic trade between the 16th and the 19th century. During its introduction, *P. falciparum* had to adapt to new environmental conditions, in particular new human populations and new mosquito species. What were the specifics of invasion history? Were the two introductions independent or from the same source? How did selection shape the *Plasmodium* genome during the colonization process? Which genes played a role in this adaptation? Have populations from different introductions adapted in the same way? We analyzed genomic variation from 1,095 isolates from the four distinct continents where it is present today. Using population genetic analyses, we analyzed the population genetic structure and demographic history of the parasite in South America. We confirm South American populations originated from Africa with at least two independent introductions. Using genome scan analyses, we looked for traces of ancient and recent positive selection along the genome of South American populations. We detected positive selection signals on genes involved in host cell interaction and resistance against malaria treatment. Among these genes, some bear traces of local adaptation while others result from adaptive introgression. Although many questions remain concerning the adaptation of *P. falciparum* to South America, functional analyses at the

scale of the parasite and host are required to further our understanding of the adaptive processes involved in this successful colonization.

Abstract ID: 1931

Parasites of isolated seal populations: patterns in species and genetic diversity

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Environmental disruption often results in profound changes in host–parasite associations. The relatively recent history of ringed seal colonization of the Baltic Sea and Fennoscandian lakes gives us a unique opportunity to study how, in a short evolutionary time, geographic isolation and shifts from marine to freshwater realms influenced the fate of various seal parasites. In the present study, we compared the species diversity and phylogeographic patterns of seal parasites with contrasting dispersal capability. Genetic diversity of permanent ectoparasites, seal louse *Echinophthirius horridus*, was closely related to the population size and genetic diversity of the host, and population genetic structure reflected barriers to host mobility. In the case of acanthocephalan worms, a gradient in species diversity was observed from four genetic lineages in the Arctic, through three in the Baltic, two in Lake Ladoga, to only one in Lake Saimaa. Also in these trophically transmitted parasites, a loss of intra-species variability and geographic structuring was observed, but not as tightly coupled to the host pattern as was the case with lice. These results demonstrate how the incorporation of population genomic data of parasites can complement our understanding of the historical processes that have acted to structure biodiversity.

Abstract ID: 1147

Genetic and distribution modeling to infer drivers shaping genetic diversity of Ixodes ricinus

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Species may respond to climate change by shifting their geographic distribution to track the changing environmental conditions. However, the impact of such changes is fluctuating as it is shaped by changes in bioclimatic conditions encountered at the different time steps investigated. We used species distribution models (SDMs) to model the distribution of the tick *Ixodes ricinus* during contemporary climate conditions and the Last Glacial Maximum (LGM). We present an approach that tackle genetic variation and evolutionary potential of the species by incorporating the genetic structure into SDMs to better reflect the geographical range of the two Northern and Southern genetic clusters

identified. Regressive and correlative methods were applied between allele frequencies and both the present vs. the shifts (since the LGM) in habitat suitability conditions. We used this approach to test the hypothesis that shifts in the species' current genetic structure are a consequence of changes in habitat suitability since the LGM, and to identify candidate loci under selection. The results show a significant variation in allele frequencies and loci under selection in response to the shifts in habitat suitability since the LGM, especially in the Northern genetic cluster. Because most of those loci were significantly related to both bioclimatic variables and changes in the overall bioclimatic niche, different selective forces would produce evolutionary variation within the species. Acknowledging this differential selection is of importance to forecast the future dynamics of species, especially so for vector-borne species like *I. ricinus*, which can carry diseases of potential threat for human health.

Abstract ID: 2014

Contrasting patterns of evolutionary diversity in migratory bird species under morphological stasis

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The comparative investigation of species complexes with wide distributions in different biogeographic realms is a promising approach to identify regional drivers of diversification and Using genome-wide data, we found contrasting diversification patterns in two bird sister species: very shallow genetic differentiation across the Holarctic sand martin *Riparia riparia* while Asian pale sand martin *Riparia diluta* represents a monomorphic species complex. Demographic inferences indicate distinct regional impacts of past climate change on evolutionary history of the two sister species. More consistent demographic change was revealed in *R. riparia* : range expansion probably with Europe as a center of origin was indicated by long-lasting increase during the Late Pleistocene. Contrary, *R. d. fohkienensis* of subtropical China showed rather constant past effective population sizes, whereas on the Qinghai-Tibetan plateau might have recently expanded to the north leading to a secondary contact zone with Central Asian *R. d. diluta* in Mongolia. Signs of only limited admixture between the two might be a consequence of different migration strategies with selection against hybrids potentially showing intermediate migration routes. Meanwhile, different phenologies might act as prezygotic isolation factors among *R. d. tibetana* and *R. d. fohkienensis* at the edge of

the Qinghai-Tibetan plateau. While the regionally heterogeneous climate during the late Pleistocene in Asia might have fostered initial population diversification, contrasting migration behavior could be an important factor in maintaining the resulting evolutionary diversity under morphological stasis in the pale sand martin.

Symposium: S09. Parallel and repeated evolution in adaptive radiation (id: 16)

Abstract ID: 1125

The role of gene exchange in parallel rapid adaptive radiations

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When provided with ecological opportunity, some lineages undergo adaptive radiation. However, the propensity to radiate differs profoundly among lineages. While most lineages speciate at a very slow pace, some lineages radiate repeatedly giving rise to similar ecomorphs in each radiation. For example, one lineage of cichlid fishes radiated repeatedly in each major lake of the Lake Victoria region in just 150,000 years. In each radiation, it has evolved cichlids feeding on algae, zooplankton, snails, insect larvae, other fish or their fry. I will show how hybridisation facilitated the rapid radiations and the high level of parallelism. In the second part of my talk, I will focus on adaptive radiations of South American butterflies that show high parallelism in wing colour patterns warning predators of their toxicity. Again, I find an important role of gene exchange in the highly similar warning colours of different species. In summary, I show that gene exchange and admixture can both fuel rapid radiations and increase parallelism in adaptive radiations.

Abstract ID: 1091

Convergent evolution of seasonal plasticity in a radiation of African *Bicyclus* butterflies

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Phenotypic plasticity in life strategy and morphology has evolved in many taxa as adaptation to seasonal habitats, where ecological threats and opportunities fluctuate throughout the year. Plasticity has enabled species to occupy new niches, and is an important contributor to species diversification. Laboratory studies have revealed genetic and developmental cascades regulating plasticity, from sensing environmental cues to producing distinct seasonal phenotypes. However, we lack important information on how these mechanisms evolve under natural conditions, whether repeated evolution of plasticity proceeds via convergent genetic routes, and what ecological factors drive the evolution of plasticity in the wild.
Here, we apply a phylogenomic approach to a classic model of plasticity, African *Bicyclus* butterflies. Species have independently evolved plasticity in reproductive strategy and wing pattern upon repeated invasions of seasonal savannahs from rainforests. The origin of these savannahs 8-10 MYA coincided with a diversification burst in this genus. We exploit a new high-quality phylogeny and sequence whole genomes of 19 *Bicyclus* species covering >18 million years of evolution, where reproductive plasticity has evolved independently at least 4 times.
First, we test whether repeated transitions to plasticity produce convergent changes in evolutionary rates, and identify evolutionary hotspots in cascades regulating plasticity. Second, we uncover ecological drivers of evolutionary transitions to plasticity by identifying climatic and habitat variables that best explain convergent genetic changes. Together, our analyses reveal to what extent repeated evolution of plasticity as a result of recurrent ecological changes has been achieved via similar genomic routes.

Abstract ID: 1251

The genomics of a great speciator provides insights into adaptations to island life

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Islands have long been recognised as natural laboratories for studying evolution, as the isolation of populations often leads to the emergence of unique and unusual forms. Repeated patterns of evolution are commonly observed across populations of island-dwelling birds; these include changes in morphology, reduced dispersal capacity, increased tameness, and a slowed pace of life. This set of repeated evolutionary changes is commonly known as the 'island syndrome'. However, whether these convergent phenotypes have the same genetic basis remains largely unexplored. Silvereyes, of the white-eye bird family Zosteropidae, show several features of the island syndrome, including an increase in body and bill size. The species is a prolific natural coloniser of southwest Pacific islands: its island populations vary in age from very recent (~100 years) to intermediate (~4000 years) and very ancient (>100 thousand years). To explore how the island syndrome unfolds at the genomic level, we have sequenced 400

silvereye whole genomes from 25 different populations. We identify loci highly associated with bill length and tarsus length. Our results suggest there may be different genetic paths to the same phenotype, indicating a rare case of incipient mutation order speciation.

Abstract ID: 1637

The origins and maintenance of polymorphisms across species radiations

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The presence of phenotypic morphs in a population is sometimes considered a precursor to speciation. Here, daughter species evolving through the fixation of different morphs and polymorphisms are expected to be lost during speciation. Despite this, a common pattern in nature is the recurrence of parallel phenotypic polymorphism in many species of a radiation. While such persistent polymorphisms are ubiquitous, there is little discussion of their evolutionary origins.
Speciation represents a barrier to the inheritance of the ancestral genetic variation underpinning polymorphisms as only a subset of the ancestral population become founders of the new species. Polymorphism recurrence across species radiations thus requires both that the genetic variation underpinning the polymorphism and the selection regime maintaining it persist through speciation. Where does that genetic variation underpinning polymorphisms originate and how does it cross speciation boundaries? Is it inherited from ancestral standing variation, reintroduced through introgression or reinvented through mutation? What selection pressures act to maintain this genetic variation in multiple members of the species radiation that may have wildly different ecologies?
Using diverse examples, I explore the characteristics of polymorphisms influencing whether their underlying genetic variation crosses speciation boundaries. I discuss how the genetic architecture and ecological context of polymorphisms are key to understanding whether polymorphisms are lost or retained during radiations.

Abstract ID: 1278

Physiological adaptation genes, not morphology, open a new perspective on adaptive radiations

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The concept of adaptive radiation has been pivotal in advancing our understanding of speciation and diversification mechanisms by uniting ecology and evolution. The emergence of a key innovation that allows a lineage to interact with the environment in a novel way, together with colonizing novel environments devoid of competitors and an

abundance of available niches, represents the kind of ecological opportunity considered the prerequisite for adaptive radiation. Besides morphological traits, key innovations could also be molecular or physiological, but this has rarely been examined. We combined genome-wide search for adaptive genes with environmental niche modelling to determine the evolutionary processes responsible for the diversification of a monophyletic assemblage of twelve morphologically conserved *Ptychadena* frog species in the Ethiopian Highlands. After a single colonization event and subsequent diversification, these species today occupy a diversity of habitats at different elevations. Using whole genome sequencing and niche identity tests we reconstructed the pattern of ecological diversification and tested whether diversification was accompanied by niche divergence and genomic adaptation, hypothesizing that evolution of physiological key innovations (metabolic changes, resistance to UV radiation, hypoxia, cold,…) facilitated the colonization of the highlands leading to ecological opportunities and diversification. We found that biological pathways and functions predominantly associated with physiological adaptation to changes in elevation, vegetation, temperature, precipitation had been the target of strong positive selection. The number of selected genes differs significantly among lineages and is related to the extent of niche divergence and harshness of the environment in terms of elevation, water household and temperature.

Abstract ID: 1370

Different ecomorphs affect the species response to ecological release in island red devil spiders

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Ecological release is defined as the expansion of range, habitat and/or resource usage by an organism following colonisation of a new region. This phenomenon is ubiquitous in oceanic islands, where colonising species whose ancestors evolved in highly competitive environments experiment relaxed selection as a result of reduced species richness. In addition, factors other than competition levels may also be involved in the species' ability to expand their niche. Ecological specialisation, for instance, has been frequently considered as an evolutionary dead end, preventing the reversal to a more generalist state even under relaxed competition.
To evaluate the relative contribution of ecological release, here we integrate geometric morphometric methods, stable isotope analyses and species distribution models. Specifically, we investigate the implications of different cheliceral morphotypes in three species of red devil spiders (genus *Dysdera*) in the Canary Islands that colonized younger depauperate islands from older and species-rich sources. These morphotypes, which they evolved convergently multiple times during the diversification of the group, are associated with different trophic specialization levels.
Our results revealed a strong influence of cheliceral types on predicting the magnitude and direction of the ecological release in the three species when colonizing low competitive islands. Interestingly, species with morphotypes associated to a more specialist diet, tend to expand the trophic niche, increase their range and change their phenotype, contrary to the ecological release expected by the colonization of more generalist species.

Abstract ID: 2231

Shared genomic targets of selection in repeated adaptive divergences of sympatric salmonid ecotypes

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Arctic charr (*Salvelinus alpinus*) is a salmonid fish that is renowned for repeated cases of parallel sympatric divergence into phenotypically and genetically distinct ecomorphs. This has occurred in numerous freshwater lakes across the northern hemisphere. Despite being a model for adaptive divergences and ecological speciation, the genetic components under selection in these parallel ecomorph divergences have not been inferred, nor the extent to which they are shared. The genetic underpinnings of these evolutionary events remain an open question. To examine this, we sequenced the whole genomes of six populations of Arctic charr including five benthic-pelagic pairs, representing independent sympatric divergences. We recovered a robust set of shared genes under selection in all replicates; these have functional roles in other organisms and lie in genomic regions of known ecologically relevant quantitative trait loci (QTL) for salmonids. A large proportion of variation was population-specific, reflecting that the ecomorphological parallelism occurs despite differing genetic histories and patterns within lakes. There were no coding region substitutions in these shared genes under selection but abundant variation in the up- and downstream regions of genes. Gene expression variation from transcriptome-wide analysis also shows significant parallelism both in level of expression and patterns of alternative splicing. The combination of population genetic metrics and overlap with functional regions, with shared expression divergence, are strong indicators of these genes playing a role in ecological adaptation of Arctic charr in replicate ecotype pairs.

Abstract ID: 2347

Genomic and transcriptomic basis underlying parallel origins of live birth

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Live-birth is a key evolutionary innovation that has evolved numerous times across the animal kingdom, but the genetic changes underlying transitions from egg-laying to live-birth are poorly understood. We analysed whole-genome sequences and transcriptomic data from four closely related species of intertidal snail (*Littorina*) that vary in their mode of female reproduction. Patterns of genome-wide variation suggests two independent origins of live-birth, but

localised genealogical analysis reveal numerous genomic regions where individuals group according to their reproductive mode. Candidate regions are widespread across the genome and show patterns of variation that are consistent with positive selection having acted on haplotypes associated with live birth. Transcriptomic analysis of reproductive organs and control tissue reveal a set gene that are differentially expressed between egg-laying and live-bearing snails. Our results show that transitions to live-birth has a complex, polygenic basis and is driven by the same allele in different clades.

Abstract ID: 1488

Genomes reveal age and demographic consequence of fast adaptive radiation

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New species typically evolve over several million years. However, rates of speciation and ecological diversification vary orders of magnitude across the tree of life, with the fastest shown by adaptive radiations. Eight hundred endemic species of cichlid fishes emerged and formed entire food webs in Lake Victoria and nearby lakes in East Africa. According to Victoria's paleolimnological history, five hundred may have arisen within the past 15,000 years, but molecular phylogenies estimated a much older origin. We use whole genomes to reconstruct the age and demography of all Lake Victoria region radiations. We show that in Lake Victoria, all major trophic guilds diverged <14,200 years ago, corresponding to at least 634 speciation events per million years, the fastest rate in metazoans. Cichlid radiations in lakes Edward, Albert, Kivu, and Saka all began <19,100 years ago, an order of magnitude faster than previously thought. Transitions between trophic levels led to divergence in effective population sizes in accord with the trophic pyramid of numbers concept, replicated across three independent food web radiations. Our results demonstrate that classical ecological theory of trophic interactions in immigration assembled food webs also applies to food webs that assembled through rapid adaptive radiation.

Abstract ID: 1872

Parallel adaptation within wild populations is a source of morphological and genetic diversity

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Parallel adaptation is often envisioned as entailing the repeated evolution of similar forms, however it can also lead to the evolution of *dissimilar* phenotypes with a shared function. In Hawaiian populations of field crickets *Teleogryllus oceanicus*, we have observed the emergence of at least five independently evolved mutant phenotypes, all of which remove males' ability to sing. This inability to sing is adaptive because singing crickets in Hawaii are attacked by a parasitoid fly. While three of these songless phenotypes involve near-identical changes to wing venation, we recently discovered two

more, morphologically distinct silent morphs – crickets unable to sing because their wings are curly, or very small. These curly- and small-wing phenotypes have emerged in populations which already harboured male-silencing phenotypes, with which they can also be co-expressed, creating the opportunity for competition between adaptive phenotypes within the same populations. Field observations indicate this competition impedes fixation of any one silent phenotype within a population, complicating coevolutionary dynamics between crickets and the parasitoid fly, and allowing singing males to persist despite strong negative selection. I will present genomic, transcriptomic, phenotypic and behavioural data for the various morphs, which we use to understand their repeated emergence and spread, quantify their relative costs and benefits, and predict future evolutionary trajectories. Crucial insights from this system are that parallel adaptation can occur within populations, through both similar and dissimilar changes in phenotype, and can create and maintain genetic diversity.

Abstract ID: 1890

Rapid parallel adaptation despite gene flow in silent crickets

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Gene flow is predicted to impede parallel adaptation via de novo mutations due to the homogenising effects of moving pre-existing adaptive alleles from population to population. This gene flow dynamic is predicted to work against adaptation and radiation via parallel evolution. However, critical tests of this assumption are elusive because it can be difficult to disentangle gene flow and independent mutation in natural systems. My talk will illustrate how we overcame this challenge using Hawaiian crickets (*Teleogryllus oceanicus*) in which 'flatwing' males that lack sound-producing wing structures recently arose. Silent flatwing males rapidly spread in different island populations under selection from a lethal, acoustically-orienting parasitoid fly. Morphometric and genetic comparisons revealed distinct silent flatwing phenotypes in these populations, localized to different loci. Nevertheless, we detected strong, recent and ongoing gene flow among the populations. Using genome scans and gene expression analysis we found that parallel evolution of flatwing on different islands is associated with shared genomic hotspots of adaptation that contain the gene doublesex, but the form of selection differs among islands and corresponds to known demographics in the wild. We thus show how parallel adaptation can occur on contemporary timescales despite gene flow, and argue that parallel evolution and the downstream evolutionary processes that rely on it could be far less constrained than previously appreciated.

Abstract ID: 1951

The role of sexual selection in shaping adaptive radiations

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Anolis lizards are famous for their diversity, their repeated parallel radiations, and their stunningly colourful dewlaps, which are thought to be used for signalling in social interactions. Previous work has indicated that sexual dimorphism and sexual selection may be crucial in shaping this radiation: for example, *Anolis* lizards are strongly

dimorphic in ecomorph-relevant traits, and across parallel radiations, sexual dimorphism contributes significantly to the amount of morphospace covered. Here, I investigate this topic using an individual based model, inspired by the adaptive radiation of *Anolis* lizards. In doing so, I explore questions such as: What role can sexual selection play in shaping an adaptive radiation? How does the co-evolution of female preference and a male trait (such as dewlaps) affect the dynamics of an adaptive radiation? What are the impacts of different mechanisms of female choice? And how can sex-specific gene expression alter the outcome? This project thus shows how sexual selection impacts two key properties of adaptive radiations: the ability to undergo adaptive evolution (also known as 'evolvability'), and the ability to diversify.

Abstract ID: 2161

The genetic bases of adaptive radiation in *Ophrys* orchids

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Sexual mimicry is a fascinating case of plant adaptation to pollinators, by mean of which plants attract insects to ensure reproductive success. This phenomenon has been deeply described in the *Ophrys* orchids, where the mechanisms of pollinator attraction and the so-called pseudocopulation are well known. It is known that sexual mimicry played a key role in driving species diversification in the *Ophrys* genus, thus causing a recent radiation (~1 Mya) that gave rise to a large number of *Ophrys* species. The rationale resides in the high specificity of sexual mimicry, for which each *Ophrys* plant attracts only one pollinator species. Changes in flower odour cause a pollinator shift, which in turn causes pollinator-driven plant adaptation, so speciation. Although the ecological aspects of this phenomenon are quite well-understood, the genetic bases remain still unclear. We close this gap by producing the first chromosome-level genome reference for the *Ophrys* genus, and analyse the genetic variation within different populations and different species among the Italian peninsula. Our dataset comprises WGS and GBS data of 127 individuals among 4 species. Results indicate that markers of differentiation particularly fall into a 20 Mb region on chromosome 2. Interestingly, none of the previously described putative genes for pollinator attraction fall into this region. Investigations of the causes and the evolutive implications for the ongoing speciation in the genus are currently ongoing.

Abstract ID: 2180

Convergent expression changes during development lead to convergent tooth morphologies in rodents

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Murinae, the family of mice and rats, represent one of the most successful radiation in mammals, possibly thanks to their new mastication mode with a new cusp row on upper molars. This innovation happened convergently in three other rodent clades. Here, we investigate if the gene expression changes underpinning the development of this new morphology are convergent. We focus on mouse and Acomys with convergent supplementary cusps in the upper molar, as well as hamster and gerbil, with the ancestral cusp number. We also study lower molars, whose cusp number is unchanged in the four species. Our approach combines comparative transcriptomics, developmental biology and genetics. We obtained RNA-seq time series of molar development for both teeth in the four species. Clusters of gene expression profiles are shared by the two teeth and highly species-specific. Interspecies similarity is not stronger for convergent pairs of teeth than for control pairs. However, by focusing on genes differentially expressed between lower and upper molar in each species, we find more genes in common for the convergent species than for any other pair. This includes Bmp6 whose spatio-temporal profile evolution and loss-of-function phenotype are consistent with a role in the convergent morphology. Furthermore, by studying the developmental mechanisms of cusp formation, we reveal a convergence in several pathways. In conclusion, we observed a marked co-evolution of the two teeth and no global pattern of convergence in gene expression. We nevertheless find some genes with convergent expression changes and clear convergence in developmental mechanisms.

Abstract ID: 2219

The genomic basis of similarity in the cichlid fishes of the Lake Victoria Region Superflock

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The extraordinary species richness of East African cichlid fishes is coupled with a large eco-morphological variation in morphology, diet, habitat preference, and behaviour. This is especially true for the Lake Victoria Region Superflock, a radiation of 700 species that evolved very rapidly over the last 100–200 ka. Most species inhabit a single lake in the Lake Victoria region (Lakes Albert, Edward, Kivu, Victoria) and the intra- and interlacustrine similarity in eco-morphology between many species is striking. How these are related to each other, however, remains mostly unknown. Their young age and many similarities make these cichlids a perfect system to investigate repeated evolution in adaptive radiations.
We performed a revision of the about 80 species of haplochromine cichlids from the Lake Edward system. From the system, we discovered 29 new species, many of which strongly resemble species from other lakes within the Lake Victoria region. We collected

morphological and genomic data from about 100 species from four distinct lakes. We are quantifying eco-morphological similarities between species using a geometric morphometric approach. Our framework currently includes 161 species and shows partial separations between eco-morphological groups across lakes and strong overlaps between similar species from different lakes. Using a whole genome sequencing approach, we investigate whether genomic regions can be identified that segregated across replicate species flocks and sorted repeatedly into species with similar eco-morphologies. This will allow us to determine the relationships between these young species and improve our understanding of repeated evolution in the Lake Victoria Region Superflock.

Abstract ID: 2261

The genomic predictability of morph differentiation in a highly polymorphic Arctic fish

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The recent and repeated evolution of multiple ecologically, phenotypically, and genetically differentiated morphs within Arctic charr (*Salvelinus alpinus*) makes this species an ideal model to investigate the genomic repeatability of morph differentiation and reproductive isolation. Labrador, Canada is home to many such charr morphs including landlocked and anadromous populations as well as sympatric small and large morphs that occur either in landlocked lakes or sea-accessible lakes (where the large morph is anadromous and the small morph is a freshwater resident). To investigate the genetic parallelism underlying these charr morphs in Labrador we used an 87K SNP chip comparing 1) replicate allopatric landlocked and anadromous populations paired by common drainage and 2) replicate sympatric small and large morphs. Despite both allopatric and sympatric morph pairs demonstrating strong genome-wide differentiation, little of this genetic differentiation was consistent across replicate morph pairs, suggesting generally limited genetic parallelism. However, several functionally-relevant genes consistently differed between replicate morph pairs. For example, the muscle-associated gene myomesin-2 repeatedly differentiated allopatric anadromous and landlocked populations while the growth-associated gene pappalysin-2 repeatedly differentiated sympatric small and big morphs. We also identified a number of genes where a different paralogous copy differentiated each replicate pair of morphs. We suggest that such parallelism at the level of the paralog may represent an

underappreciated mechanism driving consistent phenotypic differentiation, particularly in salmonids which underwent a recent whole genome duplication. Our results therefore stress the importance of considering multiple mechanistic levels (e.g., SNP, gene, paralog) when assessing the predictability of evolution.

Abstract ID: 1785

Early life parallel evolution in the sharpsnout seabream over spatial and temporal scales

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Temporal and spatial studies are crucial to understand adaptation patterns. Thus, consistent responses to similar selection pressures can unveil parallel evolutionary processes and the genomic drivers underlying these adaptive changes. In this study we combined genomics with phenotypic and environmental data to address the adaptative processes associated to early life mortality on the sharpsnout seabream, *Diplodus puntazzo*, a coastal fish species of the Mediterranean Sea. We first assembled and annotated a high quality chromosome-level reference genome (N50=6.3 Mb, 98% of the genome in 24 chromosomes, 99.3% Metazoan BUSCO genes). In addition, we analysed 116 settlers and 111 six-month survivors obtained during two consecutive reproductive seasons (2015 to 2017) from three different geographic locations in the western Mediterranean. For each individual we genotyped ~58,000 SNPs using 2bRAD sequencing and we compiled individual information from nine phenotypic early life traits and environmental variables (pelagic larval duration, pelagic larval growth, size at hatching and at settlement, sea-surface water temperature and moon illumination). For some traits, we observed similar temporal and spatial trends between settlers and survivors, such as higher survival for individuals generally hatching later and at lower temperatures, coupled with local selective mortality for other traits. We detected significant associations between several loci and the assessed variables, shedding light on the candidate genes to be involved in the selective survival at early life. These results provide clues on the genetic drivers for the evolutionary processes in early survival in fish species, as a combination of parallel evolution and local adaptation.

Abstract ID: 2376

Can synergistic pleiotropy explain the low parallelism of temperature gene expression evolution?

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Parallel phenotypic responses to similar environmental stressors have been described not only for different populations, but also between species. Since many traits are complex, it's not clear to what extent parallel evolution can be seen on a molecular level. We address this question by studying the transcriptomic response of polymorphic populations from two species, *Drosophila melanogaster* and *D. simulans,* to fluctuating high and low temperature regimes in in the laboratory. In both species a strong adaptive response was observed. 193 genes were differently expressed between high and low temperature for *D. melanogaster* and 189 for *D. simulans*. Only two and five (Jaccard index=0.01;0.03) up/downregulated genes, respectively, were shared between the species. Additionally, a correlation of the overall transcriptome responses was low (*rho*=-0.067). Evolved genes in both species were though enriched among midgut and accessory gland specific genes (J.I.=0.67). Understanding how the experimental thermal adaptation we observe is reflected in natural population is important with temperature being one of the most important environmental stressors. Interestingly, we find parallel responses between clines of the same species higher compare to our observation. Reasoning that pleiotropy may be a major factor determining the adaptive gene expression evolution, we compared the levels of pleiotropy among evolving genes. For both species, pleiotropy appeared higher in the clines than in the laboratory. This might be explained by the more complex environments in nature (synergistic pleiotropy). We propose that pleiotropy may be an important, but complex, factor contributing to the repeatability of gene expression evolution.

Symposium: S10. Eco-evolutionary dynamics in changing environments: insights from models, experiments and case studies (id: 961)

Abstract ID: 2459

Patterns and effects of gene flow on adaptation across spatial scales: implications for management and models

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Gene flow is essentially the rearrangement of a species' genetic variation across time and geographic space. Gene flow can have major effects on adaptation and remains one of the greatest evolutionary management tools available for biological conservation and restoration. Nevertheless, we are still in need of understanding and predicting gene flow effects over varying geographic scales and gradients of environmental variation. Here I discuss some empirical findings on several topics about which we still have much to learn: How is genetic variation distributed across species ranges? What are the patterns of gene flow in nature with respect to environmental gradients? And what is known about the adaptive effects of gene flow to small or marginal populations in challenging environments (e.g., at species range limits)? By understanding patterns of adaptation relative to patterns of gene flow, across steep and shallow environmental gradients, we can build a framework for how to best promote adaptive gene flow in natural and conservation contexts.

Abstract ID: 1157

Eco-evolutionary dynamics under spatio-seasonal environmental change: from theory to nature

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Eco-evolutionary responses to environmental variation and change fundamentally depend on the speed, form and consequences of environmentally-induced phenotypic and micro-evolutionary changes in key traits that shape population dynamics and distributions. Predicting complex system dynamics and feedbacks requires theory that encompasses combinations of plasticity, selection, genetic variation and movement, coupled with multi-year wild population studies designed to quantify key parameters emerging under typical and extreme environmental conditions. Yet, such integrated theoretical-empirical programmes are rarely implemented. We present key results from a theoretical-empirical programme designed to interrogate eco-evolutionary dynamics involving a key movement trait that directly shapes spatio-seasonal population dynamics and distributions: seasonal migration versus residence. First, we highlight new theory that shows how dichotomous threshold traits (such as migration versus residence) can show distinctive plastic and micro-evolutionary responses to environmental variation, and how changing migration can impact population dynamics. Second, we use >10 years of spatially extensive individual-based data from a wild partially-migratory bird population to show that extreme climatic events can induce strong spatially-structured selection on expression of seasonal migration versus residence and, notably, on expression of plasticity in migration. Further, we show that such episodes of selection can be strong enough to detectably alter phenotypic and additive genetic values, thereby causing both immediate and micro-evolutionary changes in seasonal population distributions and resulting opportunities for selection. Overall, we thereby show how interactions among environmental variation and plasticity, selection and genetic variation in movements can act to drive and constrain spatio-temporal eco-evolutionary responses of potentially mobile populations to changing seasonal environments.

Abstract ID: 2006

Rapid seasonal thermal adaptation in Chironomus riparius

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Effects of seasonal or daily temperature variation on fitness and physiology of ectothermic organisms and their ways to cope with such variations have been widely studied. However, the way multi-voltines organisms cope with temperature variations from one generation to the next was, until this point, not well understood. In the context of global climate change, the way those species cope with the seasonal temperature variations provide a good insight on their reaction range in case of exceptional temperature event. To investigate this, a multi-voltine midge *Chironomus riparius* (Meigen, 1803) was used as test species. The possibility of phenotypical plasticity was tested with a common garden approach. After three generations, significant mortality rate differences led the conclusion that the population

responded rapidly to climatic variation via adaptive mechanisms more than via phenotypic plasticity. An Evolve and Resequence (E&R) study was therefore performed to infer *C. riparius* evolutionary potential for rapid thermal adaptation. We exposed populations of C. *riparius* sampled *in naturae* to three temperatures and to cyclic varying temperature for more than two years in parallel to the genomic monitoring of a natural population. Life-cycle fitness tests and genomic analyses revealed strong, genome-wide selective response in all laboratory replicates. This confirmed a selective response to identical selection pressure(s) most likely induces by the laboratory conditions. However significant variations in SNPs frequency were observed following the temperature cycles in laboratory as well as change in haplotypes trajectories following exceptional temperature events *in naturae,* highlighting the evolutionary potential of natural populations.

Abstract ID: 1319

Experimental local plant adaptation to soil is reinforced by herbivory

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Local adaptation is a key phenomenon for the maintenance of genetic variation and ecological speciation. In plants, adaptation to local soil type has often been demonstrated, but the role of multivariate selection in this process, especially selection imposed by biotic interactions has almost never been investigated. We used experimental evolution with a starting population of fast cycling *Brassica rapa* plants, that was split into treatment groups growing on two different naturally occurring soil types, with and without bumblebee pollinators and aphid herbivores (8 treatment groups with two replicates each, and a total of ca. 800 plants per generation), to study the speed of soil adaption and the role of biotic interactions in this process. At the end of the experiment, a reciprocal transplant experiment was conducted where all plants were grown in the soil type they evolved in (local), and in the one they did not evolve in (foreign). We showed that after 8 generation of selection, plants pollinated by bumblebees with aphid herbivores had evolved significant local soil adaption. For both soil types, plants produced more flowers and attracted more bumblebees when growing in the soil they had evolved in. Plants from other treatments, for example those with bee pollination but without aphids, did not show any local adaptation in the reciprocal transplant experiment. We therefore conclude that local adaptation can evolve rapidly and can be reinforced by antagonistic biotic interactions such as herbivory.

Abstract ID: 1967

Rapid evolution in populations of a long-lived dominant grass species

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Rapid evolution in response to climate change is an important mechanism helping organisms to adapt to changing climate. While such a potential has been repeatedly

demonstrated in short lived organisms such as various microbes, to what extend we can observe it in long-lived species is largely unknown.
We used long-lived clonal hexaploidy grass Festuca rubra growing along precipitation and temperature gradients in Norway as a model. We transplanted seed mixtures produced at single localities to original localities and to localities with climate changing in the direction and degree of predicted climate change for the region (to warmer, wetter and warmer-wetter sites). All localities received seeds originating from the same maternal plants in identical proportions. We assessed trait and genetic composition of established plants after 3 years.
The traits of plants which established in the given conditions have converged towards traits of plants which originate in the given environment. Similarly, the genetic data indicated that genotypes established in the same conditions have specific sets of genes independent of seed origin. Both these datasets indicate that environment can select genotypes best suited to local conditions. This suggests that even long-lived organisms can undergo rapid evolution allowing them to adapt to novel climates. Such rapid adaptation was possible thanks to high genetic diversity of populations of the species, providing sufficiently large pool of genotypes from which to select.

Abstract ID: 2155

Adaptation to cadmium shapes coexistence patterns in herbivore species

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Recent evolutionary history in different environments is expected to lead to changes in species growth rates and competitive abilities. These traits have been identified as key ingredients in modern coexistence theory, which suggests that adaptation to new environments may shape species coexistence patterns. However, this hypothesis is poorly tested. To tackle this issue, we used two herbivorous spider mite species (*Tetranychus urticae* and *T. evansi*) experimentally evolving on tomato plants grown under high or low cadmium concentrations. After 40 generations of evolution, we observed that the strength of intraspecific interactions in the two species were higher in the absence of cadmium vs. in its presence. Furthermore, the competitive ability of *T. evansi* populations that have adapted to cadmium was lower that non-adapted ones in absence of cadmium, whereas no difference was found in its presence. Incorporating these values into modern coexistence theory, we predict that coexistence is possible without cadmium, but not in its presence. We then experimentally tested these predictions by following the populations of the two species together during two generations. As predicted, we found no exclusion in absence of cadmium, irrespective of the populations used. In its presence, *T. urticae* was generally excluded, although this was less likely if *T. evansi* was not adapted to cadmium. These results validate the use of modern coexistence theory to predict the outcome of population dynamics and highlight how adaptation to metal contaminants can alter the long-term coexistence of two herbivore species in different environments.

Abstract ID: 1275

The demographic consequences of adaptation: Evidence from experimental evolution

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The process of adaptation towards novel environments is directly connected to the acquisition of a higher fitness relative to others. Such an increased fitness is obtained by changes in life history traits that may directly impact population dynamics. From a functional perspective, increased fitness can be achieved through a higher resource use or more efficient resource use, each potentially having its own impact on population dynamics. In case of the first, adaptation is expected to directly translate into higher population growth. In the second case, adaptation requires less energy, and hence, may lead to higher carrying capacity. Adaptation may thus lead to changes in the ecological dynamics, and vice versa. Here, by using a combination of evolutionary experiments with spider mites and a population dynamic model, we investigate how an increase in fecundity (a validated proxy for adaptation) affects a population's ecological dynamics. Our results show that adaptation can positively affect population growth rate and both positively or negatively affect the carrying capacity depending on the ecological condition leading to variation in adaptation. These findings show the importance of evolution for population dynamics in changing environments, which may ultimately affect the stability and resilience of populations.

Abstract ID: 1534

Adaptive development in variable environments

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Annual killifish live in temporary ponds. Their embryos survive dry periods in soil egg banks, arrest development in different diapauses and seem to implement diversified bet-hedging. An eco-evolutionary model tailored to *Austrolebias* annual fish is presented which models spatial and temporal variation of water presence in temporary ponds explicitly. Ponds fill and dry gradually. Results from experiments on stage-specific rates of development and survival are used to model embryonic life histories and to predict developmental stages of embryos at any time and location in the soil.
Invasion fitness sensitivities of rates of development, mortality rates and hatching probabilities are estimated. An eco-evolutionary dynamics based on these sensitivities can be implemented. Whether observed developmental variation could be adaptive was

first investigated by modelling wet periods within a year and assessing the ensuing patterns of fitness sensitivities. Faster developmental rates and lower mortality rates were always adaptive such that only trade-offs and constraints could keep them at their current values. A limited hatching probability can be adaptive when a separate short wet period occurs early in the wet season.
Further modelling suggests that anthropogenic disturbances and rearrangements of the natural habitats might render observed patterns of development adaptive across a wider range of rainfall scenarios. The novel environmental regimes which result could aid in the persistence of the several hundred annual fish species occurring in South-America and Africa, often at risk of extinction.

Abstract ID: 1225

The evolution of size-dependent competitive interactions and resource use promotes coexistence

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Theory indicates that species coexist in a community when intraspecific competition is stronger than interspecific competition. In size-structured communities, however, competitive interactions between individuals and coexistence depend on how resource use and the ability to compete for these resources change with body size. Therefore, testing coexistence theory in size-structured communities requires disentangling the effects of size-dependent competitive abilities and niche shifts. Here, we experimentally tested the predictions of a coexistence model that includes variation in body size, size-dependent competitive asymmetries, and size-dependent niche shifts using Trinidadian guppies (*Poecilia reticulata)* and killifish (*Rivulus hartii)* at two competitive settings representing the early (allopatric) and late (sympatric) evolutionary stages of a killifish–guppy community. We tested whether changes in the competitive interactions across sizes increased the likelihood of species' coexistence from allopatry to sympatry. We found that guppies are competitively superior to killifish but were less so in sympatric populations. The decrease in the effects of interspecific competition on the fitness of killifish and increase in the interspecific effect on guppies' fitness increased the likelihood that sympatric guppies and killifish will coexist only if killifish have stronger shifts in resource use with body size. However, while the competitive asymmetries between the species changed consistently between allopatry and sympatry between drainages, the magnitude of the size-dependent competitive asymmetries varied between drainages. These results demonstrate the importance of integrating evolution and trait-based interactions into the research on how species coexist.

Abstract ID: 1489

Planting long-lived trees in a warming climate: investigating a trade-off in the optimal provenance

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Climate change is a threat to long-lived trees, which may not adapt or migrate fast enough to keep up. Assisted Gene Flow is a conservation and forestry tool that has the potential to facilitate adaptation of populations to future climates using managed translocation of seeds from a different location ("provenance") within the current range of a species. Finding the provenance that will perform best in terms of survival/growth is, however, complicated by a trade-off: because trees face a rapidly changing climate during their lengthy lives, the genes and adaptations that confer optimal performance may vary across their lifespan. For instance, trees from warmer provenances could suffer from the colder temperatures while still in a sensitive juvenile stage. This project uses a stage-structured modelling framework to determine which provenance would maximize the survival/growth of long-lived trees in a changing climate. We test the influence of life-cycle parameters on this optimal provenance. Models were parameterized using empirical matrices for twenty long-lived tree species. We show how the optimal provenance depends largely on the temperature sensitivity of the trees at different stages of their lives, driven towards the predicted future temperature experienced at the most sensitive stage. These theoretical predictions therefore call for increased empirical effort to investigate how thermal tolerance changes across life.

Abstract ID: 1650

Spatio-temporal dynamics of a major rice virus, highly diverse at local scale in Burkina Faso

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Virus epidemics cause major losses in agriculture. Predicting disease progression is challenging because epidemics can take different trajectories depending on host and pathogen genetic diversity, host density or environmental conditions. The rice yellow mottle virus (RYMV) constitutes a threat to the actual development of rice cultivation in Africa. As climate change and agricultural intensification increase the risk of epidemics, there is an urgent need to understand the spatio-temporal dynamics of RYMV at local scale. This study includes a five-years monitoring of RYMV incidence in six sites, characterized by two rice growing systems (irrigated vs. rainfed lowland), in western Burkina Faso. This allows confirming the highly local patterns of prevalence, and to identify a disease hotspot. A screening of RYMV genetic diversity was then performed in this site, revealing a very high genetic diversity with the co-occurrence of four distinct lineages at small geographical scale (within one irrigated perimeter). A few isolates from each group was fully sequenced, revealing that one of these lineages results from a

recombination event between two others. Temporal dynamics suggest an evolution of RYMV population (modifications in the relative frequencies of each genetic lineage) within the five-years studied period. In controlled conditions, we evaluated the virulence of viral isolates from each genetic groups on a set of rice cultivars. Induced symptoms, as well as viral load were affected by the rice cultivar, the viral isolate and their interactions. The implications of these results, and the consequences of genetic and pathogenic diversity on disease dynamics, are discussed.

Abstract ID: 1529

Niche shifts promoting the native range expansion, but not yet invasion, of an annual plant

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Although ecological niche models have been instrumental in projecting species distribution shifts under global change, growing evidence of niche shifts during range expansion is a key source of uncertainty in model forecasts. Rapid evolution has been studied extensively in invasive species, but may also occur in native populations tracking climate change. We compared niche shifts during both types of range expansion in the Mediterranean annual plant *Dittrichia graveolens*. Previous work has found that this species' recent native range expansion coincided with rapid evolution of earlier flowering time at the leading edge, suggesting that a climatic niche shift may have contributed to the rapid range shift. We asked whether the native range expansion of *D. graveolens* tracked climate change, whether further range expansion was promoted by niche expansion, and how these results changed forecasts of two ongoing invasions by this species in Australia and California. Niche shifts were quantified in both environmental and geographic space, comparing the historic (1901-1930) and present (1990-2019) climate and distribution. We found that *D. graveolens* expanded its native range well beyond the expectation under climate change, associated with a 5.5% niche expansion towards more temperate climates. In contrast, we found niche conservatism in the invaded ranges in Australia and California, where *D. graveolens* is still constrained to climatic areas matching the historic native niche. We conclude that native populations may track climate change and adapt to novel conditions in parallel, causing further range expansion than expected based on climate change alone.

Abstract ID: 2048

Evolution of plasticity prevents post-invasion extinction of a native forb

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Exotic plant invaders pose a serious threat to native plants. However, despite showing inferior competitive ability and decreased performance, native species often subsist in invaded communities. The decline of native populations is hypothesized to be halted and eventually reversed if adaptive evolutionary changes can keep up with the environmental

stress induced by invaders, i.e., when population extinction is prevented by evolutionary rescue (ER). Nevertheless, evidence for the role of ER in post-invasion persistence of native flora remains scarce. Here, I explored the population density of a native forb, *Veronica chamaedrys*, and evaluated the changes in the shade-responsive traits of its populations distributed along the invasion chronosequence of an exotic transformer *Heracleum mantegazzianum*, which was replicated in five areas. I found a U-shaped population trajectory that paralleled the evolution of plasticity to shade. Whereas *V. chamaedrys* genotypes from intact, more open sites exhibited a shade-tolerance strategy (pronounced leaf area/mass ratio), reduced light availability at the invaded sites selected for a shade-avoidance strategy (greater internode elongation). Field experiment subsequently confirmed that the shifts in shade-response strategies were adaptive and secured post-invasion population persistence, as indicated by further modeling. Alternative ecological mechanisms (habitat improvement or arrival of immigrants) were less likely explanations than ER for the observed population rebound. These results suggest that *V. chamaedrys* survived because of adaptive evolutionary changes operating on the same time scale as the invasion-induced stress, but the generality of ER for post-invasion persistence of native plants remains unknown.

Abstract ID: 1514

Gone but not forgotten: Entire adaptive radiation retains genomic variation from extinct species

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Anthropogenic environmental change is causing the loss of biodiversity at an unprecedented rate. When reproductive isolation between species is contingent on features of the environment, environmental change can weaken reproductive isolation and result in extinction through hybridization, a process called speciation reversal. The extinction of species results in vacant niche space, and its re-population by adaptation of related or evolutionary new species can enhance the ecological resilience of ecosystems. In Lake Constance, a deep-water whitefish species went extinct through speciation reversal during the period of anthropogenic eutrophication mid last century. Using historical and contemporary samples, we sequenced genomes of all species of the Lake Constance whitefish radiation from before and after the eutrophication period. We show that despite the extinction of the deep-water species, fractions of its genome including regions shaped by positive selection and thus potentially adaptive in deep water, persist within surviving species as consequence of introgression. By sampling a depth transect ranging from shallow to deep water, our data suggests that introgressed variation from the extinct species may potentially facilitate rapid adaptation to the vacant deep-water niche in one of the surviving species. Thus, introgression of old variants derived from extinct species and selection on this introgressed variation within their new bearers can improve the ecological resilience of ecosystems. Given the prevalence of environmental change, studying the genomic consequences of speciation reversal provides fundamental insights into the evolution of biodiversity, especially its dynamics under environmental change, and informs biodiversity conservation.

Abstract ID: 1327

Temporal changes in the roles of species sorting and diversification determine community dynamics

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Competition and predation are two major processes structuring natural communities through species sorting (ecology) and their role as major drivers of diversification (evolution). The contribution of ecology and evolution to shaping communities needs further elucidation as the relative importance of competition and predation can change along environmental gradients, and selection by competition and predation often favours different traits. Furthermore, the interactions between species sorting and diversification are largely unknown. Predation has, for example, been found to increase the rate of molecular evolution, and bacterial populations are known to rapidly evolve anti-predator defences during co-evolution with (protist) predators. Whether predation in complex bacterial communities selects for defence or competitive and/or cooperative types is unknown. To estimate the contributions of species sorting and diversification during predation on bacterial communities, we co-evolved twelve rich bacterial communities (24 species) for 60 days with their protist predator *Tetrahymena thermophila*. We found that species sorting and prey adaption shaped the community composition. While community dynamics were initially explained by species sorting, changes in defence and competitive ability (growth rate) contributed to the community dynamics later in the experiment. In contrast to observations from single bacterial populations, bacterial anti-predator defences declined rapidly, whereas higher levels of competitive ability were measured, suggesting competition as the main driver of selection. Overall, we show that temporal changes in species sorting and evolution determine the dynamics within the bacterial prey communities resulting in selection for prey traits that are qualitatively different from those that emerge under simple pairwise predator-prey coevolution.

Abstract ID: 979

Fundamental processes of eco-evolutionary community dynamics

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Unprecedented environmental changes induce strong selection pressures on species. Studies have shown both ecological and rapid evolutionary responses of species to these ongoing environmental changes. Increasing evidence that ecological and evolutionary processes can occur at similar temporal and spatial scales and might thus frequently interact has raised the concern that these processes should not be studied in isolation from each other, but instead integrated if we attempt to better understand species responses to environmental change. Even more so, because species are embedded within communities, environmental change does not act on single species, but acts simultaneously on all species within the community, giving rise to potentially complex eco-evolutionary dynamics. We currently still lack a coherent framework to address and study eco-evolutionary dynamics within communities, despite the many theoretical and conceptual advances made during the last decades. Following a synthesis by M. Vellend which showed that community ecology could be organized along analogous processes of evolutionary biology (i.e., selection, migration, drift and diversification), we argue that by explicitly considering interactions between these processes of evolutionary biology and community ecology, it may facilitate our understanding of eco-evolutionary dynamics in multi-species communities. Focusing on interactions between processes of evolutionary biology and community ecology may enable explorations of the full range of eco-evolutionary community dynamics, may provide a way forward to reveal generalities and formulate hypotheses about eco-evolutionary community dynamics and guide the design of novel theoretical models that explicitly take these interactions into account.

Abstract ID: 1407

The impact of life history, species ecology and humans on the population decline of extant megafauna

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The late Quaternary extinction event, strongly supported by the fossil record, is characterized by selective extirpation of large-bodied animals at a global scale. While fossils provide valuable glimpses into histories of species, the fragmentary nature of such data limits precision of past population dynamics inferences. We therefore analysed genome sequence data of over 100 extant megafauna species using pairwise sequentially Markovian coalescent (PSMC) models to infer past changes in population sizes. We employed a Bayesian statistical framework to infer population trajectory differences between species while taking into account differences in life history traits, ecological parameters, as well as paleoclimate and hominin impact. We find a global trend of megafauna decline towards present time during the last million years, with larger species experiencing the strongest decline. Furthermore, we find that the rate of population decline intensified approximately 65,000 years ago, with species native to Australasia and Neotropics experiencing the sharpest shift towards population decline. Additionally, the decline in population size was strongest for carnivores and mildest for generalist species. Finally, we developed predictive models based on temperature fluctuations and human population sizes to assess their relative impact on megafauna population dynamics. We find that the paleoclimate has limited explanatory power for recent shifts in megafauna population sizes, which largely coincide with human arrival

times and expansion. Our results provide unique insight into factors governing population shifts in large animals and have important implications for the global restructuring of our ecosystems.

Abstract ID: 1338

Changes in global avian functional diversity over the last million years

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Despite evidence of declining biosphere integrity, we currently have limited understanding of how the functional diversity associated with changes in abundance among ecological communities has varied over time and before wide-spread human disturbances. We combine morphological, life-history, and ecological trait data for >230 bird species with genomic-based estimates of changing effective population size (N_e) to quantify shifts in avian functional diversity over the past million years. We show that this period of the Pleistocene was relatively stable in terms of avian functional diversity, but that significant changes occurred in rarer regions of the avian global functional trait space and among key ecological/life-history strategies. We detected overall declines in representation within functional trait space among larger-bodied species with larger eggs and larger clutch sizes from more ancient time to more recent time, as well as overall increases among large-bodied species with longer incubation durations and a larger hand-wing index, indicative of stronger dispersal ability. Waterbirds and seed-eating species likewise declined over time, while migratory and altricial species were always better represented over the past million years. Changes across zoogeographic realms revealed the erosion of multiple hotspots of functional trait space in the past, particularly within the Paleartic and the Neartic. Tracking temporal changes in functional diversity provides a method to establish baselines and quantify losses of biosphere integrity before human-related disturbances became widespread. The integration of paleodemographic dynamics with functional trait data will enhance our understanding of functional diversity and help improve estimates of biodiversity declines over time.

Abstract ID: 1901

Dynamic eco-evolutionary fitness landscapes display complex trajectories and sustained diversity

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Genotype-fitness maps and ecological interactions are usually studied separately. We introduce a model that combines probabilistic fitness landscapes and ecological interactions to generate a dynamic co-evolutionary fitness landscape. This model allows us to quantify long-term diversity and coexistence in a population from a fitness landscape perspective. We combine a Rough Mount Fuji genotype-phenotype map with an ecological phenotype-fitness resource-competition model. Through the multidimensional Rough Mount Fuji genotype to phenotype map we can tune epistasis

(i.e., non-additive fitness interactions on the genotype level) and correlations between traits (i.e., whether there is a trade-off between performing well with respect to different phenotypes). We find that ecological interactions increase the observed epistasis in the genotype-fitness map at the steady-state over the same model without ecological interactions. Long-term diversity is largest when there are phenotypic trade-offs. However, epistasis in the genotype-phenotype map enables long-term coexistence of multiple genotypes also in the absence of phenotypic trade-offs.

Abstract ID: 1834

What limits a species' range?

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We know that heritable variation is abundant, and that selection causes all but the smallest populations to rapidly shift beyond their original trait distribution. So then, what limits the range of a population? There are physical constraints, and also population genetic limits, ultimately set by population size. Global adaptation, where the same genotype is favoured over the whole range, is most efficient when based on a multitude of weakly selected alleles, and is effective even when local demes are small, provided that there is some gene flow. In contrast, local adaptation is sensitive to gene flow, and may require alleles with substantial effect. How can populations combine the advantages of large effective size with the ability to specialise into local niches? To what extent does reproductive isolation help resolve this tension? I address these questions using eco-evolutionary models of polygenic adaptation.

Abstract ID: 1307

Genetic load and extinction in peripheral populations – eco-evolutionary dynamics

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We analyse how migration from a large mainland influences genetic load and population numbers on an island, in a scenario where fitness-affecting variants are unconditionally deleterious, and where numbers decline with increasing load. Our analysis shows that migration can have qualitatively different effects, depending on the total mutation target and fitness effects of deleterious variants. In particular, we find that populations exhibit a genetic Allee effect across a wide range of parameter combinations, when variants are partially recessive, cycling between low-load (large-population) and high-load (sink) states. Increased migration reduces load in the sink state (by increasing heterozygosity) but further inflates load in the large-population state (by hindering purging). We identify various critical parameter thresholds at which one or other stable state collapses, and discuss how these thresholds are influenced by the genetic vs. demographic effects of migration. Our analysis is based on a 'semi-deterministic' analysis, which accounts for genetic drift but neglects demographic stochasticity. We also compare against simulations which account for both demographic stochasticity and drift. Our results

clarify the importance of gene flow as a key determinant of extinction risk in peripheral populations, even in the absence of ecological gradients.

Abstract ID: 1350

How do species ranges respond to the effects of counteracting environmental gradients?

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Future change in environmental conditions may lead to the extinction of a population due to decreased fitness. Extinction may be avoided by adaptation to new conditions, or by a range shift to track favorable conditions. Due to current climate change, with temperatures warming poleward, many species are expected to track their current temperature range by moving poleward. However, not all environmental changes are expected to cause range shifts in the same direction. In the Baltic Sea, for example, salinity decreases in the south-north direction, and while temperature is expected to increase, salinity is expected to decrease. The former will tend to push species towards the north, while the latter will tend to push them towards the south, unless adaptation with respect to either factor can be more readily attained. It is unclear how species' range dynamics will play out in presence of such contrasting environmentally driven tendencies. Here, we perform spatially explicit simulations of a population whose range is determined by adaptation along two separate environmental variables acting on polygenic adaptive traits. We will specifically use the monitored temperature and salinity data from the Baltic Sea to reproduce the environmental gradient, and we will also model expected changes in these variables in the next 100 years. We will compare this to a scenario in which only one of the two variables imposes selection. We will evaluate how different species-specific variables will impact on the interplay between expected temperature and salinity changes, and outline implications for forecasting future species' distribution.

Abstract ID: 1922

From genotypes to demography: eco-evolutionary dynamics in Atlantic salmon

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Ecological and evolutionary processes can occur on the same timescale and influence each other. Yet, few models have been developed to quantify feedback between ecological and evolutionary processes in wild populations. Such models often require data from long-term populations monitoring and a good understanding of the genetic basis of life history traits. In Atlantic salmon, large effect genes are associated with age at maturity. Interestingly, one of these genes, in the *vgll3* region, displays a sex-specific effect with reversal dominance, potentially reflecting sexually antagonistic selection. Here, we developed an eco-evolutionary dynamics model, combining 40 years of genetic and demographic data, to quantify sex-specific selection at these large effect genes, their allele frequency dynamics and influence on population growth. We discuss results obtained from the Imsa population (Norway), and compared them with assumptions based on the genetic architecture.

Abstract ID: 1660

How does radioactivity impact the evolution of tree frogs in the Chernobyl exclusion zone?

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The Chernobyl nuclear accident (Ukraine, 1986) lead to the contamination of the environment by radionuclides. For several years, in the vicinity of the power plant, a territory called Chernobyl exclusion zone has been abandoned by humans. Wildlife living in this territory is still chronically exposed to ionizing radiation. Such zone appears interesting case study to analyse the eco-evolutionary dynamics at work in changing environment. In particular, we investigated the evolution of tree frog (*Hyla orientalis*) populations after the Chernobyl nuclear accident by combining population genetics and transcriptomic analysis. We first explored the intensity of evolutionary processes in the Chernobyl exclusion zone. We showed a decrease of nuclear genetic diversity (transcriptome-based SNP) and an increase of relatedness along the contamination gradient and the existence of limited asymmetrical gene flows towards the most contaminated places. We concluded to the existence of small effective population size in the most contaminated places. The analysis of a mitochondrial genetic marker (cytochrome b coding gene) points towards a substitution rate hundred times higher for mitochondrial DNA, and also confirms a likely reduced effective population size. We then evaluated the potential parallel functional processes that could be affected in tree frogs and showed by combining differential gene expression analysis, dose-response modelling and co-expression network analysis the impairment of mitochondrial energetic processes. Together, these results display the central role of mitochondria and ATP synthesis as the target of the disturbance due to ionizing radiation, and question the interplay between plasticity and evolutionary processes in this response.

Abstract ID: 1308

Indirect effects of abiotic conditions slow down eco-evolutionary dynamics of host and virus

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The pattern and pace of host-parasite coevolution can be affected by the abiotic environment if the host and/or parasite are poorly adapted to their local environment, for example when environmental conditions change. Because the completion of the parasite's life cycle depends on the fitness of the host, the evolutionary dynamics of the parasite are also indirectly influenced by the degree of host environmental maladaptation, even when the abiotic environment does not directly affect the parasites' fitness. The dependency of the parasites' evolution on the hosts level of maladaptation is not fully understood. Here, we examined the pattern (Arms Race, Red Queen Dynamics), the repeatability and pace of host-parasite coevolution in an algal-virus system along a gradient of four abiotic conditions that directly affect the algal host. We followed the eco-evolutionary dynamics of host and virus in replicated populations over dozens of generations and determined host resistance and virus counter-adaptation through time-shift experiments. We found signatures of Arms Race Dynamics, but the evolution of the virus slowed in treatments where the host was poorly adapted to its environment. In contrast, the pace of host resistance was unaffected, as the host population quickly evolved resistance to the counter-adaptations in the virus population, independently of the environmental gradient. In our experiment, the failure of the host to adapt to the changed environmental conditions resulted in differences in the overall population sizes of the virus. This suggests that limited mutation supply due to lower population sizes affected the adaptability of the virus population.

Abstract ID: 1224

Indirect evolutionary facilitation in a predator-prey system facing an environmental perturbation

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Genetic diversity is a fundamental requirement for adaptation and it has been suggested that evolution in an interacting species can buffer environmental perturbations to prevent population decline and extinction. However, the conditions for when and how this happens are not completely understood. Building on the concept of indirect evolutionary rescue (Yamamichi & Miner 2005), we present a study combing results from experiments and model simulations to introduce the idea of indirect evolutionary facilitation. Specifically, we present experimental results testing how genetic variation in defense (i.e., protection against the predator) and competitiveness (i.e., growth) traits in a prey population contributes to the rescue a predator population when exposed to a perturbation. We used different clones of the green algae *Chlamydomonas reinhardtii* that differ in their defensive and competitiveness traits as prey, the rotifer *Brachionus calyciflorus* as predator and microplastic particles as an external perturbation. The microplastics directly affects the predator food acquisition and thus indirectly its growth. We tested how the persistence of the predator depended on the combinations of traits and the strength of the perturbation. We found that microplastics

reduced both ingestion and growth rates of the predator with different patterns depending on prey traits. We then found that large genetic variation in the prey population allowed the persistence of the predator population up to a certain amount of microplastics. Overall, the recognition of indirect evolutionary processes will provide important new insights for predicting the survival of populations after a disturbance and future responses to environmental changes.

Abstract ID: 2300

Experimentally evaluating the impacts of immigration on adaptation to a novel environment

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A critical goal of modern evolutionary ecology is to establish how to effectively manage populations in human-altered environments. When the environment suddenly worsens and populations begin to decline, extinction will occur unless populations can adapt in response to natural selection (i.e., evolutionary rescue). After environmental change, theory predicts that immigration can delay extinction and provide novel genetic material that may reduce inbreeding depression and facilitate adaptation. However, when migrants are not adapted to the new environment, immigration can also counteract selection and constrain adaptation. This study evaluated these theoretical predictions using the red flour beetle, *Tribolium castaneum,* as a model system. Initially small populations were exposed to a novel insecticide, and three immigration rates were implemented with migrants from a benign environment: 1 migrant/generation, 5 migrants/generation, one large migration event, and no migration (control). Population size and fitness were measured throughout the experiment. Following an initial decline across all treatments, control populations recovered the fastest, illustrating the constraining effects of immigration on adaptation. After seven experimental generations, a reciprocal transplant study revealed that all populations were adapted to the insecticide regardless of immigration, and a fitness cost to adaptation was revealed when populations were reared in the benign environment. Potential benefits of immigration such as increased genetic variation may become apparent through future genomic analysis. Overall, this work seeks to determine the utility of immigration as a management strategy for recovering fitness, maintaining genetic health, and promoting adaptation to a novel environment.

Abstract ID: 1556

The effect of bottleneck size and antibiotic-induced selection on antibiotic resistance evolution

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Bacterial populations undergo several bottlenecks during infection of host populations, imposed by the transmission of pathogens between hosts, an activated host immune response, or the antibiotic treatment employed. Bottlenecks—catastrophe events that drastically reduce bacterial population size—can increase the influence of random effects during bacterial evolution, directly affecting the diversity of resistance alleles. In evolution experiments, bottlenecks typically occur periodically in time. Between bottlenecks, factors such as antibiotic-induced selection, competition or clonal interference directly affect bacterial growth and, consequently, resistance evolution. Despite the relevance and presence of bottlenecks in antibiotic resistance evolution, their effect, along with such factors, has been largely ignored in the literature. Recent evolution experiments have demonstrated that bottleneck size and antibiotic-induced selection reproducibly impact the evolutionary path to resistance in pathogenic *Pseudomonas aeruginosa*. In particular, these experiments found that resistance is favoured—expectedly—under high antibiotic selection and weak bottlenecks, but—unexpectedly—also under low antibiotic selection and severe bottlenecks. An understanding of this observation is missing, and mathematical modelling can aid in explaining it. In this talk, I will present progress made in the theoretical modelling of these evolution experiments to explain their outcome. The model I will present is based on a multi-type non-homogeneous birth-death-mutation process in continuous time. The model takes into account the lag phase experienced by the bacterial population before entering the exponential growth phase and resource competition between strains. At the end of the talk, I will discuss several model extensions that may inspire new experiments.

Abstract ID: 1007

Towards the prediction of the epidemiological dynamics of *E.coli* during infection by phages T7

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Measure, describe and predict the co-evolution of bacteria and their phages is essential for the development of bacteriophages as clinical antibacterial treatments. When studying epidemiological dynamics of bacteria/phage systems, one of the main issues is to find a precise and high throughput, yet not too laborious measurement, as a proxy of the bacterial population size over time while phage infection occurs. In our study, the production of living cells and biomass of Escherichia coli in the presence of bacteriophage T7 were measured in parallel on a real-time basis, using several fluoro-luminometric measurement (Fluorescence with CFP and bioluminescence), combined with optical density that is a rough proxy of the bacterial population kinetic. We evaluate the ability of the main epidemiological models of type Sensitive/Infected/Phage (SIP) found in the litterature to jointly fit these distinct measured bacterial kinetics and their mutual consistency as a test of model validity. Using these three fluoroluminometric measurements combined with their theoretical modelisation allow to describe the dynamics of infections with accuracy. Such parameterization of the epidemiological dynamic opens the perspective of predicting with good confidence the kinetics of co-evolution in bacteria/phage systems.

Abstract ID: 2145

Life-history evolution in response to foraging risk, modeled for Northeast arctic cod (*Gadus morhua*)

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Fisheries management do not presently account for evolutionary adaptation of fish stocks, despite the strong theoretical foundation showing that evolution is likely have long-term impacts on fish stocks. A key tradeoff driving evolution is the decision of how much to forage. Increased foraging effort increase energy intake, which is useful for growth and reproduction, but comes at the cost of increased mortality due to increased exposure to predators. We present an individual-based, mechanistic modeling framework, adapted to Northeast Arctic Cod. The model incorporates life-history traits, mortality trade-offs and heritability, allowing evolution to occur as the consequence of individual trait combinations and the interactions between them. By altering the interaction between foraging and mortality, we simulate various levels of risk associated with foraging effort. We find that with increased risk, and the subsequent increase in mortality, fish scale down their foraging effort. This combination of decreased energy availability and higher mortality in turn select for faster maturation and higher reproductive investment. These results fit well with expectations, given that increasing time spent at smaller, more vulnerable, sizes would also reduce the likelihood of surviving to mature later. Given that natural mortality among fish is generally poorly understood, these results highlight an interesting point of further research, that could help future modeling approaches make more accurate assumptions about natural mortality and its components.

Symposium: S11. Adaptation and evolution across environmental gradients (id: 26)

Abstract ID: 1933

Thermal performance, plasticity, and adaptive potential across environmental gradients

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Environmental conditions in nature are highly variable in space and time, yet organisms must adapt to them in order to succeed. On-going climate change poses further challenges for adaptation as both the means and the variability of environmental conditions are shifting. It is becoming increasingly evident that successful adaptations often require both local adaptation and adaptive plastic responses, latter which may also include transgenerational effects. I will present some on-going work in the classic model in eco-evolutionary dynamics, the Glanville fritillary butterfly, where we address the role of local adaptation and plastic responses in relation to climate change adaptation. We

combine experimental manipulations with genomic analyses using individuals originating from natural populations across environmental gradients. Generally we find evidence for local adaptation as well as strong within-generation plasticity for temperature. Individuals from populations across the environmental gradient vary in plasticity with the Northern populations showing both higher plasticity as well as higher intra-population variation for plasticity. Evidence for adaptive transgenerational plasticity in this population is, on the other hand, generally weak, presumably due to low predictability of temperature fluctuations within the growing season. Whole genome sequence data revealed evidence for local adaptation to climate but only few candidate loci overlapped between two altitudinal gradients, in the Alps and Pyrenes, suggesting divergent adaptive responses.

Abstract ID: 1068

Change from early to adult environment affects aphid transcriptome, fitness and endosymbiont density

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Environmental conditions experienced during early development are a key predictor of an organism's adult phenotype. Such early environmental effects may prime an organism to anticipate specific conditions during adulthood and can be adaptive if the actual conditions match those for which the organisms were primed. While phenotypic plasticity (adaptive or not) in response to changing conditions has been demonstrated in a range of organisms, the underlying mechanisms of the responses to either matching or mis-matching conditions remain largely unclear. Focussing on a temperature gradient reflecting good and poor developmental conditions, we tested key predictions of how a change in thermal conditions from early to adult environments affects fitness using a fully factorial experiment in a clonally reproducing pea aphid system with different life histories. We further investigated the underlying molecular mechanism using RNAseq, predicting that transcriptomic changes underpin differential responses and ultimately fitness. Our results demonstrate that, in contrast to our predictions, better early conditions provided a fitness advantage regardless of whether or not these conditions match with the adult conditions; whereas fitness always improved with better adult conditions. The transcriptome profile of aphids that developed in identical or changing environments reveals a genotype-specific response to environmental conditions as well as distinct environmental effects independent of genotype. We also found associated changes in aphid endosymbiont density, which suggest that the environmental impact on the endosymbiont community directly or indirectly affects how aphids respond to environmental conditions.

Abstract ID: 1130

Genome-wide detection of selection and local adaptation in *Temnothorax longispinosus* to its parasite

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Parasitism is a highly specialized and evolutionarily successful lifestyle that requires remodelling of phenotypic traits and underlying genomic basis for host exploitation. Social parasites exploit the altruistic behaviours of their hosts, so behavioural adaptations are of particular importance in these parasites and their hosts. In the case of the obligate dulotic ant, *Temnothorax americanus* and its host *Temnothorax longispinosus*, their shared phylogenetic ancestry and shared environments facilitates investigating the molecular underpinnings of the evolutionary arms race and geographic mosaic of coevolution of this social parasite and its host. With this plan in mind, we collected host and parasite colonies from ten populations throughout the north-eastern United States. We used a Pool-Seq approach to determine the population structure of the host and to infer local adaptation patterns. Moreover, we conducted Pool-GWAS analyses to identify candidate loci associated with i) parasite prevalence, ii) parasite recognition via antennal transcriptomes, iii) host aggression based on behavioural assays, iv) diversity of chemical profiles, and finally v) environmental variables such as climate. These results give some first insights into the genomic basis biotic interactions by looking at the coevolution between host and parasite and taking into account local adaptation patterns along environmental gradients.

Abstract ID: 1284

A population genomic approach of bumble bee responses to urban ecosystems

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Human settlements and urban growth have profound effects on natural ecosystems. Urban development results in loss, degradation and fragmentation of natural habitats, increase in impervious surfaces, as well as in environmental effects associated with the heat island effect, water, air, noise and light pollution. Ultimately, urbanisation leads to the creation of novel ecosystems that exhibit novel abiotic and biotic characteristics and pose a challenge to many organisms including wild pollinators, whilst also imposing altered selective regimes. Among wild pollinators, bumble bees are a model system for studies on behavior, ecology and evolution, in part because of their ecological and economic importance. Here, we used whole genome sequencing to generate SNP data for 200 *Bombus terrestris*, 200 *Bombus lapidarius* and 221 *Bombus pascuorum* individuals, sampled from nine cities in Germany and nine paired rural sites. We then employed a comparative population genomic approach to study their responses to urban ecosystems. Millions of SNPs were identified and used to assess genome-wide genetic diversity and to partition diversity into neutral and adaptive, identifying both key demographic parameters from neutral markers and candidate loci undergoing selection for urban habitats.

Abstract ID: 1292

How insect chemical profiles unify signaling & adaptation: Evolutionary conservation of a dual trait

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Cuticular hydrocarbons (CHC) form the basis for a wide array of chemical communication systems in insects while primarily functioning as desiccation barrier. Conserved signaling properties in CHC profiles can range from nestmate recognition in eusocial insects to sex pheromones in solitary insects. Simultaneously, CHC profiles have been postulated to display considerable flexibility to allow insects to adapt to a wide range of different climatic conditions. However, preservation of encoded signaling functionalities might constrain the adaptive flexibility in this dual trait postulated to be crucial for adaptation and insect survival in varying environmental desiccation conditions. To shed light on these seemingly contradictory selective pressures, we analyzed CHC profile variation across different environmental gradients in two representative hymenopteran species and isolated the particular CHC compound classes correlating with factors most closely associated with desiccation. In the invasive Argentine ant *Linepithema humile*, huge super colonies partially transcending continents retain the capability of widely expanded nestmate recognition while adapting to vastly different micro-climates, whereas in the cosmopolitan parasitoid wasp *Nasonia vitripennis*, CHC function as universally recognized female-specific sex pheromones. By unraveling the compounds with the most potential for adaptive flexibility in both species, we were also able to narrow down the CHC compounds most likely encoding and conveying the conserved signaling function, revealing interesting similarities despite the actual communicated information varying so widely between both species. This suggests that the main signaling properties in CHC profiles can be evolutionary conserved across vast phylogenetic boundaries, delivering intriguing potential hints at a unified, common “chemical language”.

Abstract ID: 1447

Heliconius butterflies: colour, altitude, and thermal tolerance

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With the onset of climate change, understanding insect thermal responses has become an increasingly relevant topic for investigation. *Heliconius* butterflies, famous for their müllerian mimicry and polymorphism, have a wide distribution across the neotropics and occupy a wide range of temperatures, mainly due to their distribution on the slopes of the Andes. However, the mechanisms that underpin *Heliconius* thermal adaptation have been relatively understudied. Environmental gradients, such as altitude, can be used as a fantastic proxy to understand temperature-driven responses due to possible local adaptation within species across the gradient. Here we investigate the effect of altitude on the wing colour variation of *H. erato* and *H. melpomene*, distantly related mimics often found in the same locations. Specifically, we present evidence that there is variation in the extent of black coverage and the hue of red colour, associated with elevation, with individuals from higher elevations being darker, with increased black coverage, consistent with “thermal melanism”. This was done by processing standardised digital photographed wings with a “K-distance clustering approach”, in which similar pixels in standardised images are made to cluster together to give the percentage and hue of each colour in the image. We used individuals from common-garden and temperature-controlled rearing to establish the extent to which this variation is due to genetic

differences between populations, versus environmental effects. We then test for a relationship between wing colour and thermal tolerance. Overall, our results indicate local adaptation to altitude in *Heliconius* butterflies.

Abstract ID: 1457

Cross-seasonal trade-offs in two closely related butterflies

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Classic niche theory tells us that species can co-exist by occupying different regions of a multidimensional niche space. They could be separated in space or utilize different resources that potentially fluctuate over space and time, and the extent of a species' niche should be governed by trade-offs. But what is the role of seasonal variation in this equation, and is season-specific performance constrained by cross-seasonal trade-offs? We here present a system of two closely related butterflies (*Pieris rapae* and *P. napi*) that co-occur in Sweden both geographically and phenologically, share host-plant preferences, and have seemingly similar life-histories. Yet, by analysing citizen-science data over 11 years, we show that they display remarkably different population dynamics. Throughout the species' common bivoltine range, *P. rapae* have a relatively small first generation, but a second generation of quadruple the size. In contrast, *P. napi's* second generation is only marginally larger than the first. Using a combination of field and laboratory experiments, we show that *P. rapae* prefer to oviposit in warmer microclimates than *P. napi*, and perform better in multiple growth season-related traits, particularly at warm temperatures. Instead, *P. napi* survive diapause overwintering better than P. rapae. Our results point towards *P. rapae* being better than *P. napi* at utilizing growth season conditions, with emphasis on warm temperatures. However, this comes with poor performance during the cold winter months, indicating the presence of cross-seasonal trade-offs. We highlight seasonality as promoting thermal niche-separation, and suggest that the species are displaying two alternative stable evolutionary strategies.

Abstract ID: 2353

Identifying candidate genes for adaptation to a light gradient in a group of Malawi cichlids

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Ecological gradients play a significant role in species diversification. Yet, we are still lacking a uniform view regarding which genes and molecular pathways are relevant for this process. Here, we focused on a group of deep-water adapted cichlids from Lake Malawi, the clade Diplotaxodon, to investigate genomic changes associated with differences in water-depth distribution among species. Using whole-genome resequencing data, we analyzed genome-wide associations (GWA) between SNP variation and a proxy for habitat depth – eye size – among 9 Diplotaxodon species. We

found multiple association peaks along the genome, containing SNPs enriched for GO categories related with visual perception and photoresponse. Annotation of the 0.01% top-most significant SNPs showed an overrepresentation of non-synonymous changes, compared to the genome-wide background. A large proportion of the SNPs with a predicted non-synonymous effect map to cone-specific phototransduction genes, including *arr3a*, *gucy2d*, *gnat2*, *cnga3a* and *pde6h*. These results support previous findings, suggesting a prominent role of cone vision for depth adaptation in this clade. Additionally, we found strong allele frequency differences among *D. limnothrissa* and representatives of the D. macrops 'complex' (e.g., *D. sp. 'macrops black dorsal'*) at the top GWAS SNPs. We propose that this could be an indication of adaptive divergence among Diplotaxodon species linked to differences in light conditions related with contrasting depth distributions. Whether allelic variation in these genes has a functional impact in visual sensitivities remains to be tested; however, our findings provide valuable insights into the role of environmental gradients in cichlid visual system diversification.

Abstract ID: 1626

Climatic gradients shape macroevolutionary patterns of chemical signal diversity across *Drosophila*

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Selection consistently favours efficiency in biological signals, yet these traits are remarkably diverse among closely related species. This perplexing diversity might be understood by considering additional sources of selection on signals, including sources that vary along environmental gradients. One class of traits that is shaped by multiple, potentially environmentally variable forms of selection are the sexually dimorphic cuticular hydrocarbon (CHC) profiles of insects. These profiles act as both sexually selected signals and naturally selected waterproofing barriers. Sexual selection favours low boiling point CHCs that partially melt at natural temperatures, whereas natural selection favours high boiling points because melting jeopardizes desiccation resistance. To understand how sex and environment shape signal diversity by influencing this trade-off, we analyzed CHC boiling point data for over 500 male and female *Drosophila* representing 95 species. We categorized species along an aridity gradient as arid, temperate, tropical, or cosmopolitan, and performed sex-specific phylogenetic ANOVAs to test for boiling point differences among habitats. We also fit a set of likelihood-based models to test whether habitat influences sex-specific evolutionary rates. Our results indicate that arid-habitat flies evolve faster and have higher boiling points than flies from other habitats, consistent with greater desiccation stress and stronger natural selection in those environments. The latter trend was, however, only significant for males. Collectively, our results suggest that climatic gradients shape the diversity of a complex chemical signal, with sex-specific environmental effects contributing to the vast CHC variation we see between sexes and among species.

Abstract ID: 1962

Thermoregulation, transparency and altitude in clearwing butterflies

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In contrast to most butterflies which harbour colorful wings and a wide variety of patterns, some species display transparent wings to various extents, for which light absorption is limited. Transparency raises questions regarding potential costs for vital functions, such as thermoregulation. Moreover, many neotropical clearwing butterflies can be found at high altitudes, with cooler conditions, where species are expected to harbour darker colour pattern. Understanding the complex processes involved in thermoregulation in these butterflies requires a multidisciplinary approach, combining the study of the physical phenomena of light radiations absorption by wings, associated with the exploration of thermal needs and behaviors that the different species perform to thermoregulate. The neotropical butterfly tribe Ithomiini includes almost 300 clearwing species, distributed from sea level to high altitudes in the Andes. We undertook a comparative study of the optical and thermal properties of the wings of several Ithomiini species, from highly transparent to fully opaque, and from low to highlands. We also tested the thermal tolerance to temperature extremes of two communities living at different altitudes in Ecuador. We were able to show that while transparent parts of the wings are less efficient to collect heat, Ithomiini harbour more transparency in altitude. Meanwhile, highland species have the same performances in the cold as lowland species, but are less resistant to heat. Our study depicts for the first time a physical study of the thermal properties of transparent butterfly wings, associated with insight of their physiological ability, linked to the environment of such peculiar animals.

Abstract ID: 1977

Seasonally varying selection drives supergene-based adaptation in overwintering *Drosophila*

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Drosophila melanogaster living in temperate regions adaptively evolve as they track seasonal fluctuations in the strength and direction of selection. Yet, we lack a detailed understanding of the functional genetic architecture of seasonal adaptive tracking. This gap in knowledge is compounded by seasonal boom-bust population cycles, a process that may alter levels of standing genetic variation. We characterized the genomic signal of boom-and-bust cycles and identified candidate loci that drive seasonal adaptation from multiple, densely sampled orchard populations collected across several years. PCA reveals temporal structure, and using genetic simulations, we show that this temporal structure is consistent with cyclical population collapse. The boom-bust signal is observed genome-wide except for chromosome 2L, where allele frequencies of the cosmopolitan inversion In(2L)t drive genetic structure. Loci inside In(2L)t are strongly associated with temperature in the weeks prior to sampling and these temperature associated loci are clustered into multiple regions inside the inversion. These clusters are

in high linkage at distances >1 Mb, suggesting that In(2L)t could harbor a supergene. Several of these regions are associated with recent partial selective sweeps occurring only on the inverted karyotype. Our results provide new insights about *Drosophila* seasonality and rapid evolution. First, we show that demographic contractions and expansions are an important, and measurable, component of the seasonal dynamics of temperate Drosophilids. Second, we provide strong support for candidate regions that underlie seasonal adaptative tracking. Finally, this work supports the general hypothesis that supergenes are important drivers of rapid adaptation.

Abstract ID: 2013

Sensory adaptation and perceptual thresholds across an ecological gradient in *Heliconius* butterflies

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Diverging populations often experience different sensory conditions which may impose divergent selection on the sensory systems. Most examples of sensory system adaption come from the sensory periphery, but fewer studies have considered the behavioural implications of changes within the brain. *Heliconius erato cyrbia* and *H. himera* are two closely related butterflies distributed across an environmental gradient in western Ecuador. *H. e. cyrbia* occurs in low-elevation wet forests, whereas *H. himera* is found in higher semi-arid forests. Neuroanatomical differences and recent behavioural work suggest sensory system adaptation: for *H. e. cyrbia*, brain regions associated with visual processing are larger, and in choice assays, visual stimuli are preferred over olfactory stimuli; for *H. himera*, olfactory processing brain regions are larger, and olfactory signals are preferred over visual signals. These data suggest habitat-associated sensory system adaptation via differential sensory investment, but whether or not this translates into differences in sensory perception has not been established. We test insectary-reared *H. e. cyrbia* and *H. himera* in parallel assays, training both species to differentiate between two visual or two olfactory stimuli and then sequentially testing with increasingly similar stimuli to determine sensory perception thresholds. Sensory adaptions in different species may also converge under similar environmental conditions; we test this by including *H. e. lativitta*, another low-elevation species from wet forests East of the Andes Mountains. Finally, we assay F1 hybrids of all three species to observe signatures of disruption among divergent eco-types that may contribute to extrinsic post-mating isolation.

Abstract ID: 2085

Hybridization in closely related wood ants with different climatic adaptations

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Hybridization and the following introgression can cause negative fitness effects and hybrid breakdown, but also potentially help populations adapt to a changing environment. To better understand the consequences of hybridization, we need knowledge on naturally hybridizing non-model organisms. Here we examined hybridization in five keystone *Formica* wood ant species that co-occur in Finland across a climatic gradient. Whole-genome data from 77 individuals, one per population across Finland, comprised five species: *F. aquilonia*, *F. polyctena*, *F. rufa*, *F. lugubris*, and *F. pratensis*. It revealed widespread hybridization among three species. All studied populations of the southerly adapted *F. polyctena* were admixed. In addition to it hybridizing with northerly adapted *F. aquilonia*, also southerly adapted *F. rufa* was involved in the hybridization. Moreover, climate analyses show that the hybrid populations nest in warmer locations than sympatric populations of *F. aquilonia*, the northern parental species. Thus, at the northern edge of the *F. polyctena* and *F. rufa* ranges hybridization is more extensive than previously observed and the results reveal a mosaic hybrid zone. Considering the widespread effects of the revealed hybridization, it may impact adaptation possibilities of the *Formica* species in the face of warming climate. It will also be of interest to study in future, how the hybrid zone will move with the ongoing climate change.

Abstract ID: 2379

Multispecies comparative analysis of phenology variation along altitudinal gradients in butterflies

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In temperate regions, butterfly phenologies are known to be diverse, varying in the wintering stage, voltinism, timing of generation(s), and environmental clues. Latitudinal changes in phenology are well understood, but altitudinal variations tend to be more difficult to predict as they vary on short spatial scales with fast-changing environmental factors, such as temperature, exposure, orientation, vegetation cover, land use. The way those phenologies change relative to these environmental factors may have an important impact on local adaptation, gene flow, and speciation. There are to our knowledge no generalized analysis of species phenology variation and their drivers. Here, we explore the diversity of phenologies in relation to altitude. Using participatory data from French programmes and repositories, we analyzed the variation in phenology for more than 150 species, using 3d representations of variations in the timing of adult butterfly occurrence relative to environmental factors. We then constructed a phenotypic landscape (or “morphospace”) providing a generalized view of species phenologies, and allowing extracting the main descriptors of their variation across the species studied. Different phenology types could be recognized along those main axes, associated with specific

aspects of the biology of the species (phylogeny, wintering stage, hostplants). This analysis allows formulating testable hypotheses regarding the main drivers of phenological adaptation along the altitudinal gradient in mountain regions, and provides insight on patterns of gene flow and speciation among populations adapted to different altitudes.

Abstract ID: 2393

Going deeper: molecular adaptation to hypoxia in African crater lake cichlids

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In this study we are trying to understand the molecular background which underlies the establishment of adaptation in fish that inhabit deep-water environment. We focused on the monophyletic species flock from Barombi Mbo lake which is characterized by a relatively big depth (110 m) and provides a wide range of habitats with various oxygen and light conditions. Cameroonian crater lake cichlids are a celebrated example of sympatric speciation. During their rapid evolution they adapted to the various ecological niches within the same waterbody and every species became specialized for a particular trophic niche in absence of spatial separation. Two cichlid species (*Konia dikume* and *Myaka myaka*) inhabit deeper water layers and are adapted to the reduced light, oxygen and high hydrostatic pressure. Here, we discuss the role of the mutations in hemoglobin genes and try to provide a link between structural changes in the amino-acid sequence and adaptation to deep-water habitat. We report that deep-water specialists *Konia dikume* and *Myaka myaka* possess a high number of specific amino-acid substitutions in four hemoglobin genes that are expressed in adult fish. We performed functional tests of the blood in five Barombi Mbos cichlids and identified that there are interspecific differences in isoform composition of hemoglobins and that blood of *Myaka myaka* demonstrates a higher responsiveness to the presence of allosteric cofactors. In addition to that, we performed swimming performance and hypoxia tolerance tests and observed that fish with mutated hemoglobins reach higher critical swimming speed and tolerate lower oxygen concentrations.

Abstract ID: 1886

Adaptating to oncogenic pollution in two flatfish species: why (and how) can one but not another?

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Tackling cancer is considered a global challenge that calls for integration of diverse fields. Studying cancer in wild species in ecological settings is one yet underexplored direction. Majority of human cancers are caused by environmental factors, including oncogenic pollutants, which also cause cancer in wild animals. In ecological settings, natural selection can produce solutions to negative impacts of environmental change, given enough time. The increase of oncogenic substances in natural habitats has therefore unintentionally created opportunities for using polluted habitats as "natural laboratories" for studying cancer defence mechanisms. The Baltic and North Sea are among the most polluted marine areas, having a long history of contamination. Two flatfish species (*Platichthys flesus* and *Limanda limanda*) inhabit a whole gradient of contamination, creating opportunities for studying populations that have, for a long time, been exposed to differing selection pressures. Both species are used as ecotoxicological indicator species due to pollution-induced liver cancer, which is much more prevalent in dab, suggesting that flounders are better protected against pollution-induced cancer. By conducting gene expression analyses, we were able to suggest the genetic mechanisms behind pollution-induced cancer in both species, but also the mechanisms that protect flounders (but not dabs) against cancer development. The finding that from two closely related species, one can develop defences against pollution-induced cancer and the other cannot, and the ability to suggest the genetic mechanisms behind this, is one of the first demonstrations of the usefulness of the "natural laboratory" approach in cancer biology.

Abstract ID: 1804

Genome-environment associations in herring and horse mackerel: implications for climate change

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Abundant marine species offer ideal systems to discover selection signatures and, thus, study molecular mechanisms underlying ecological adaptation. Here we integrate whole-genome sequencing, oceanographic data, and environmental modelling to uncover the genomic basis and environmental correlates of local adaptation in two iconic marine fish species, Atlantic herring and horse mackerel. These species have wide geographic distributions and inhabit a variety of environments, but have marked differences in life history. Herring spawn in shallower offshore/nearshore waters and exhibit substantial homing behavior and spawning-season fidelity. Horse mackerel spawn on deeper shelf waters and are not presumably faithful to spawning grounds. In herring, our genomic analysis revealed a striking association between adaptive genetic variation and

environmental factors varying between spawning sites. Relevant factors include temperature, salinity, oxygen, turbidity, and tidal range. In horse mackerel, a similar association was observed but to a much lesser extent, perhaps due to lower habitat variability and selective pressures during early-life. In both species, putative chromosomal inversions underlined climate-related clines. We found several candidate genes that could play critical roles in energy metabolism, cellular function, and light sensitivity. An analysis of the magnitude of mismatch between current adaptive genetic variation and future climate projections suggested differential climate change response between populations. We discuss the relative role of life history, selection, and gene flow in shaping adaptive genetic variation, and implications of our findings for future climate scenarios. Our studies provide insight into the molecular and ecological mechanisms underlying adaptation and the evolutionary response to climate change.

Abstract ID: 1553

The European native oyster's (*Ostrea edulis*) current genetic structuring.

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Endemic to European coasts, *Ostrea edulis* represents a luxury good since the Romans Empire. *O. edulis* is distributed across multiple environmental gradients, but we know very little about if and how populations have adapted to local environmental conditions. Furthermore, abundances are at historic lows due to overfishing and disease outbreaks. We also know that extensive translocations of *O. edulis* have and are occurring between the European countries, spreading lethal infectious parasites in natural remnant populations. But our knowledge about how translocations have affected the distribution of natural genetic diversity is limited.
Previously applied methods are done with allozymes, microsatellites and moderate numbers of SNPs. Although those studies showed significant structuring on large spatial scales (three distinct European genetic clusters) and have suggested adaptation in local populations, the limited genomic resolution and geographical scales of sampling have challenged the more detailed investigation of local adaptation on fine geographic and genomic scales.
Our study, based on low-coverage whole-genome resequencing of ~850 individuals across a dense sampling of 50 European localities, leverages novel high-resolution genomic techniques to address practical management needs in an emblematic European commercial species. Taking advantage of a new reference genome, our preliminary results show differences in previously uncharacterized putative chromosomal inversions between sampling locations and genetic differentiation between locations at finer geographical scales. Conservation planning efforts will benefit from a better understanding of the genetic structure, degree of local adaptation and molecular mechanisms for the establishment and maintenance of oyster populations and their parasites

Abstract ID: 1035

Do fisheries influence adaptation to climate change?

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Overfishing may be the biggest threat to aquatic ecosystems; indeed, the extremely high mortality rates and distinct size selectivity can cause evolutionary change in exploited populations. Consequently, fished populations may become more vulnerable to other anthropogenic stressors due to reduced genetic variation and selection towards certain life-history strategies. We utilise three populations exposed to size selective harvesting: large-selected (removing 75% of the smallest individuals from the population, leaving the largest individuals), small-selected (removing 75% of largest individuals from the population, leaving the smallest individuals, mimicking fisheries), and random-selected (removing 75% of a population at random). Five generations of size-selective harvesting induced numerous phenotypic changes in exploited populations together with large-scale genetic changes. These populations have now recovered from harvesting stress for nine generations. To determine the vulnerability to thermal stress of size-selectively exploited fish populations, we exposed individuals to three temperature treatments (34°C; 28°C; 22°C). We assessed differences among the selection lines in life history traits (growth and reproduction), physiological traits (metabolic rate and CTmax), behavioural traits (activity and feeding behaviour), and genetic traits. We found that selection lines showed different responses to the thermal stressors, with particularly strong responses at 34°C, showing large alterations in life history traits. Furthermore, our control line (random-selected) showed greater resilience to thermal stress, particularly in relation to growth and metabolism suggesting fisheries-induced selection can erode adaptive potential. Our results allow for a greater understanding of synergistic stressors on fish populations under future climatic scenarios.

Abstract ID: 1028

Genomic divergence across southern African marine thermal gradients

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The southern African coastline is a marine biodiversity hotspot of global importance, which is partly due to the region being an area of overlap of Atlantic and Indian Ocean fauna and flora. However, numerous smaller-scale biodiversity patterns exist that often separate closely related and morphologically cryptic sister species, and their existence is best explained by thermal gradients. Here, I summarise recent advances into furthering our understanding of how such spatial patterns were driven and are maintained. In addition to data based on traditional genetic methods suitable for summarising large-scale biogeographical patterns, I focus on findings based on genome-wide data from RADseq and RNA-Seq studies. These are particularly useful to identify differences between recently diverged populations or species that are not yet distinct based on selectively neutral or morphological data. They provide insights into early-stage divergence that takes place in portions of the genome that are under thermal selection, generating unique geographically constrained biodiversity in the face of often substantial

gene flow. Examples of how such information can be used to improve the management of exploited or threatened species are discussed.

Abstract ID: 1245

In Humboldt's footsteps: using gradients to make sense of ecosystem functions

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Nitrogen (N) fixation by moss-associated cyanobacteria is a main source of N input to pristine ecosystems such as arctic tundra and boreal forest. While we have a good understanding of the abiotic factors that control this ecosystem process in these northern, cold biomes, we have hardly touched upon the controls of N2 fixation activity in other pristine systems like tropical forests. Further, most of our current knowledge is based on single-factor experiments, while studies on the combined effects of various factors on N2 fixation are scarce. Here, gradients can serve as tools to identify driving factors behind ecosystem functions and their susceptibly to change.
I will present results on N2 fixation activity in mosses assessed along various gradients ranging from arctic tundra to tropical cloud forests using elevation as well as natural fertility gradients as natural laboratories. Our results show that moisture is a key factor controlling N2 fixation activity along gradients across ecosystems, but temperature shapes cyanobacterial community composition colonizing mosses. Increased N availability inhibits N2 fixation activity, while the effects of other nutrients such as phosphorus and molybdenum on N2 fixation in mosses depends on the nutrient status of the ecosystem. Taken together, moss-associated N2 fixation is driven by a range of abiotic and biotic factors, with moisture being the pivotal one. No N2 fixation without liquid water. Hence, climate change will drastically lower N input via moss-associated N2 fixation to ecosystems that are currently characterized by a humid climate, i.e. tropical forests.

Abstract ID: 1759

The potential for evolutionary rescue in an arctic seashore plant under climate change

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Climate change poses a particular threat to natural populations incapable of tracking suitable conditions by dispersing to new favourable areas. For such populations to persist in a warming world requires that they can adjust their phenotype in situ, through either plastic response, evolutionary genetic adaptation, or both. Here, we study a variety

of an arctic seashore plant, *Primula nutans* ssp. *finmarchica* var. *jokelae,* which occurs by the Bothnian Bay in Fennoscandia, and already shows signs of maladaptation to altered climatic conditions. We evaluate the potential for these populations to evolve through time to increase their likelihood of survival in novel conditions, i.e., their potential for evolutionary rescue. We utilize manual crossing experiments in a nested half-sibling breeding design and employ quantitative genetics methods to estimate G-matrices and evolvability. We compare evolutionary potential in vegetative versus reproductive traits and evaluate constraints on evolution given genetic correlations in traits with potentially competing selection pressures. Based on previous evidence from translocation trials indicating strong selection pressure posed by climate change, and our estimates of evolutionary potential from crossing data, we show that these threatened populations may not be able to evolve to an adaptive phenotype in the foreseeable future. The study addresses the urgent need to obtain a more predictive understanding of the adaptive potential and extinction risk of populations in the face of ongoing anthropogenic climate change.

Abstract ID: 1589

Genetic changes over time and space reveal candidate SNPs for local adaptation in *Laminaria digitata*

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Tracking genetic changes over time within populations allows exploration of how genetic drift and selection interact to shape patterns of genetic diversity. Here, we address these issues using thousands of SNPs (dd-RAD-sequencing) across four populations, at two-time steps (separated by about 10 years) in the cold-water kelp *Laminaria digitata*. These populations were sampled along a latitudinal gradient. Different outlier detection tests, including simulations to analyse neutral trajectories of allele frequencies, were ran at both temporal and spatial scales. These tests led to the identification of 52 outlier SNPs. Temporal and spatial candidate loci did not overlap, but the same two temporal outliers were identified in two different populations exposed to the highest mean sea-surface temperature. This correlated signal agrees with the hypothesis that these SNPs may be subject to similar selective pressures in these populations. On the contrary, in the smallest population (with an effective population size three to seven times smaller than that of other study populations), temporal analyses failed to detect any outliers, supporting the hypothesis that drift is probably the major factor driving the pattern of genetic diversity in this population. Using RAD loci mapping on protein-coding genes of related species, ten candidate SNPs were identified as belonging to a family of enzymes involved in metabolic processes. Their frequency in space and time was better explained by variation in sea-surface temperature rather than by geographical clines in allele frequency. Our results suggest that habitat heterogeneity may be accompanied by changes in selective pressures on a short timescale.

Abstract ID: 1073

The drivers of fast evolution in genetically depauperate Lupinus species from the Andean sky-islands

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The high-elevation flora from tropical mountains is recognized by its outstanding diversity, which evolved exceptionally fast within the last five million years. Ecological opportunities afforded by the emergence of island-like habitats and distributional changes induced by Pleistocene climate change are believed to have promoted species diversification. We focus on the microevolutionary drivers underpinning the Andean *Lupinus* radiation, which has become a model group to address fast and recent speciation. We study intraspecific patterns of genetic variation and reconstruct the demographic history of populations in three Andean *Lupinus* species, two of which, *Lupinus alopecuroides* and *Lupinus nubigenus* are very rare and endemic species. We find unprecedented low levels of within-population genetic diversity and high genetic differentiation between the populations. In *Lupinus microphyllus*, we detect signatures of historical gene flow, but negligible contemporary gene flow, and signals of an ancient decline in population size that may be lasting until today. Pleistocene climate change shaped intraspecific genetic patterns depending on local environmental factors, such as volcanic activity or glacier coverage, and on species-specific traits, such as the reproductive and dispersal strategies. In the case of the Andean lupines, our study shows that intraspecific patterns of genetic variation were mainly determined by episodes of geographic isolation during past cold periods, which were accompanied by restricted gene flow and enhanced genetic drift. Alarming low genetic diversity has been reported recently in several other tropical-alpine plants indicating that the tropical-alpine flora may be extremely vulnerable and prone to extinction.

Abstract ID: 1195

Genomic local adaptation of a generalist plant species to pollinator communities, soil, and climate

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The combined effect of changes in pollinator communities, and the direct impact of soil and climate variation on plant-pollinator interactions can strongly affect the reproductive success of flowering plants. However, knowledge of the adaptative potential of plants to complex ecological networks and the underlying genetic mechanisms is still limited. Based on a pool-sequencing approach of 21 natural populations of *Brassica incana* in Southern Italy, we combined a genome-environmental association (GEA) analysis with a

genome scan for signature of selection to discover genetic variants associated with pollinator communities, edaphic and climatic variation. We demonstrated that *B. incana* is locally adapted to both single pollinator species and the overall pollinator interactions. Interestingly, we observed a significant number of genetic variants shared between the soil texture (fine silt) and the visits of bumblebees and hoverflies, while few genetic variants involved in both pollinator and climate variation were identified. Our results highlight the adaptive potential of generalist species to complex biotic interactions, and the importance of considering multiple environmental factors to describe their adaptive landscape.

Abstract ID: 1232

Parallel adaptation to environmental gradients in Arabidopsis: role of standing vs. de-novo variants

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Parallel adaptation provides valuable insight into the predictability of evolutionary change through replicated natural experiments. We investigated the strength and genomic underpinnings of repeated local adaptation of two outcrossing *Arabidopsis* species towards challenging environments. Based on structured sampling of 13 pairs of ecologically divergent populations, ecological experiments and population genomics, we discovered rapid multi-parallel adaptation towards both high-alpine sites and toxic serpentine soils and detected significant over-representation of shared adaptive candidate genes for each environment. Although vast majority of the parallel candidates sourced on shared allelic variation, we also discovered a small fraction of genes exhibiting convergent evolution from independent *de novo* mutations. In alpine adaptation, we complemented our investigations with published gene lists from five additional alpine Brassicaceae and found that the extent of genomic parallelism significantly decreased with increasing divergence between the compared lineages. This relationship was explained by decreasing probability of repeated selection on the same standing or introgressed alleles. We therefore conclude that genetic divergence between populations, species and genera, affecting the pool of shared variants, is an important factor in the predictability of genome evolution.

Abstract ID: 1959

The effects of global urbanization on demographic processes in Trifolium repens

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Urbanization is a worldwide phenomenon driving changes in the biotic and abiotic environment at an unprecedented rate. Evidence is growing that these urban environmental changes drive species' evolution, yet little is known about how urbanization affects the demography of populations. Demographic events, including population bottlenecks, expansions, divergence, and gene flow are among the most important evolutionary processes shaping the genetic diversity within and among populations, with important consequences for the future evolutionary potential of

populations. Here we build on the Global Urban Evolution project to understanding how urbanization affects population demography and if it leads to similar evolutionary processes among cities.
Using the plant white clover (*Trifolium repens*), we performed whole genome sequencing on >2500 plants sampled from urban and rural populations across 25 cities. We then quantified genetic diversity within and between habitats and performed demographic modeling. White clover populations had high levels of genetic diversity in both habitats and in the majority of cases, did not experience bottlenecks when first colonizing urban habitats, yet experienced modest population expansion through time. Additionally, even populations that were clearly structured, urban and rural populations showed evidence of extensive ongoing gene flow. These results show that urbanization drives similar demographic events in replicated cities and do not lead to strong isolation between urban and rural populations. Our results suggest that unlike some native species that experience population bottlenecks, restricted gene flow and reduced evolutionary potential in urban aeras, urbanization may promote population expansion and migration, and enhance evolutionary potential in cosmopolitan species.

Abstract ID: 1218

Global urban envionmental change drives adaptation in white clover

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Urbanization dramatically transforms environments in ways that alter the evolution of life. We examined whether urban environmental change drives parallel evolution by sampling 110,019 white clover (*Trifolium repens*) plants from 6,169 populations spanning urban-rural gradients in 160 cities across diverse climates. Plants were assayed for hydrogen cyanide, an antiherbivore defence that also affects tolerance to abiotic stressors. Urban-rural gradients were associated with the evolution of phenotypic clines for hydrogen cyanide in 47% of cities throughout the world. Variation in the strength of clines among cities was explained by environmental changes in drought stress and vegetation cover that varied among cities. Sequencing 2,074 genomes from 26 cities revealed that clines were best explained by adaptive evolution. Our results demonstrate that urbanization is driving adaptation on a global scale.

Abstract ID: 1620

Evolutionary adaptive potential enlighten by genome–environment associations

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Leveraging innovative tools to speed-up the pre-breeding discovery of natural sources of adaptation from landraces, crop-wild relatives and orphan crops is a key prerequisite to accelerate the genetic gain of abiotic stress tolerance. In order to fill this scientific research gap, here we review modern inter-disciplinary approaches that combine ecological climate data with last generation evolutionary genomics under the paradigm of Genome–Environment Associations (GEA). We first exemplify how GEA utilizes *in situ* geo-referencing from genomically characterized gene bank accessions to pinpoint genomic signatures of natural selection while assessing its genetic basis. We later discuss the necessity to update current GEA models to predict both regional and microhabitat local adaptation with mechanistic eco-physiological climate indices and cutting-edge GWAS-type models. To account for polygenic evolutionary adaptation, we encourage the community to start gathering Genomic-Estimated Adaptive Values (GEAVs) from Genomic-Prediction (GP) and multi-dimensional Machine-Learning (ML). The latter two should ideally be weighted by *de novo* GWAS-based GEA estimates, and optimized for a scalable marker subset. We close envisioning avenues to make adaptation inferences more robust by merging high-resolution data sources, such as environmental remote sensing and summary statistics of the genomic site frequency spectrum, with epigenetic molecular functionality responsible for plastic inheritance in the wild.

"I shall endeavor to find out how nature's forces act upon one another, and in what manner the geographic environment exerts its influence on animals and plants. In short, I must find out about the harmony in nature" Alexander von Humboldt – Letter to Karl Freiesleben, Jun 1799

Abstract ID: 2212

Genetic basis of adaptation across aridity gradients in a new *Arabidopsis thaliana* diversity panel

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Drought is expected to intensify in many locations worldwide as a consequence of ongoing global warming. Understanding how populations adapt to drought across spatial gradients can provide clues about how they may adapt over time. The model plant species, *Arabidopsis thaliana,* is globally distributed across five continents, but previous species-wide studies have focused on only a subset of the natural range, mainly in Eurasia and North America. As part of the *Arabidopsis thaliana* African Genomes Project, we have expanded sampling to include populations from some of the most extreme climatic locations, mainly from Africa and other peripheral populations of the species range. This new diversity panel provides an opportunity to examine global as well as region-specific clinal patterns. Here, we investigate the response to drought and its genetic basis in this new global diversity panel. Analyses of worldwide and region-specific population sets reveal evidence for clinal patterns in drought tolerance with

precipitation and aridity, such that plants in more drought-prone locations tend to grow more slowly and reach a more compact final size. Trait-mapping reveals that parallel and convergent genetic changes are responsible for clinal patterns across regions. Overall, we clarify how plant populations adapted to climatic variation over space, information which can be applied to infer how populations might adapt to future climatic change.

Abstract ID: 1478

Local adaptation and environmental effects on the parasitic bacterium *Pasteuria ramosa*

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Local adaptation occurs when separated populations of a species, which are widely distributed and experience a variety of environmental conditions, adapt to their local environment. While numerous studies have investigated the local adaptation of hosts to their parasites and/or parasites to their hosts, only a handful of studies examined the local adaptation of endoparasites with free-living stages to their external (off-host) environment. *Pasteuria ramosa* is an endoparasitic bacterium that infects the water flea *Daphnia* across ponds in Eurasia and North America in different geographical areas, thus experiencing varying water regimes. We examined four groups of parasite populations that differ in their environmental regime origin – all year wet, summer dried, winter freeze, and winter freeze and summer dry. Our goal was to examine how the combination of temperature and dryness affects the parasite's ability to attach to its host and to infect it. We subjected the four groups to temperatures of 20, 33, 46 and 60˚C in dry and wet conditions, and exposed *Daphnia magna* individuals to the treated spores. We found that both temperature and dryness affected the attachment ability and the infectivity of the parasite. Even under high temperatures (60˚C), exposed spores from all populations attached to the host, mostly when dried, albeit they were unable to establish infection. Furthermore, desiccation of the spores helped them endure higher temperatures. However, our results provide little to no support for local adaptation of *P. ramosa* spores from highly disturbed pools to extreme conditions.

Abstract ID: 1562

Genome-wide association mapping for growth rate at fluctuating and extreme temperatures

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Climate change is predicted to increase both the number and the frequency of fluctuations in temperature. Due to increased variation, organisms are forced to tolerate more extreme temperatures, which can be harder to adapt to than the rising mean temperature. Furthermore, it has been suggested that different genetic mechanisms are used in adaptation to fluctuations with varying frequency compared to constant conditions. This can affect species' ability to confront climatic changes, and also complicate predicting their survival. We investigated if distinct genetic architectures or

constraints for adaptation (negative genetic correlations or low amounts of heritable genetic variation) are found at fluctuating and constant temperatures. To answer these questions, we used nested association mapping and quantitative genetics in a fungal model system. Growth rates were measured for a panel of 428 *Neurospora crassa* strains under fast and slow frequency fluctuations, at high and low temperature range with respect to the species' tolerance. The measurements were also made at constant mean and extreme temperatures of these ranges. The genome-wide association mapping discovered that the same loci were associated with growth rate at constant and fluctuating environments, indicating mostly common genetic background. Supporting these findings, we found strong positive genetic correlations between fast and low frequency fluctuations, and between fluctuating environments and their mean values. High heritability values across environments neither provided evidence for genetic constraints. Our results contradicted the theory concerning thermal fluctuations, which is best explained by the lack of strong selection on natural variation in wild-collected populations.

Abstract ID: 2452

Detecting parallel adaptation in clonal lineages of a plant pathogenic fungus

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Although ascomycete fungi can undergo sexual and asexual reproductive cycles, asexuallity is the pervasive mode of reproduction of field isolates of globally distributed fungal pathogens such as the rice blast fungus Magnaporthe oryzae. Three genetically differentiated clonal lineages of M. oryzae have successfully colonized different environments and rice hosts in the last couple of hundred of years. Detecting particular genomic regions under positive selection that contribute to this success is hampered by strong genome-wide patterns of linkage disequilibrium that have arisen due to the absence of meiotic recombination. To overcome this difficulty, we take advantage of the broad global distribution of clonal lineages and annotate homoplasies in each clonal lineage phylogeny. We hypothesize that homoplasy patterns can be used to detect cases of parallel adaptation, where similar hosts or climatic constraints are present in distant geographic regions colonized by a particular clonal lineage. By combining genomic annotation with comparison of population frequencies and ages of homoplasies, we generated candidate regions that could have arisen via parallel adaptation and might have played important roles in the successful expansion of this economically important fungus.

Abstract ID: 1341

Local genetic adaptation in chimpanzees along a habitat gradient

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Chimpanzees, along with bonobos, are our closest living relatives and are endangered, with numbers in continuous decline. They inhabit a diversity of habitats in sub-Saharan

Africa across the gradient from cool wet rainforest to hot dry savannah, which provides the opportunity for local genetic adaptations. Understanding such adaptations would provide fundamental insight into chimpanzee evolution and essential information for planning conservation efforts. However, studies of fine-scale adaptation in chimpanzees have been hindered by the difficulties associated with accessing genetic samples from endangered wild populations. Our work analyses a new dataset of unprecedented scale, consisting of 828 exomes from non-invasive samples of wild chimpanzees, together with newly collected data on the environmental gradient variables, to investigate local adaptation in chimpanzees. We found that SNPs with exceptionally large allele frequency differences between populations were enriched for virus response functions, highlighting the importance of pathogen-mediated adaptation in chimpanzees. We next investigated the evidence of adaptation along the rainforest-savannah environmental gradient by performing a genotype-environment association (GEA) analysis. We identified candidate targets of selection underlying adaptation to different habitats along this gradient, within subspecies and convergently across the four subspecies. I will discuss these results, together with the key biological pathways that we identify as facilitating adaptation to habitat type and the most likely selection pressures.

Abstract ID: 1624

Feather growth and quality across passerines is explained by breeding rather than moulting latitude

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Tropical bird species are characterised by a comparatively slow pace of life, being predictably different from their temperate zone counterparts in their investments in growth, survival and reproduction. In birds, the development of functional plumage is often considered energetically demanding investment, with consequences on individual fitness and survival. However, current knowledge of interspecific variation in feather growth patterns is mostly based on species of the northern temperate zone. We evaluated patterns in tail feather growth rates (FGR) and feather quality (stress-induced fault bar occurrence; FBO), using 1518 individuals of 167 species and 39 passerine families inhabiting Afrotropical and northern temperate zones. We detected a clear difference in feather traits between species breeding in the temperate and tropical zones, with the latter having significantly slower FGR and three times higher FBO. Moreover, trans-Saharan latitudinal migrants resembled temperate zone residents in that they exhibited a comparatively fast FGR and low FBO, despite sharing moulting environments

with tropical species. Our results reveal convergent latitudinal shifts in feather growth investments (latitudinal syndrome) across unrelated passerine families and underscore the importance of breeding latitude in determining cross-species variation in key avian life-history traits.

Abstract ID: 2003

Standing variation and adaptation of a small mammal to climate change

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The most likely pathway for many species to survive future climate change is for pre-existing trait variation to provide a fitness advantage under the new climate conditions. Here we evaluate the potential role of haemoglobin (Hb) variation in bank voles (*Clethrionomys glareolus*) under future climate change. We model gene-climate relationships for two distinct Hb types HbS and HbF, which are distributed from north to south in Britain presenting an unusually tractable system linking genetic variation in physiology to geographic and temporal variation in climate. Projections for future climates indicate that the relative climatic suitability of haemoglobin types will change, resulting in the poorly adapted HbS being displaced by the advantageous HbF in much of Scotland and northern England. This would facilitate adaptation of populations to future climatic conditions - without HbF, voles in northern Britain would likely be poorly adapted in the future because their Hb would not match local climatic conditions. Such a scenario is consistent with the previously described displacement of HbS by HbF in southern Britain during end-glacial climate warming. Our study demonstrates how pre-existing differences in physiological tolerance can determine the adaptive capacity of populations to changing climatic conditions.

Abstract ID: 2370

Improved habitat quality benefits mothers but has a fitness cost for Soay sheep offspring

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Spatial and temporal differences among habitat quality, along with a variation in resource accessibility and availability, generate a strong selective pressure on habitat usage. This greatly influences fitness trade-offs associated with allocating energy and resources within individuals and for their subsequent offspring. To investigate the effect of habitat quality on annual and lifetime breeding and reproductive success (LBS and LRS), survival probability, parasite burden (FEC) and longevity, a Bayesian modelling framework was fit to data collected from a population of 1175 wild Soay sheep off the west coast of Scotland. We found that higher LBS and LRS was associated with better quality habitats; four-year old ewes grazing more on good-quality and less on poor-quality grass had an increased probability of reproducing and weaned offspring, but not

for recruiting offspring. We suggest that this may be linked to a higher longevity in ewes on good quality habitats, and an effect of vegetation on twinning. Over their lifetime, ewes grazing on better quality habitats recruit more lambs, however, offspring on good quality habitats have lower survival rates. This may be mediated by parasite burden as it is largely invariant to vegetation in ewes, but lambs have higher FEC counts on better quality patches, which leads to decreased chances of survival. Overall, this study suggests that offspring may incur fitness costs, while their mothers benefit. This is possibly in relation to the drastic overwinter mortality rate, as mothers may instead choose to invest in their own energy acquisition rather than parental care.

Abstract ID: 2043

Latitudinal but not elevational variation in blood glucose is linked to life history in passerines

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Macrophysiological research is vital to our understanding of mechanisms underpinning global life history variation and adaptation under diverse environments. Birds represent an important model taxon in this regard, yet our knowledge is limited to only a few physiological traits, mostly studied in temperate and Neotropical species. Here, we examined latitudinal and elevational variation in an emerging biomarker of physiological pace of life, blood glucose concentration, collected from 61 European temperate and 99 Afrotropical passerine species. Our data suggest that the slow physiological pace-of-life syndrome, indicated by lower baseline glucose level and stronger stress response, evolves convergently in lowland tropical birds across continents and is shaped by their low fecundity. In contrast, elevational variation in blood glucose levels implied a unique montane pace-of-life syndrome combining slow-paced life histories with fast-paced physiology. The observed patterns suggest an unequal importance of life history in shaping physiological adaptations associated with latitude and elevation.

Abstract ID: 1956

Herbivores adapt to metal-accumulating plants but lose their non-linear response at low metal doses

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Organisms are expected to respond linearly to linear gradients of a given stress. However, non-linear patterns such as hormesis have been observed in response to several abiotic stresses. These non-linearities emerge as an overcompensation of the organisms following a stress response, allowing them to maintain their fitness along a stress gradient. Yet, if organisms become tolerant to the stress, this overcompensation may be lost. Thus, non-linear responses may be contingent upon the recent evolutionary history of the populations. Here, we performed experimental evolution of two species of herbivorous spider-mites (*Tetranychus urticae* and *T. evansi*) on high concentrations of cadmium, without cadmium and on heterogeneous environments with and without cadmium. We then measured performance on plants exposed to several concentrations of cadmium at generations 11 and 33, to assess adaptation (performance at high cadmium concentrations), a cost thereof (performance in absence of cadmium) and the linearity of the response (the response to increasing concentrations of cadmium). We found adaptation to cadmium in populations of both species evolving at high concentrations. Moreover, our results show that populations evolving in absence of cadmium have a non-linear response to this stress, but this is lost in populations evolving with metal-accumulating plants, highlighting the dependence of non-linearities upon the evolutionary history of populations. For *T. urticae* adaptation to high cadmium occurred at no costs, suggesting that these populations would explore the gradient more efficiently, while for *T. evansi*, adaptation to high cadmium is costly at lower concentrations, possibly fostering specialization on high cadmium.

Symposium: S12. Resurrection ecology as a tool for the study of rapid evolution (id: 42)

Abstract ID: 1235

Resurrection ecology for environmental health: a perspective on biomonitoring and bioremediation

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Despite available technology and the knowledge that chemical pollution damages human and ecosystem health, chemical pollution remains rampant - ineffectively monitored, rarely prevented and only occasionally mitigated. In our pioneering work on waterfleas (*Daphnia*) resurrected from sedimentary archives dating back several decades, we discovered that historical exposure to chemical stress causes reduced genome-wide diversity in modern strains, leading to lower cross-generational tolerance to novel chemical stress. Lower tolerance is underpinned by reduced gene diversity at detoxification, catabolism and endocrine genes. Conversely, historical natural strains were more resistant to chemical stress. These discoveries enabled by resurrection ecology led to a novel framework, in which we broaden the use of the sentinel species *Daphnia* as a monitoring agent of water pollution. And where prevention has failed, to the application of *Daphnia* as a bioremediation agent to help combat the hazards of chemical mixtures in the environment. Applying modern 'omics' technologies

to *Daphnia* exposed to real-world ambient chemical mixtures, we can effectively detect chemical mixtures occurring in the environment, predict the effects of untested chemicals within mixtures, and identify diagnostic indicators for toxicological adverse outcomes and molecular signatures of toxicity. Where prevention is no longer an option, we show that using historical *Daphnia* strains naïve to chemical pollution as removal agents of ambient chemical mixtures can sustainably improve environmental health protection, preventing long-term exposures to chemicals. Expanding the use of *Daphnia* beyond its current applications empowered by resurrection ecology has the potential to transform both assessment and remediation of environmental pollution.

Abstract ID: 1987

Spatio-temporal genome dynamics of *D. magna* populations in multifarious environments

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Typically, the study of adaptive responses to environmental change focuses on single stressors because understanding the molecular mechanisms underpinning adaptation to complex environments is challenging. However, understanding responses to multifarious environments is paramount to gauge the adaptive potential of natural populations to human-driven changes.
Here, we use resurrection ecology and landscape ecology to study genome dynamics of 18 populations of *Daphnia magna* responding to three orthogonal gradients of selection, including natural (Predation and Parasites) and anthropogenic (Land-use) stressors. We validate spatial patterns with temporal dynamics observed in populations exposed through time to one of the three stressors. We reveal patterns and processes responsible for local adaptation, identifying both divergent and balancing selection as processes underpinning landscape evolution. Capitalizing on the properties of *Daphnia*, we link the genome-wide elements of adaptation to phenotypic plastic and constitutive fitness traits. Our study provides an integrative understanding of processes and mechanisms of adaptation to complex environments.

Abstract ID: 1246

Demographic and genomic consequences of a rapid adaptation event in the poplar rust pathogen

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The intense and unidirectional selection pressure caused by the massive deployment of resistant plants can result in rapid adaptation of pathogen populations[1]. Such rapid evolution was documented for the poplar rust fungus. In 1994, poplar rust populations suddenly overcame the RMlp7 qualitative resistance carried by poplar cultivars planted widely in Western Europe[2,3]. This recent event of adaptation from standing genetic variation caused a selective sweep on the rust genome[4]. We study a 25-year temporal sampling of poplar rust populations to decipher the demographic and evolutionary history of this pathogen while overcoming its host genetic resistance. Using a resurrection ecology approach, we examine phenotypic and genetic variations throughout this adaptive event. Our analyses reveal that a unique and homogeneous genetic group overcame RMlp7 resistance and replaced the ancestral genetic group within five years. We then use forward simulations to 1) understand the interplay between demography and genetic evolution underpinning the rapid evolution of poplar rust populations, and 2) disentangle the polymorphism signatures of selection from that of stochastic processes due to demographic changes. We show high stochasticity in evolutionary trajectories with the notable effect of evolutionary rescue scenarios on polymorphism signatures. Finally, we integrate our simulator in an Approximate Bayesian approach (ABC) to infer the demographic and selection parameters from temporal genetic data. Our statistical framework coupling modelling with temporal data is powerful to understand recent events of rapid adaptation.

[1]Saubin *etal*.DOI:10.24072/pcjournal.10
[2]Louet *etal*.DOI:10.1111/mec.16294
[3]Persoons *etal*.DOI:10.1111/mec.13980
[4]Persoons *etal*.DOI:10.1093/gbe/evab279

Abstract ID: 1877

Resurrecting plants for climate change research

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Climate change may cause rapid evolutionary changes in plant populations. The resurrection approach, in which individuals raised from ancestral propagules are compared with individuals raised from descendants of the same population, is a powerful and direct method to reveal evolutionary changes over time and can therefore be used to investigate how recent environmental dynamics affect rapid evolution. I will show that conventional seed banks are a valuable source of ancestral propagules for resurrection studies. Furthermore, I will provide evidence from resurrection studies that rapid evolutionary changes took place in various plant species across Europe, possibly as adaptive response to climate-change related environmental changes. Finally, I will show how resurrection ecology can adopt classical methods from experimental plant ecology and modern molecular techniques to increase our understanding of rapid evolutionary processes.

Symposium: S13. Evolutionary ecology of chemically-mediated species interactions in plants (id: 936)

Abstract ID: 1254

Adapting to increasing herbivory under climate change: the role of intraspecific trait variation

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Ongoing climate change may impact alpine plant populations via both direct effects of increased temperature and climate-driven changes in interactions between plants and other organisms, such as insect herbivores. Rates of herbivory in high-elevation environments are predicted to increase with warmer temperatures, yet, we currently know little about whether existing variation in defence traits within species might facilitate rapid adaptation to these changes. Using field surveys and greenhouse experiments, we tested for variation in herbivore resistance traits within and among populations of a perennial alpine plant, *Arabis alpina* (Brasssicaceae), from different elevations. Rates of herbivore damage declined with increasing elevation in the field, and plants from low elevations were generally less palatable for specialist herbivores than those from higher elevations. Elevational trends were also observed in constitutive and induced expression of glucosinolate defence compounds, though significant variation in glucosinolate production was also observed among populations from similar elevations. Growth chamber experiments suggest changes in non-defensive polar metabolites, rather than defence compounds, were associated with the elevational trends in specialist herbivore performance. To examine the evolutionary drivers of this variation, patterns of genetic diversity and structure are being estimated using RAD-seq genotyping and compared to patterns of trait divergence across the elevational range of *A. alpina*. Together, these results will offer insight into the factors driving intraspecific variation in defence, as well as the potential for species in high-elevation environments to respond to the changing herbivore pressure predicted with ongoing climate change.

Abstract ID: 1279

Effects of intraspecific plant chemodiversity on the attraction and occurrence of aphids

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Few plant species show an extraordinarily high intraspecific variation in plant compounds, which may influence interacting species. Individuals of the plant *Tanacetum vulgare* differ in the composition of terpenoids in their leaves and thus form so-called chemotypes. These differences have been shown to affect the attraction and performance of herbivores, including aphids. However, little is known about the effects of chemodiversity at the individual versus the population level on aphids specialised on *T.*

vulgare. To investigate this question, we set up a common garden containing 60 plots, each containing either five plants of the same or five different chemotypes, and scored the aphid abundance on each plant weekly. From leaf terpenoid profiles of the individuals, the pooled α-chemodiversity per plot was calculated. Winged individuals of *Metopeurum fuscoviride* showed a significant preference for (i.e. higher abundance of) certain chemotypes regardless of the plot-type. In contrast, the total number of *Uroleucon tanaceti* was affected by the chemotype-plot-type interaction: on plot level, a significant negative correlation between their number and the pooled α-chemodiversity was found. Yet no single terpenoid could explain the variance, highlighting the importance of compound combinations. Our results indicate that chemodiversity influences plant-aphid interactions on an individual and population level of the plants, depending on the aphid species and whether individuals are winged or not. Thus, chemodiversity of plants is an important dimension influencing an insect's niche, whereby the chemical composition needs to be considered on an individual and populational plant level, as both can affect the herbivore's performance.

Abstract ID: 1222

Real-time adaptation to evolutionary novel toxins in an insect herbivore

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A central challenge for empirical studies of plant-herbivore co-evolution is to infer evolutionary history from current interactions. Plant chemical defences likely played a central role in the plant-herbivore arms race, yet current interactions are dominated by specialized herbivores that are largely resistant to these defences. However, plants may occasionally escape from their co-evolved herbivores by gaining functionally novel types of defences. Such gains represent unique opportunities to study the consequences of phytochemical diversification for non-adapted herbivores. We study the evolutionary consequences of a recent gain of novel plant defences in the genus Erysimum (Brassicaceae). These plants uniquely produce two types of chemical toxins: evolutionary conserved glucosinolates and evolutionary novel cardenolides. Consistent with a co-evolutionary escape, several glucosinolate-adapted herbivore species no longer accept Erysimum as host plant, and no Erysimum herbivore has yet evolved specific resistance to cardenolides. The diamondback moth (DBM), Plutella xylostella, is notorious for its ability to rapidly evolve resistance to insecticides. Using 20 wild DBM populations, we demonstrate that this Brassicaceae specialist is currently quantitatively susceptible to cardenolides. Despite minor variation among populations, feeding on Erysimum plants consistently reduces survival and fitness of these insects. Moreover, naïve larvae actively avoid feeding on Erysimum when provided choice. To study the mechanisms of insect resistance evolution to novel plant toxins, we are conducting a large-scale selection experiment where we aim to evolve increased resistance against cardenolides in replicate DBM selection lines. Will we see a rapid response to selection for cardenolide resistance in this Erysimum-associated insect herbivore?

Abstract ID: 1371

Pollinator shifts and the evolution of specialized floral scent rewards

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Floral scent can serve to attract or reward pollinators and evolves in response to shifts in pollinator communities. Even small changes in the scent profile can lead to the attraction of different pollinators. Pollinator shifts may involve small changes in the relative abundances or phenotypic trait distributions of pollinators (quantitative pollinator shift), or immediate changes in the functional group of pollinators (qualitative pollinator shift). Most neotropical species of *Dalechampia* (Euphorbiaceae) are pollinated by euglossine bees, which collect resin- and scent-rewards. Qualitative pollinator shifts from resin-collecting female euglossine bees to scent-collecting male bees have occurred three or four times independently. I consider two hypotheses for the evolution of scent rewards: evolution via exaptation (indicated by overlap in scent compounds in scent-and resin-rewarding species), or evolution as a biosynthetic novelty (indicated by distinct scent profiles in scent-and resin-rewarding species). Disentangling evolutionary novelty from exaptation is an empirical challenge and requires good knowledge of the evolutionary history of the study system. Also, I assess scent variation among *Dalechampia* taxa in a greenhouse common garden and relate it to quantitative shifts in pollinator communities and variation among species, populations, and mating systems. In this system, floral scent variation was not associated with quantitative pollinator shifts. However, qualitative pollinator shifts between female and male euglossine bees were associated with compounds that appear to have evolved as a biosynthetic novelty from pre-existing biosynthetic pathways. Overall, despite limited scent variation across ancestral species, the flexibility of plant biosynthetic pathways mediated scent evolution, thus allowing qualitative pollinator shifts.

Abstract ID: 1741

Mechanisms of trade-offs between defense and life history strategy in monkeyflowers

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Trade-offs between life history strategy and investment in defense against herbivory have been characterized in multiple plant species, but the underlying molecular mechanisms are often unknown. Here, we use coastal and inland populations of the yellow monkeyflower, *Mimulus guttatus* to investigate the molecular mechanisms underlying adaptive variation in allocation among rapid reproduction, long-term vegetative growth, and herbivore resistance. Inland monkeyflower populations allocate resources primarily to rapid growth and reproduction to escape from seasonal drought while investing little in herbivore resistance. In contrast, coastal populations have evolved to invest more in vegetative growth and herbivore resistance as a result of higher herbivore pressure and a longer growing season. Gene interactions in the gibberelic acid (GA) pathway have previously been shown to affect resource allocation trade-offs in plants. Here, we describe the results of a manipulative field reciprocal transplant experiment designed to assess the roles of the GA pathway on monkeyflower flowering

time, biomass, herbivore defense, levels of herbivory, and fitness in coastal and inland habitats.

Abstract ID: 1761

Genetic architecture of leaf specialized metabolites in sessile oak (*Quercus petraea*)

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Specialized metabolites contribute to plant defense against pathogens and herbivores, and to their protection against abiotic stresses (e.g. UV radiation, drought). In the context of global change, natural variation of these traits may become even more important to mitigate extreme climatic and biotic events and be a source of adaptive solutions in natural populations. Leaf specialized metabolites (LSM) were previously shown to be variable and to impact herbivore damage in populations of European white oaks. Here, we aim to describe the natural variation of LSM in sessile oaks across Europe and identify the underlying genetics to better understand the evolutionary forces shaping this variation. We sampled 225 individuals from nine provenances growing in a common garden in France and used high-throughput liquid chromatography coupled to non-targeted mass spectrometry to quantify 219 molecules. In addition, we performed whole genome sequencing of all individuals at low-coverage (~10X) to generate 1,4 millions markers (SNPs). We found that linkage disequilibrium decreased over 3 kb and that oak provenances displayed little genetic differentiation (pairwise FST<0.05). Genetic variation explained over 50% of the variation for 187 molecules and a genome-wide association study identify significant associations for 147 LSM. Overall, our results suggest that sessile oak provenances display extensive variation for LSM and that this variation has a very strong genetic component with many LSM having simple genetic architectures. On-going analyses of the signatures of natural selections and genes at these loci will help better understand the selective forces maintaining variation within provenances.

Abstract ID: 1015

The key to a good relationship: inter-kingdom communication in a fungus-ant nutritional symbiosis

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Communication is fundamental to a good relationship, regardless of the interacting partners. In the attine ant-fungus symbiosis, the fungal symbiont faces the challenge of communicating its nutritional needs to a superorganismal, decentralised, ant colony. Despite these challenges, the ants successfully provision their fungus within the very

specific nutritional parameters necessary for optimal fungal growth. Exactly how the fungus can communicate its nutritional needs to the ant foragers, who do not interact directly with the fungus, is unclear. We utilise a two-pronged approach to test the hypothesis that the expression profile of fungal signalling compounds changes with the nutritional composition of provisioned diets. First, we screen the transcriptome of the fungal symbiont to identify differentially-expressed genes linked to diet changes. We then build on this, using a metabolomic approach, to identify candidate signalling compounds produced by the fungus, with a particular focus on fatty acids present on the surface of the fungal mycelium. These variable compounds can be transferred to the ants' cuticle, potentially influencing the ants' foraging choices. This result could provide a pathway for the fungus to communicate its nutritional needs to its symbiotic partners.

Symposium: S14. Ecological drivers and evolutionary consequences of within-population colour variation (id: 7)

Abstract ID: 1768

From genes to pattern formation: explaining a color pattern polymorphism in a reptile

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Animal coloration is often expressed in periodic patterns that can arise from differential cell migration, yet how these processes are regulated remains elusive. In the brown anole, *Anolis sagrei*, females are polymorphic and can exhibit either a diamond- or chevron-like dorsal pattern, while males invariably show the chevron-like pattern. We show that this female-limited polymorphism is controlled by a single Mendelian locus. This locus contains the gene *CCDC170* that is adjacent to, and co-expressed with, the *Estrogen receptor-1* gene, explaining why the polymorphism is female-limited. *CCDC170* is an organizer of the Golgi-microtubule network underlying a cell's ability to migrate and the two segregating alleles encode structurally different proteins. Our agent-based modeling of skin development demonstrates that, in principle, a change in cell migratory behaviors is sufficient to switch between the two morphs. These results suggest that *CCDC170* might have been co-opted as a switch between color patterning morphs, likely by modulating cell migratory behaviors. This kind of genetic architecture provides a high degree of controllability and ultimately evolvability of color patterns.

Abstract ID: 2029

A complex colour polymorphism is associated with a single gene in male wood tiger moths

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Colour is often used as an aposematic warning signal, with predator learning expected to lead to a single colour pattern within a population. However, there are many puzzling cases where aposematic signals are also polymorphic. The wood tiger moth, *Arctia plantaginis*, uses bright hindwing colours as a signal of unpalatability. Males have discrete colour morphs which vary in frequency geographically. In Finland, both white and yellow morphs can be found within the same populations, and these colour morphs also differ in behavioural and life-history traits which contribute to the maintenance of this polymorphism. In similar cases, such complex polymorphisms are controlled by supergenes. We show that male colour is linked to a duplicated copy of a *yellow* family gene that is only present in the white morphs. This white-specific copy, which we name *valkea,* is highly upregulated during wing development, and could provide a region of reduced recombination, thus providing some aspects of a supergene. The *yellow* family genes have been linked to melanin synthesis and behavioural traits in other insect species. Our results add to only a few examples of seemingly paradoxical and complex polymorphisms which are associated with single genes.

Abstract ID: 2332

Molecular Basis of Continuous Flower Colour Variation in Oncocyclus Irises

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Flower colour is an adaptive trait enabling the plant to interact with its environment, resulting in a dazzling variety of flower colours. While the mechanisms that create and maintain discrete colour variation among populations have been well studied, less attention has been paid to cases where colour variation is maintained within populations. Oncocyclus irises display flower colour variation on a continuous scale within a single population, a rare phenomenon. Anthocyanins are the main pigment compounds responsible for flower colour variation and the genes underlying its biochemical pathway, the Anthocyanin Biosynthesis Pathway (ABP), are widely studied. We aim to understand how the interaction of pigment synthesis and ABP gene expression result in the continuous range of flower colours in these irises. We found ABP genes sitting at pathway branchpoints to be differentially expressed. Branchpoints are the spot where the pathway flux can be directed towards different branches and therefore can cause a change in anthocyanin composition and thus a change in colour hue. Finally, to understand the evolutionary significance of the continuous colour variation in these irises, we compare ABP gene expression to the colour phenotype and fitness measurements of the entire population. Thereby considering the entire path of selection; from genotype, to phenotype, to fitness. Flower colour sits at the intersection of ecological interactions, genetics and evolution, and thus provides an excellent system to understand the causes of variation, and more importantly, what maintains or erodes it.

Abstract ID: 1333

Wing-spot and good-gene hypothesis: it’s not that simple

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Wings play an important role in dipteran life. Wings are primarily used in flight and also play a part in mating behaviour. *Drosophila* species exhibit a variety of wing pigmentation patterns. Some display a male-specific spot that appears on the top-right edge of the male wings and others polka patterns. In this work, the males of *Drosophila biarmipes* were exposed to three different growth temperatures to understand the thermal plasticity of wing-spot. The wing spot showed a plastic response to temperature conditions. We observed a non-linear pattern where wing pigmentation was maximum at the mid-thermal range. It was different to the patterns observed for body-tergite pigmentation in several *Drosophila* species where it increases with decreasing temperatures. Further, the wing-spot area was examined for chemical composition using Raman spectroscopy. The spectral peaks showed carbon-carbon double bond formation. We also tested the wing-spot associations with male fitness by exposing recently collected lines to a range of environmental stresses. The results were then observed in the light of '*good gene hypothesis*'. A negative trend was observed between dark wing-spot and a range of fitness traits. Males with darker wing-spot pigmentation did not associate with better stress handling except for desiccation tolerance. Interestingly, higher desiccation tolerance and larger body size were found to be positively correlated with darker wing-spot. Our results indicated a complex interaction between male ornamentation and fitness.

Abstract ID: 1212

How frogs get their stripe: evolution of a widespread color pattern polymorphism

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Polymorphisms shared among distantly related lineages are indicators of ancient balancing selection or repeated evolution under common evolutionary constraints at the ecological, physiological or molecular level. The vertebral stripe is a widespread color pattern in anurans, which is often present in only a subset of the individuals within a population and can assume several discrete morphs. When present, the pattern is believed to act as a substrate-matching and/or a disruptive camouflage and its polymorphism could be maintained by frequency-dependent predation and/or habitat heterogeneity. Here we combine histology, genome- and transcriptome-wide analyses with order-scale phylogenetic comparative analyses to investigate this common color pattern polymorphism. We demonstrate that variation near the Agouti signaling protein gene (*ASIP*) is responsible for the different vertebral stripe phenotypes in the Ethiopian grass frog *Ptychadena robeensis*. Surprisingly, and although the stripe phenotypes are shared with closely related species, we found that the *P. robeensis* alleles are not under long-term balancing selection and are private to the species, thus indicating that the morphs result from parallel evolution within the *Ptychadena* radiation of the Ethiopian Highlands. Finally, we show that the vertebral stripe has evolved hundreds of times in the evolutionary history of anurans and is selected for in terrestrial habitats. Our findings demonstrate that this cryptic color pattern evolves rapidly and recurrently in terrestrial anurans, leading to a shared polymorphism between distantly-related species across the order.

Abstract ID: 2460

Concealing 3D shape: Camouflage in *Cepaea* snails

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Predator-mediated selection has led to an impressive array of adaptations in prey, the remarkable colour polymorphism of the *Cepaea* land snails often being used as a textbook example of such adaptation. Surprisingly, however, empirical studies looking at the survival of these colour morphs from the view of their natural predators are still lacking. Here, we use machine learning combined with classic avian predation experiments in the field to study habitat-specific optimal camouflage strategies in this famous system. We systematically collected calibrated photos of nearly 1000 snails of various colour morphs of both *Cepaea hortensis* and *Cepaea Nemoralis*, along with thousands of background images obtained from the three most common habitat types where these snails are commonly found in nature: grassland, woodland, and hedgerows. We use visual modelling to establish the visibility of each morph in each given habitat from the perspective of their natural predators. With our substantial image database, we can estimate the selection pressure imposed on different appearances of each colour morph, as seen from their own predators' perspectives, and compared our predicted survival differences between colour morphs for each given habitat type with our observed morph frequencies in the wild, as well as the observed survival of each morph from our avian predation experiments in the field. Our final aim is to use machine learning-generated morphs (predicted best camouflage versions), to investigate optimal camouflage for each habitat type and compare this with what the snails look like in reality.

Abstract ID: 1101

Estimates of selection and dispersal from a flower color hybrid zone of snapdragons

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Studies of colour variation have made an important contribution to our understanding of how natural selection shapes variation in natural populations. However, we usually lack a detailed understanding of the nature and strength evolutionary forces involved. Here, we use 11 years of data (~22,500 individuals) collected from the hybrid zone of *Antirrhinum majus* (snapdragons) to study the mechanisms that maintain the flower colour variation despite gene flow. The two hybridizing subspecies of *A. majus* exhibit strong differences in flower colour (magenta vs yellow) and produce intermediate coloured hybrids, but are indistinguishable for other traits and across most of the genome, suggesting that flower colour is the primary target of selection. Using geographic cline anlaysis, steep coincident clines are observed at loci contributing to flower colour variation, from which

selection strength is estimated to be 1.5%. We also find non-random associations between alleles among colour loci (i.e., linkage disequilibria, LD), generated by mixing populations, from which short range dispersal is inferred to be 50m. Finally, simulations of multilocus cline models will allow more detailed inferences, including the effects of long-range dispersal, dominance and epistasis. Together, these results provide strengths of different evolutionary forces and show how they interact to maintain the phenotype divergence within a single species.

Abstract ID: 1829

Ecological consequences of colour polymorphism in spiders

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It has been suggested that the presence of multiple colour morphs within a population facilitates the use of diverse environments and increases colonization success leading to range expansion. However, this hypothesis has been tested in few lineages, comprising species where colour is likely to be involved in sexual selection. Arachnids can present extensive colour polymorphism, often linked to prey capture and anti-predator defences, but no studies to date have tested whether such colour variation is linked to ecological success. Using comparative and meta-analytical approaches, we tested the association between colour polymorphism and ecological success in web-building spiders. We performed a global systematic literature search in which we identified 117 colour polymorphic spider species, belonging mainly to the families Araneidae and Theridiidae. We found weak evidence that polymorphic species have wider latitudinal ranges than lineages without colour variation, after controlling for phylogenetic relationships. Additionally, colour polymorphic species have a higher number of geographical records on islands compared to monomorphic species, which could suggest higher success in island colonisation. Nevertheless, we did not find differences in other indirect measures of ecological success, such as range size. Overall, our results show that within-population colour variation is a common phenomenon in web-building spiders, and it could be associated with ecological success. However, the effects reported seem to be weaker than those presented in other lineages, suggesting that the ecological role of colour could moderate the strength of association between colour polymorphism and ecological success, and lead to variation in patterns between clades.

Abstract ID: 1648

Phenomics of sexual conflict: how integrated are colour and shape in a female limited polymorphism?

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Sexual conflict, arising from antagonistic selection between the sexes, can lead to the formation and sympatric coexistence of stable colour polymorphisms within natural populations. Often, seemingly discrete colour morphs show continuous variation in colour traits that covary with other characters like morphology, behaviour or life history. Such

phenotypic integration can result from correlational selection, which is thought to counteract the eroding effects of recombination and drift and thus stabilise polymorphisms over evolutionary timescales. However, due to longstanding difficulties in measuring many phenotypic traits simultaneously, there are only few quantitative studies of phenotypic integration in polymorphic species. Here we conducted a comprehensive study to quantify phenotypic integration between colour and morphology traits in the colour-polymorphic damselfly *Ischnura elegans*, where one of the three female morphs is a male-coloured mimic. Specifically, we used a deep-learning powered computer vision toolchain to extract a large array of traits related to colour (body pigmentation and texture) and morphology in over 15000 specimens from digital images. We found evidence of phenotypic integration between colour and shape traits in all three female morphs, with stronger integration in the male mimicking morph, and strongest integration in males. Male mimicking females with a stronger integration of colouration and specific shape traits also showed higher fecundity than androchrome females with weaker integration. Overall, our results underscore the potential importance of phenotypic integration in this trimorphic species, with potential implications for other colour polymorphic systems. Moreover, we demonstrate a novel approach for mapping out phenotypic landscapes on a massive scale.

Symposium: S15. Rapid evolution of color patterns (id: 954)

Abstract ID: 1193

Rapid evolution of flower color

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Variation in flower color due to transgenerational plasticity could stem directly from abiotic or biotic environmental conditions. Finding a link between biotic ecological interactions across generations and plasticity in flower color would indicate that transgenerational effects of ecological interactions, such as herbivory, might be involved in flower color evolution. We conducted controlled experiments across four generations of wild radish (Raphanus sativus, Brassicaceae) plants to explore whether flower color is influenced by herbivory, and to determine whether flower color is associated with transgenerational chromatin modifications. We found transgenerational effects of herbivory on flower color, partly related to chromatin modifications.

Abstract ID: 2249

Color adaptation during the repeated domestication of grain amaranth

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Colors fulfill important functions that allow populations to adapt to their environment. In addition to their obvious functions, e.g., camouflage, pollinator attraction and UV protection, colorants can alter physiological traits in plants. The domestication of plants is a well-suited model to study plant adaptation and to identify the genetic basis and regulatory networks of adaptation. We study the ancient grain crop amaranth which has been domesticated three times in Central and South America from one wild ancestor. All three grain species display a distinct seed color compared to wild *Amarnathus* species. While all wild amaranths have dark seeds, cultivated amaranths have pale seeds. The pale seed color has likely been selected independently, on different genetic backgrounds but altering the same genomic regions. We were able to map the genetic control of the seed color adaptation to two genomic regions and identify a MYB transcription factor gene as potential regulator for the seed color change. A long-read transcriptome assembly and differential gene expression analysis identified variation in flavonoid-pathway genes between individuals with pale and dark seeds. Our results link the genomic change in a transcription factor gene to altered expression in color pathway genes and metabolites with multiple physiological functions. We show that white seeds have reduced seed dormancy, which likely increased their fitness in agricultural environment. We speculate that rather than color itself seed dormancy was under selection. This shows that trait changes can be the result of pleiotropic effects of metabolic networks rather than selection on the observed trait.

Abstract ID: 1472

Predicting the rate and direction of bird colour evolution under natural and social selection

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To fully understand the striking variety of colour in nature, we need to know how such colour diversity evolved and the factors that drove its evolution. Indeed, studying both the rate and direction of colour evolution across species in relation to shifts in natural and social selection can provide insight into the drivers of rapid colour evolution and whether replicated shifts typically result in convergent or divergent evolutionary trajectories. Here, we study these questions using a new dataset of sex-specific plumage colouration for >4,500 species of passerine birds, capitalising on recent advances in UV-Vis imaging technology and Deep Learning approaches for efficient phenotyping. Using this information, we first use comparative methods to characterise variation across species in recent trajectories of plumage evolution, separately for male and female colouration. Then, by considering variation in the rate and direction of colour evolution separately, we assess the degree to which these two components are related and predictable based on shared or divergent characteristics of species' ecological and social conditions. Overall, our results provide insight into the predictability of avian plumage colour evolution under different forms of selection (natural and social), as well as revealing the dominant factors promoting and constraining rapid colour changes within lineages.

Abstract ID: 1616

Mapping the heritability of highly variable guppy color with deep learning

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Color traits play a crucial role in ecological interactions, and are subject to both natural selection through predation and sexual selection through mate choice. Guppies (*Poecilia reticulata*) are a key model for the ecology and evolution of coloration, in large part due to their extreme polymorphism in color patterns within and across populations. However, this extreme variation in the number, size and color of ornaments also makes their coloration difficult to analyze and understand, which has proved to be a major obstacle to genetic mapping efforts. Here, we leverage deep learning-enabled phenotyping to overcome these challenges, and study the color patterns in all their complexity. We performed a replicated artificial selection experiment on total carotenoid coloration, resulting in a 70% difference after just two generations. We photographed the color patterns of ~3,500 males from these lines across generations, analyzing >12,000 photos. Using high-resolution spatial maps of color traits across the guppy body we demonstrate that the response to selection is heterogeneous, with some areas even responding opposite to the direction of selection. Combing our spatial maps with a full pedigree, we map the heritability and sex-linkage of color across the body, illustrating large differences in the genetic architecture across ornaments. Finally, we summarized the color patterns in two-dimensional pattern space, using metric learning, and show how selection moved populations through pattern space. Our results show how selection on a global color measure alters pattern components differently, and we provide tools to better understand color patterns and other high-dimensional traits.

Abstract ID: 2046

Natural selection, not sexual selection, likely maintains a regionally isolated sexual dimorphism

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In many species, males and females experience divergent selection pressures, often resulting in the evolution of sexually dimorphic traits. For example, female green-veined white (*Pieris napi)* butterflies exhibit a highly melanized sex-limited color form called *adalwinda*. However, females of this form only occur in the northernmost part of Scandinavia, whereas males are white throughout the species range, resulting in a regionally isolated sexual dimorphism. While little is known about the adaptive benefit of this morph, it presents an opportunity to investigate whether this regional sexual dimorphism is maintained by isolation and sexual selection within the population, or by local adaptation to the abiotic environment. To this end, using genetic data and a series of field trials, we are able to show that males, irrespective of origin, prefer unmelanized females. Furthermore, using both a pangenome approach that integrates a new ultra-long read nanopore assembly for the *adalwinda* morph with other regional *P. napi* assemblies and bulk segregant analysis, we identify a single genomic locus, near the gene *cortex,* that is associated with the *adalwinda* morph. As *cortex* has previously been associated with a range of color polymorphisms in other Lepidopterans, our results further support *cortex's* role as a hotspot locus for the repeated evolution of color variation.

Abstract ID: 1609

Characterization of the transcriptome of the color-polymorphic sipder *Gasteracantha cancriformis*

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Color polymorphism in animals is a useful system to study evolutionary and developmental processes. However, the study of this trait is biased towards model organisms, while coloration in arachnids is less explored. Gasteracantha cancriformis is a neotropical spider that displays color polymorphism with at least 16 known morphs but, to date, the genetic basis underlying such polymorphism are unknown. We used RNAseq to generate a de novo transcriptome assembly for G. cancriformis and assess differential gene expression between three different color morphs: white, yellow, and orange. We also explored whether single nucleotide polymorphism (SNPs) across the transcriptome display any association with coloration. Overall, the gene expression profile of the yellow and orange morphs was similar, and they both differed from the white morph. Consistently, we found that SNPs in the differentially expressed transcripts clustered the orange and yellow morphs together while the white morph appeared more differentiated. Also, we detected higher expression of astacin and vitellogenin genes in the yellow and orange morphs, suggesting these colorations in G. cancriformis are due to carotenoids. Our data provide a valuable genetic resource for future studies on neotropical spiders and constitute a step towards the identification of the genetic basis of color polymorphism in these animals.

Abstract ID: 1984

Eco-evo-devo of seasonal plasticity in insect color patterns

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Color patterns provide amongst the most visually compelling examples of adaptive evolution, with coloration playing key roles in visual communication (e.g. predator avoidance and sexual selection), as well as in how organisms interact with abiotic properties of their environment (e.g. thermo-regulation and protection against UV). Color and color patterns differ between and within species, and are affected by genetic and environmental factors. Seasonal plasticity in pigmentation is common in insects, including examples where the temperature experienced during development determines adult coloration, adjusting it to the alternative seasonal conditions and corresponding strategies for survival and reproduction. I will describe work using insect models of pigmentation plasticity to illustrate both its adaptive significance and genetic basis.

Abstract ID: 1908

Modular regulation and convergent evolution of ASIP underpins color variation in wheatears

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Adaptation to novel environments is likely to be faster if selection can act on segregating variation, present either from pre-existing standing genetic variation or introduced through introgression, as opposed to variation that needs to arise by mutation. Determining the circumstances under which each of these evolutionary routes fast-tracks evolution is best addressed in systems with abundant phenotypic parallelism. Here, we made use of two powerful natural laboratories – phenotypic parallelism and hybrid zones – to investigate the molecular basis and evolutionary history of coloration in wheatears (genus Oenanthe). First, by leveraging a color polymorphism and hybrid color phenotypes within the *hispanica*-complex we inferred strong associations of three plumage traits with coding and non-coding SNPs, all located within or upstream of the ASIP gene. We then show that across the genus, the very same phenotypes are not associated with SNPs uncovered in the *hispanica*-complex. Instead, we find additional non-coding variation in the ASIP region that might underly the evolution of throat coloration outside the *hispanica*-complex. Taken together, our results show that i. within- and between-species variation in plumage coloration is determined by modular regulation of ASIP expression in the *hispanica*-complex, and ii. convergent genetic bases underpin plumage color parallelism at the phylogenetic scale in wheatears. By combining a population genomic with a comparative approach, our study provides insights into how regulatory variation at a master locus, likely derived from shared ancestral variation within the *hispanica*-complex, but not across the genus controls wheatear coloration.

Abstract ID: 1833

Diversity of carotenoid-based body color in cichlid fish: molecular basis and evolutionary history

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Heritable differences in carotenoid-based body coloration occur between many closely related taxa of birds and fish and testify to the rapid evolvability of this trait. The hue of carotenoid-based body coloration ranges from bright yellow to deep red and is determined by the types and concentrations of carotenoids deposited in the integument. Here, we present two case studies which address the molecular basis and the evolutionary history of the diversification of carotenoid-based body coloration in cichlid fishes. We studied the composition of integumentary carotenoids and integumentary gene expression patterns in pairs of closely related populations of cichlid fish

(genera *Tropheus* and *Aulonocara*). Color contrasts (red versus yellow) were associated with the presence/absence of red keto-carotenoids in all three pairs. Unexpectedly, gene expression differences between red and yellow fish varied among taxon pairs, suggesting variation in the genetic basis of integumentary carotenoid metabolism among similarly colored populations. We also studied the evolutionary history of color pattern differentiation in populations of the highly polymorphic cichlid fish species *Tropheus moorii*. Population genetic signatures suggested that the evolution of a particular color pattern phenotype occurred by ancient hybridization between distinctly colored populations and that the underlying secondary contact was facilitated by climate-induced changes in habitat structure. Experimental crosses between the parental phenotypes indeed re-created the hybrid color pattern. In the reconstructed scenario, the evolution of the novel color phenotype was driven by shifts of dispersal barriers in an unstable environment and represents a selectively neutral process of color pattern diversification.

Abstract ID: 1446

Fine-mapping of color pattern variation and its genomic bases in a rapid radiation

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Color pattern plays a fundamental role in the ecology and evolution of a broad range of organisms. Nevertheless, colour pattern is a complex trait – often a collection of traits – that is difficult to analyse quantitatively, and whose genetic bases can also be complex. Here, we leverage one of the fastest fish radiations on Earth (the hamlets, *Hypoplectrus* spp), to address these two issues. We dissect color pattern variation with a standardized, pixel-resolution approach that we complement with whole-genome sequencing to run a multivariate Genome-Wide Association Study (GWAS) for color pattern variation. This approach allows to i. analyse colour pattern variation objectively and quantitatively, ii. identify sharp association peaks for color pattern variation along the genome, and iii. visualize the phenotypic effects of the Single Nucleotide Polymorphism (SNP) markers that are most strongly associated with colour pattern variation at each association peak. The results indicate that the modular combination of a small number of large-effect loci that are each associated with different components of colour pattern variation (bars, spots, colour, …) underlie phenotypic diversification in this group.

Symposium: S16. Predator cognition and the evolution of prey defence strategies (id: 938)

Abstract ID: 2461

Predator selection on phenotypic variability of cryptic and aposematic moths

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Selection by predators is among the strongest forces shaping phenotypes of prey animals. Negative frequency-dependent selection is expected to drive phenotypic variability among cryptic species as variation hinders the predator search image formation. Aposematic species, on the other hand, face positive frequency-dependent selection as they benefit from similar warning signals due to a shared cost of predator education. These mechanisms have been successfully shown to work in the laboratory conditions, but can we observe evolutionary consequences of predation from the wild? We analyzed the pattern and colour variability of aposematic and camouflaged moths taking into account their phylogenetic relationships. Camouflaged moths showed more variable wing patterning than aposematic moths, as expected under the negative frequency dependent predation. Against our initial expectations, aposematic moths were characterized by higher wing colour saturation and pattern contrast variation. I will discuss about these results in the light of the signal theory and present a hypothesis why aposematic organisms are not less variable *per se*. I will also discuss about possibilities to use dated, geo-referenced, digitalized museum specimens as a rich data source for reconstructing past selection episodes.

Abstract ID: 2026

Selection on individual warning signal elements in the aposematic moth

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Aposematic prey advertise their unprofitability with conspicuous warning signals that are often composed of several colour pattern elements. Many species show intraspecific variation in these colour patterns even though selection is expected to favour invariable warning signals that enhance predator learning. However, if predators acquire avoidance to specific signal elements, this might allow variation to exist in other colour patterns. Here we investigated this in the aposematic *Amata nigriceps* moths that have black and orange colouration in the wings and the abdomen. Orange spots in the wings are highly variable among individuals, with the proportion of orange varying from 10-30%, whereas the number of orange stripes in the abdomen remains consistent. We conducted preference tests with noisy miners (*Manorina melanocephala)* and artificial moths to investigate how different warning signal elements influence predators' attack decisions. When moths had orange stripes in the abdomen, birds did not discriminate between

different wing signals. Instead, the proportion of orange in the wings was found to be important only when the stripes in the abdomen were removed. In addition, we found that birds were more likely to attack moths with a smaller number of orange stripes. Together, our results suggest that stripes are an important warning signal element in the *A. nigriceps,* and this could relax selection for consistent wing colouration. Our study highlights the importance of considering individual warning signal elements if we are to understand how predation shapes selection on prey warning colouration.

Abstract ID: 2287

Do predators maintain polymorphism in an invasive moth?

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Polymorphism under selection allows studying phenotype-fitness relationships in a controlled environment. In some species, the polymorphism plays a pivotal role in their ecology with complex evolutionary forces acting together. The Box Tree Moth, *Cydalima perspectalis* (Crambidae), is an Asian moth invading Europe and North America, displaying a colour polymorphism with a white form and a melanic form. However, the ecological forces maintaining this polymorphism are still unknown. To investigate the role of predators in maintaining this polymorphism, we tested 1) for the palatability of both forms to avian predators, 2) whether the melanic coloration was associated with decreased detectability and therefore with improved survival via crypsis, and 3) for a role of bird experience causing negative frequency-dependent selection. We performed predation assays in experimental arenas, using adult moths of both forms presented at varying frequencies, and blue tits (*Parus caeruleus*) as model predators. Our results suggest that both forms are highly palatable to birds, ruling out aposematism as a factor in survival. We found that bird predators detected the melanic form at a lower rate, with a slight effect of negative frequency-dependence. These results support a role for predation and crypsis in the maintenance of the melanic form, but suggest that the white form might be enjoying other benefits balancing the frequencies in nature. Frequency differences between the native and invasive ranges might reflect variation in selection associated with the invasion.

Abstract ID: 972

Parallel, repeated co-option of a sexual ornament for a defensive signal in mimetic evolution

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Animal signals are dynamic traits that respond to multiple selective pressures. Traits used for signalling may sometimes differ between sister species, serving myriad functions such as mate choice and anti-predator defences. What evolutionary mechanisms shape the lability of these traits? Do natural and sexual selection act synergistically or antagonistically to bring about de novo evolution of signalling traits, or do they work on the existing trait variation to shape signal evolution? In *Papilio* butterflies, we show how natural selection over-rides sexual selection by trading sexual ornaments for defensive signals. We demonstrate experimentally that the ancestral bright creamy-white/yellow patches on the wings of *Papilio* swallowtail butterflies act as sexual ornaments and influence male mating success. We identified the fluorescing papiliochrome-II pigment as the chemical basis of these ornaments. Yet, in several species across *Papilio*, these colour patches have repeatedly lost the papiliochrome-II pigment and turned UV-reflective during the independent, parallel evolution of Batesian mimicry. Vision modelling showed that the UV-reflective patches of mimics improve mimetic resemblance in the eyes of avian predators. Thus, the ancestral colour patches which were used as sexual ornaments, served as a preadaptation, and natural selection repeatedly co-opted them for defensive signalling during mimetic evolution.

Abstract ID: 1781

Predator responses to real and hypothetical 3D printed phenotypes within a Batesian mimicry complex

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Batesian mimics vary widely in the accuracy of their resemblance to their models. Suggested explanations for this variation include limitations of predators' sensory and cognitive abilities. Just how good are predators at distinguishing mimics from their models? At what point are mimics for practical purposes "perfect", beyond which any further improvement in similarity is irrelevant to predators? Answering this question requires experiments involving stimuli that vary over realistic phenotypic ranges, but that also encompass novel phenotypes not seen in nature. To achieve this, we have created detailed digital 3D insect reconstructions of model (wasp; Vespidae), mimic (hoverfly; Syrphidae) and non-mimic (fly; Muscidae) species. We then used cutting-edge 3D printing technology to build real, life-sized versions of these insects. These stimuli were used to train wild great tits Parus major to distinguish non-mimetic flies from wasps, using mealworms as a reward. We then tested the birds' response to a range of intermediate stimuli created through smooth interpolation of shape, colour, pattern and size from one phenotype to another. This allowed us to explore realistic but novel mimetic stimuli, including some that are considerably more wasp-like than any seen in nature. We found a range in levels of protection across the different artificial mimics, but birds preferred even the highly accurate mimics over the models themselves. Our experiment shows a remarkable ability of avian predators to discriminate among very similar prey stimuli, and demonstrates a powerful new approach for exploring novel areas of phenotypic space in studies of visual signals.

Abstract ID: 2094

The effect of predator population dynamics on Batesian mimicry complexes

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Understanding Batesian mimicry is a classic problem in evolutionary biology. In Batesian mimicry, a defended species (the model) is mimicked by an undefended species (the mimic). Prior theories have emphasized the role of predator behavior and learning, and evolution in model-mimic complexes, but have not examined the role of population dynamics in potentially governing the relative abundances and even persistence of model-mimic systems. We examined the effect of the population dynamics of predators and alternative prey on the prevalence of warning-signaling prey comprised of models and mimics. Using optimal foraging theory and signal detection theory, we found that the inclusion of predator and alternative prey population dynamics could reverse traditional theoretical predictions: as alternative prey increase in numbers, mimics suffer because larger populations of predators are maintained, resulting in apparent competition. Under some circumstances, apparent competition affects model populations as well, although not as severely as it affected mimics. Our results bear on the intriguing puzzle that in nature, warning signals are relatively scarce, yet experiments suggest that such signals can be highly advantageous. The availability of alternative prey, and numerical responses by predators, can overwhelm advantages observed in experiments to keep warning signals in model-mimic systems relatively scarce.

Abstract ID: 1031

Sensory drive as a framework for understanding the effectiveness of warning signals

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The diversity of species appearance and signalling in nature seems almost boundless. Whilst our knowledge of signal content is growing fast, the forces that underpin signal design and make them effective are often elusive. The sensory drive hypothesis explains how sexually selected signals can be understood from the perspective of the receiver's sensory system given the constraints of the sensory environment. Can the logic of sensory drive be applied to other classes of signals such as warning signals?
Here we present computational evidence that the effectiveness of visual warning signals can be understood as the result of the pressure to exploit pattern features that the brain of the receiver is most sensitive too. We first show that visual warning signals particularly stimulate a generic model of (avian) brain functions, compared with patterns of

undefended species. We next derive a quantitative framework to predict what stimuli are likely to maximally exploit a sensory system, making them maximally conspicuous. When applied to a sensory system made for processing natural scenes efficiently (i.e., maximising information and minimising metabolism), the framework delivers stimuli that are reminiscent of warning signals. This shows that the visual features of warning signals can be driven by the properties of visual systems, which in turn are known in neuroscience to reflect the visual regularities in the environment.
Our study suggests that sensory drive could underpin the design of warning signals and predict what signals should be effective in specific environments and for specific receivers.

Abstract ID: 1796

Adaptive search and habituation to stimuli: a Bayesian approach

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If you are searching for a lost object in a given location then the longer you look for it there without finding it, the less likely it is to be present. Likewise, if you are placed in an arena with a potentially harmful object, the longer you remain without being attacked by it, the less likely the object will hurt you. Bayes' rule shows us how we can continually update our prior beliefs based on new information, such as how long has passed without an event happening. In this talk I show how we can apply Bayes' rule to understand two different phenomena, namely flash behaviour in otherwise cryptic prey and the habituation of would-be predators to novel, potentially harmful, prey. I show that any cryptic prey that gives the impression it is conspicuous while fleeing will subsequently be searched for a shorter time when it settles, thereby enhancing the prey item's survivorship. I also show that if there is a risk that an unfamiliar object could flee, then a naïve predator should approach the object once sufficient time has passed that the object is first estimated to be profitable to draw closer. In this way, I show that predators can use simple Bayesian rules to maximize their payoff when searching for prey and when encountering potentially threatening stimuli, but that prey can exploit these rules.

Symposium: S17. Brain, behaviour and cognitive evolution (id: 932)

Abstract ID: 2462

The effects of the high energy needs of neural tissue on brain size variation in vertebrates

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Brains provide information about the world, steer the ability to act upon it, and make decisions. Comparative work shows that bigger brains are better at these tasks. Yet, brains show remarkable taxonomic variation in size, even at the same body size. Opportunities to turn cognitive abilities into fitness may vary across lineages and niches, but here we focus on another major reason for this variation: brains generally need high

and uninterrupted energy inputs. Hence, a species' brain size may depend on its ability to bear the costs of maintaining the brain. Comparative studies show that higher seasonality in food intake (and perceived temperature in ectotherms) is correlated with smaller relative brain size. In addition, high energy costs should also make brain development more difficult without parental provisioning. Indeed, in a detailed study of birds, we find that the amount of parental provisioning in a given species is clearly correlated with its brain size. The expensive brain hypothesis therefore suggests that the ecology-dependent ability to bear the energy costs of brain maintenance and development may strongly influence brain size, on a par with the environmental potential to harvest cognitive benefits. This idea leads to various further predictions.

Abstract ID: 1004

Social and ecological factors predict variation in brain size across birds

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Conflicting theories have been proposed to explain variation in relative brain size across the animal kingdom. Ecological theories argue that the cognitive demands of seasonal or unpredictable environments have selected for increases in relative brain size, whereas the 'social brain hypothesis' argues that social complexity is the primary driver of brain size evolution. Here, we use a phylogenetic comparative approach to test the relative importance of ecology (diet, foraging niche and migration) and sociality (social bond, breeding system and territoriality) in driving variation in brain size across 1,886 bird species. Across all birds, we find a highly significant effect of foraging niche on brain size, suggesting that selection for complex motor skills whilst foraging generally imposes important selection on relative brain size in birds. We also find effects of social bond type and territoriality on brain size, but the nature of these effects do not support the social brain hypothesis. At the same time, we find extensive heterogeneity among major avian subclades in the relative importance of different variables, implying that the significance of particular ecological and social factors for driving avian brain size evolution is often clade and context specific. Overall our results demonstrate the potentially important and complex ways in which ecological and social selection pressures shape brain size evolution across birds.

Abstract ID: 1022

Learning from lizards: Lacertidae as a model system in comparative cognition?

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Cognition is essential for animals to deal with the challenges the environment poses. Despite its importance, the ecological driving forces of cognitive evolution throughout the animal kingdom remain largely unclear. Many studies have proposed and tested

hypotheses on the role of social and ecological challenges on the evolution of cognition. However, these have yielded mixed results and thus the answer of what drives cognitive evolution remains enigmatic. Large-scale comparative studies involving multiple species and cognitive characteristics have been advanced as the best way to understand cognitive evolution, but such studies are rare and challenging. In our study, we tested thirteen lacertid lizard species (Reptilia: Lacertidae) for their cognitive skills, using a battery of tests measuring inhibitory control, problem-solving, and spatial and reversal learning, to try and link the species' performance to interspecific variation in environmental quality, complexity, and habitat variability, as well as to their life-history. Although species clearly differed in their cognitive abilities, this variation was mostly unrelated to their environmental and life-history characteristics. We did find that species living in more variable habitats exhibited lower behavioural flexibility. Most importantly, we established lacertid lizards as an appropriate model system to study cognitive evolution. In addition, the standardised approaches in our study provide opportunities for large-scale collaborative research to increase sample size and replication, essential for advancing the field of comparative cognition.

Abstract ID: 1221

Enhanced memory in *Heliconius* butterflies linked with increased mushroom body size and plasticity

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There is significant variation in cognitive ability between species, yet the neural traits determining these differences are only partly understood, particularly in an evolutionary context. In *Heliconius* butterflies, the mushroom bodies, a region of the insect brain associated with learning and memory, are dramatically expanded, being 3-4 times larger than in closely related genera. *Heliconius* are therefore an ideal system for investigating cognitive evolution, particularly mushroom body expansion.
We present the results of visual, long-term memory trials across six Heliconiini species (three *Heliconius* and three non-*Heliconius*), in addition to neuroanatomical data from *Heliconius erato* and *Dryas iulia*. We trained butterflies to associate food with a specific colour and tested their ability to recall this learned association after eight days. The three *Heliconius* species significantly outperformed the non-*Heliconius* species, suggestive of mushroom body expansion facilitating improved visual, long-term memory in the genus.
To determine whether *Heliconius* mushroom bodies exhibit greater learning-induced plasticity, brains of trained *Heliconius erato* and *Dryas iulia* individuals were compared with control individuals raised in a non-learning environment. Using immunocytochemistry and confocal microscopy, we show that learning is associated with an increased number of synapses in the mushroom body calyces of *Heliconius erato*, but not *Dryas iulia*. This suggests that the mushroom bodies of *Heliconius* are not only larger, but more plastic in response to learning.
This is the first study to combine cognitive and neuroanatomical data in a comparative framework across two closely-related insects, providing new insights into mushroom body evolution.

Abstract ID: 1332

The evolution of brain neuron numbers in amniotes

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The evolution of brain processing capacity has traditionally been inferred from data on brain size. However, similarly sized brains of distantly related species can differ in the number and distribution of neurons, their basic computational units. Therefore, a finer-grained approach is needed to reveal the evolutionary paths to increased cognitive capacity. Using a new dataset comprising over 250 species, we analyzed brain cellular composition across amniotes. Compared to reptiles, mammals and birds have dramatically increased brain neuron numbers, particularly in the cerebellum, where they have on average more than 50 times more neurons than non-avian reptiles of comparable body mass. Moreover, these independent changes resulted in similar neuron-body scaling in the two endotherm lineages. Two other major increases in the number of neurons for body mass occurred in core landbirds and anthropoid primates, two groups known for their smarts. Interestingly, the relationship between relative brain size and relative neuron density also differs within amniotes – some groups show a positive correlation, while others do not. This highlights the need for caution when using relative brain size as a proxy for cognitive capacity.

Abstract ID: 1476

What cognitive abilities might differentiate endotherm and ectotherm vertebrates?

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The average mammal or bird has a roughly ten times larger brain relative to body size than the average ectotherm vertebrate. It has been surprisingly challenging to determine how this translates into increased cognitive performance. In particular, it is unclear whether the brain size differences translate into qualitative differences in specific cognitive abilities. A brief summary on the current evidence on fishes strongly suggests that they match endotherms with respect to the presence of supposedly 'advanced' cognitive processes, i.e. the cognitive tool kit beyond classical and operant conditioning. In contrast, a first exploratory study opens the possibility that only the larger brains of endotherms support a centralised processing of information. In all mammal species tested so far, individual performance across domain-general cognitive tasks is positively correlated, resulting in the psychometric 'general intelligence' factor *g.* Across mammalian species, the value of *g* is positively correlated with brain size. In contrast, in a first study on a fish species, wild-caught cleaner wrasse *Labroides dimidiatus* yielded no evidence for a g factor across three tasks testing for different cognitive dimensions. All pairwise correlation coefficients were close to zero. The results provide a first

indication that endotherm and ectotherm vertebrates may process cognitive tasks in fundamentally different ways due to differences in brain organisation.

Abstract ID: 2001

Brain size evolution is shaped by life history in lizards

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Knowledge about the relationship between key life-history traits and brain size in terrestrial ectotherms is critical to our understanding of vertebrate brain size evolution. Here, we address existing hypotheses about brain size evolution in vertebrates by exploring the link between brain size and longevity, age at sexual maturity, clutch/litter size, foraging mode, substrate affinity, and reproductive mode in 145 species of lizards. In contrast to other terrestrial vertebrates, brain size variation was unrelated to longevity or age at maturity, but was correlated with foraging and reproductive mode. Sit-and-wait foraging predators had larger brains than active foraging predators and viviparous species had smaller brains than oviparous species, likely because live-bearing tends to evolve in cooler climates. These results suggest that brain size may be subject to specific selective pressures in lizards, where classic life history trade-offs seem to extend to the brain, highlighting the need to incorporate cognition into life history theory.

Abstract ID: 2308

To choose or not to choose? Personality & cognition as drivers of decision-making in wild zebrafish

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Although correlations between personality and cognitive ability have been observed across multiple taxa, the extent and direction of such correlations are not always consistent, indicating varying evolutionary implications. Personality could drive the evolution of cognitive ability, as bolder individuals are more likely to take risks and hence require better cognition to survive, or better cognitive ability could result in an enhanced assessment of risks, allowing cognitively advanced individuals to be bolder. In this study, we test whether personality (boldness) or cognitive ability (numerical discrimination) has a more consistent effect on choices made in a decision-making task involving various risk-reward conditions. Individuals from a wild-caught zebrafish population were characterized for boldness and numerical ability and then tested in multiple scenarios with varying combinations of risk (high, medium, low) based on predator size and reward (high, medium, low) based on stimulus shoal size. First and preferred choices were noted. We found that bolder individuals showed better numerical discrimination and made faster choices, but were less consistent, and did not necessarily choose the high

reward choice. However, shy individuals made slower choices, were more consistent with their preferred choice, and were more likely to choose a more rewarding option. This indicates that decision-making in a risk-reward situation is not driven by simple cognitive ability, but could be a more complex process that involves personality as well. This study is the first of its kind to elucidate the directionality of these correlations, paving the path for further studies on the evolution of cognitive decisions.

Abstract ID: 1391

Cognition in the wild: Ecology dictates the value of memory for foraging bees

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"Ecological intelligence" hypotheses posit that animal learning and memory evolves to meet the demands posed by foraging, and together with the social intelligence hypotheses, provide a key framework for understanding cognitive evolution. However, identifying the critical environments where cognitive investment reaps significant benefits has proved challenging. Here, we capitalise upon seasonal variation in forage availability for a social insect model (the buff-tailed bumblebee, *Bombus terrestris*) to ask whether the benefits of short-term memory vary with resource availability. We test individual bees on a short-term memory task in the laboratory, and then analyse their foraging efficiency in the wild, by observing over 1700 foraging trips from 25 colonies over a two-year period. We show that short-term memory predicts foraging efficiency for nectar – a key determinant of colony fitness – in plentiful spring foraging conditions, but that this relationship is reversed during the summer floral dearth. Short-term memory does not appear to predict pollen foraging efficiency. Our results suggest that selection for enhanced cognitive abilities is unlikely to be limited to harsh environments where food is hard to find or extract, highlighting instead that the complexity of rich and plentiful environments could be a broad driver in the evolution of certain cognitive traits.

Symposium: S18. The evolution of behavioural adaptations: Genes, neurons and ecology (id: 31)

Abstract ID: 1482

Genetic basis and physiological role of increased sensory pooling in an ecological specialist

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Comparative studies of closely-related species offer an excellent opportunity to reveal diversification in neural circuit organisation. However, the mechanisms and consequences of species-specific neural circuits evolution remain largely unknown. We are addressing these questions comparing the olfactory system of the extreme specialist, *Drosophila sechellia* – which feeds on a single host fruit – to that of the closely-related ecological generalists *D. simulans* and *D. melanogaster*. We recently developed neurogenetic tools in *D. sechellia* to reveal how multiple changes in *D. sechellia's* olfactory system are linked to host fruit attraction. We hypothesised that one of these traits – the increase in olfactory sensory neuron (OSN) numbers – is a key adaptation for host specialisation, but testing this idea requires a deeper understanding of its molecular basis. We show that *cis*-regulatory sequences at the corresponding receptor genes have little contribution to interspecific OSN number differences. Instead, we uncovered a complex genetic architecture of this trait via quantitative genetic mapping. To determine the functional significance of OSN number increases in *D. sechellia*, we employed comparative physiology of OSNs and partner projection neurons (PNs) and behavioural assays. Our data indicate that an increased sensory neuron population reduces short term depression at the OSN-PN synapse, and may result in more robust tracking of odour plumes during food searching. Together, this work provides insights into how neural circuits can be modified structurally and functionally over relatively short time scales to allow ecologically-important behavioural changes.

Abstract ID: 1009

The genetic basis of spatial cognitive variation in a food-caching bird

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Spatial cognition is used by most organisms to navigate their environment. Some species rely particularly heavily on specialized spatial cognition to survive, suggesting that a heritable component of cognition may be under natural selection. This idea remains largely untested outside of humans, perhaps because cognition in general is known to be strongly affected by learning and experience. We investigated the genetic basis of individual variation in spatial cognition used by non-migratory food-caching birds to recover food stores and survive harsh montane winters. Comparing the genomes of wild, free-living birds ranging from best to worst in their performance on a spatial cognitive task revealed significant associations with genes involved in neuron growth and development and hippocampal function. These results identify candidate genes associated with differences in spatial cognition and provide a critical link connecting individual variation in spatial cognition with natural selection.

Abstract ID: 2106

Molecular and epigenetic mechanisms underlying individual differences in cognitive flexibility

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Cognitive flexibility allows animals to adapt to environmental challenges and individuals within species show considerable variation in cognitive flexibility. Understanding the causal mechanisms that underlie individual variation provides an important basis for understanding the evolution of cognitive traits. Molecular interactions between genes and experience, mediated by epigenetic mechanisms, are known drivers of individual variation. Where the neural mechanisms involved in cognitive flexibility are increasingly revealed, the extent to which epigenetic mechanisms act as regulators in gene transcription to cause individual cognitive variation remains enigmatic. In order to address this, we assessed how chromatin accessibility and DNA methylation interact to affect gene expression related to natural variation in cognitive flexibility in great tits (*Parus major*). By comparing individuals of extreme high and low cognitive flexibility, we show how differential gene expression is associated with differences in both chromatin accessibility and DNA methylation in three brain regions (striatum, hippocampus and cerebellum). We identified candidate genes involved in neurodifferentiation and neurotransmitter functioning as well as the epigenetic pathways through which they are expressed. These new insights into the molecular causes of individual variation in cognition shed light on how epigenetic mechanisms that shape the expression of cognitive flexibility, might be important processes in environmental adaptation, generating phenotypic variation that is selected upon without changing the DNA sequence.

Abstract ID: 1605

How collective behavior evolves? Mechanistic insights from artificial selection in guppies

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The study of how social interactions evolve is fundamental to understand the nature of social groups and how it might affect individual cognitive abilities. Yet, it remains enigmatic how such interactions evolve. Here, we studied the relationship between collective motion, behavior and cognition using female guppies artificially selected for higher polarization, a physical property of group motion that quantifies how aligned are individuals while shoaling. After three generations of artificial selection, female guppies

showed a 15% increase in polarization in relation to control females. This resulted in crucial changes in brain anatomy. Specifically, region size shifted approximately 5% between lower-order and higher-order cognitive areas of the brain. Using automated fish tracking we also studied ecologically relevant behaviors and found that polarization-selected fish presented more cohesive shoals, spent less time inspecting an imminent predation threat, and showed a higher readiness to shoal with unfamiliar conspecifics. These findings were complemented with the largest to date direct estimation of heritability in social tendency. Specifically, we found an overall moderate heritability and strong sex-specific differences of social tendency after phenotyping over 1500 individuals in approximately 200 families. Moreover, we used artificially selected female guppies to study the genetic architecture of social tendencies and how genes in the brain are expressed and interconnected when fish are exposed to different social contexts. Our comprehensive study on this system provides distinct knowledge on proximate and ultimate mechanisms of social behavior, highlighting the central role that cognitive ability plays in the evolution of collective motion in animal groups.

Abstract ID: 1428

Untapping the genetics of vertebrate dispersal combining RNAseq, RADseq and quantitative genetics

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The genetic basis of animal dispersal, particularly in vertebrates, remains largely unknown. This contrasts with the key role that dispersal has in both ecological and evolutionary processes and in the dynamics of population colonization, extinction and local adaptation. Untapping the genetic basis of dispersal should deepen our understanding of how dispersal behaviour evolves, the molecular mechanisms that regulate it and link it to other phenotypic aspects in order to form the so-called dispersal syndromes. We used a comprehensive approach combining quantitative genetics, genome-wide and transcriptome sequencing to study the genetic basis of natal dispersal in a known ecological and evolutionary model of vertebrate dispersal: the common lizard *Zootoca vivipara.* Our study supports the heritability of dispersal in our semi-natural populations, with lesser variation due to maternal and natal population effects. We found genetic variation around the *Carbonic Anhydrase* gene (*CA10*) to be associated with natal dispersal, which together with differential expression of several genes (*SLC6A4*, *NOS1*) involved in the functioning of the central nervous system suggest that

neurotransmitters (serotonin and nitric oxide) are involve in the regulation of dispersal and potentially dispersal syndromes. Several genes from the molecular clock (*CRY2, KCTD21*) were differentially expressed between disperser and resident lizards, supporting that the circadian rhythm; known to be involved in long-distance migration, might affect dispersal as well. Because of their conserved roles across taxa, the highlighted pathways hold the potential to generally regulate dispersal in vertebrates.

Abstract ID: 1501

Patterns of gene expression in a migratory divide between songbirds

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Behavioural traits are critical for adaptation and can facilitate speciation. Many of these traits are innate and yet knowledge of their genetic basis and connection with gene expression is limited. Here, we examine gene expression in hybrid zone between two subspecies of songbird that exhibit dramatic differences in their migratory behaviour, breeding next to one another but using different migratory routes. Hybrids between these subspecies take intermediate and ecologically-inferior routes, helping maintain reproductive isolation between pure forms. We compare the expression profiles of pure forms during the migratory and non-migratory season using RNAseq data. We focus on brain regions linked to migration and use complementary data from hybrids to (1) distinguish between the effects of cis- and trans-regulatory elements and (2) connect patterns of gene expression with reproductive isolation. We will report several findings from this work, including the fact that genes that are differentially expressed between the seasons and subspecies are enriched for neuro-developmental GO terms, suggesting differences in migration derive from changes in neurogenesis. The former genes do not exhibit allele-specific expression in hybrids, suggesting divergence in seasonally dependent gene expression is caused by changes in trans- not cis-regulatory elements. This result is supported by the fact that these genes do not co-localize with areas of genomic divergence between the subspecies and misexpression is not observed in hybrids at these genes. Misexpression is documented in genes that are not differentially expressed between pure forms but are season-specific, highlighting an unexpected form of selection against hybrids in this system.

Abstract ID: 1075

Genetic and neuronal mechanisms of circadian plasticity loss in the equatorial *Drosophila sechellia*

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Species with broad geographic distributions often accommodate environmental variation with behavioral plasticity. This ability to adjust behaviors to match the environment is integral to fitness, but we still have little understanding of its molecular basis. Determining how behavioral plasticity is achieved, both genetically and by the nervous system, is key to understanding how cosmopolitan organisms evolved to handle variable environments and predicting how they will persist in increasingly volatile climates. One

factor that varies seasonally and by latitude is photoperiod (length of day). Many drosophilids, including the cosmopolitan *Drosophila melanogaster*, display plasticity in circadian activity, allowing them to adjust to fluctuating day lengths by varying the timing of their morning and evening activity peaks to coincide with changing photoperiods. *D. sechellia*, however, is an equatorial island endemic experiencing almost no variation in day length throughout the year. Accordingly, we show that *D. sechellia* displays minimal circadian plasticity when faced with longer days. We examined the expression of a key neuropeptide gene, *Pigment dispersing factor* (*Pdf*), in two populations of circadian neurons with roles in morning and evening peak timing. Using immunofluorescence, single-molecule RNA FISH, and transgenic reporter labelling of these cells, we identify differences in *Pdf* expression and obtain evidence that these differences are due to *cis*-regulatory evolution of the *Pdf* enhancer. Ongoing experiments test the hypothesis that *cis*-regulatory evolution of *Pdf* is causal for interspecific differences in circadian plasticity. Our findings have broad implications for understanding how selection from variable environments drives gene expression evolution resulting in phenotypic plasticity.

Abstract ID: 1142

Selection, drift, and constraint and the evolution of mating behaviors in bioluminescent ostracods

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Connecting genetic processes to the evolution of complex phenotypes is nontrivial. Animal behaviors, like the communication signals used between sexes, can be extremely complex because they are emergent across levels of biological organization. Here, we begin to explore how diversification of bioluminescent mating behaviors across species of cypridinid ostracods (“sea fireflies") was influenced by evolution of a single gene, the enzyme *c-luciferase*. Comparative analyses of *c-luciferase* orthologs identified from *de novo* transcriptomes suggest some amino acids evolved under episodic diversifying selection and may be associated with changes in both light production and color, two functions that impact bioluminescent signaling. Other sites evolved neutrally or under purifying selection, and may have shifted color across genera. Our statistical results also corroborate the importance of epistatic interactions between sites identified from previous mutagenesis experiments in the literature; such interactions could constrain the evolution of enzyme function, and subsequently phenotypic diversity of mating signals. By expressing c-luciferase orthologs *in vitro*, we report a preliminary correlation between differences in the duration of discrete bioluminescent secretions (pulse duration) and enzyme activity, supporting the hypothesis that substitutions in *c-luciferase* genes influence mating display diversity. Our behavioral data indicate that variation in pulse duration affects female swimming behavior, and may be important in mate choice. All together, we conclude that myriad evolutionary forces jointly influence behavioral diversity. These results set up additional behavioral and genetic studies that could explicitly link selection such as mate choice, drift, and constraint to the evolution of behavior.

Abstract ID: 1357

Visual specialisation and explosive expansion of the mushroom bodies in *Heliconius* butterflies

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Neural innovation, elaboration and refinement underpins behavioural diversity. Yet our understanding of how neural systems evolve, and the mechanisms that govern links between brain and behavioural change remain underdeveloped. We describe a dramatic example of neural elaboration, linked to the evolution of a novel behaviour. *Heliconius* are the only butterflies known to actively collect and digest pollen. This dietary innovation is linked to restricted individual home ranges, and a spatially and temporally faithful foraging behaviour that is reliant on visual cues. We show that across the tribe of Heliconiini, the mushroom bodies (MBs), a major insect learning and memory centre, vary in raw volume by over 25-fold. Rapid bursts in mushroom body size occurred in multiple branches of the Heliconiini, but the largest coincides with the origin of pollen feeding and, even after accounting for brain size, results in a doubling of MB size at the base of *Heliconius*. This volumetric expansion is driven by concomitant increases in intrinsic MB neurons, but consistent scaling of MB components and synaptic densities. Strikingly, much of this variation can be linked to increased visual input to the MB in *Heliconius*, altering the dominant sensory modality processed by the MB. We further show that MB expansion is accompanied by increased performance in multiple, visually based cognitive assays, consistent with theoretical expectations that cognitive capacity increases with MB size. Our data highlight Heliconiini as a tractable system for comparative, detail-rich analyses aimed at understanding the adaptive and mechanistic basis of neural and behavioural evolution.

Abstract ID: 1543

Social plasticity in signals and preferences enhances signal-preference co-divergence

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Evolutionarily relevant variants arise from plasticity when variation in the environment exposes hidden genetic variation to the action of selection. Here we tested whether plasticity arising from variation in social environments, often the most dynamic and fitness-relevant environment animals experience, promotes assortative mating. Interactions in mixed social aggregations could reduce, create or enhance signal-preference differences. In the latter case, social plasticity would have the immediate effect of impeding gene flow. Rearing two recently diverged species of Enchenopa treehoppers—sap-feeding insects that communicate with plant-borne vibrational

signals—in mixed-species versus own-species aggregations resulted in enhanced signal-preference species differences. We also found that the form of plasticity did not differ between individuals from sympatric and allopatric sites. Our results support the hypothesis that social plasticity can create or enhance signal-preference differences. Such social plasticity may facilitate rapid bursts of diversification, even in cases where gene flow would be expected to hinder signal-preference genetic covariance, which is normally assumed to underlie speciation by divergence in sexual traits.

Abstract ID: 1602

Mate choice in the brain: Species differ in how male traits turn on gene expression in female brains

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Substantial research demonstrates the importance of female mate choice to speciation, yet we know little about the cognitive mechanisms that underpin female decision-making or its genetic basis. For example, how does gene expression help regulate mate choice decisions? Prior research revealed that limnetic and benthic female sticklebacks use different male displays to evaluate prospective partners and reject heterospecific males based on display differences. We predicted divergent female preferences would result in divergent gene expression patterns in brains of benthic and limnetic females, and would be especially pronounced when evaluating displays known to cause sexual isolation. To test this, we coupled behavioral data from a mate choice experiment with gene expression data from female brains. We find substantial differences between species in which genes are expressed, suggesting strong divergence in gene expression in female brains. Importantly, we also find expression differences between females courted by conspecific versus heterospecific males, suggesting their involvement when females differentiate between species, and thus their importance for speciation. Our most novel findings are that we connect gene expression levels to female choice behavior when evaluating male morphological and behavioral displays. Certain genes and modules respond to variation in specific male displays, and species express them in opposing directions, suggesting male display variation elicits a transcriptomic response that in turn influences female decision-making. For example, nuptial color ‘turns on’ expression of some genes and modules in limnetic females but ‘turns off’ expression in benthic females, thus linking these genes to divergent female preferences and sexual isolation.

Abstract ID: 2385

Unveiling the processes that drive divergent behaviour to shared chemistry in Heliconius butterflies

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Chemical signals can contribute significantly to fitness via their influence on the behaviour and physiology of other organisms. The influence of pheromones towards

securing mates bears particular relevance to the study of behavioural evolution, due to its direct influence on reproductive success. *Heliconius* butterflies have frequently been the focus of evolutionary research because of their extraordinary intra- and interspecific wing colour pattern variation, which are crucial for mate choice and sexual selection. However, there is also a clear role for chemical signalling by *Heliconius*, which possess both courtship and antiaphrodisiac pheromones. Such antiaphrodisiacs are transferred from males to females during mating to reduce further male mating attempts, simultaneously reducing male-male competition and female harassment. The best-studied antiaphrodisiac pheromone is that of *H. melpomene*, which has been identified as the monoterperne (E)-beta-ocimene. We find this same compound in the male genital bouquet of multiple species across the *Heliconius* phylogeny, which poses the question of whether male behavioural responses to (E)-beta-ocimene are preserved between distantly related species. Here, we use a combination of behavioural, electrophysiological, phylogenetic and selection analyses to show how and why a shared chemical signal produces divergent behavioural responses between species.

Abstract ID: 2423

The genetic and neural basis of female mate preference in *Drosophila*

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Female preference usually determines whether or not mating occurs within a species, and can serve as a barrier between species. However, very little is known about the genes and neurons affecting female receptivity. We identified the specific transcripts of a gene affecting variation in female mate rejection behaviour in *Drosophila*. We then identified individual neurons that affect female receptivity, and the neurons our transcript is acting through to influence female behaviour. Lastly, we categorized these neurons by determining the neurotransmitters and receptors influencing behaviour via these neurons.

Abstract ID: 1143

Ancestral proxy for the vasopressin/oxytocin system functions in male but not female parental care

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Gene duplication is thought to allow for the origin of novel gene functions. However, the evolutionary trajectory of duplicated genes can be difficult to determine, as the ancestral state is often unknown. Here, we leverage a system for which behavioral functions have been well-characterized in the duplicates – the oxytocin/vasopressin system in vertebrates – but that exists in a single copy – inotocin – in insects. How are the phenotypic functions of a single copy partitioned prior to gene duplication? To answer this question, we first survey conserved functions of the oxytocin/vasopressin system across vertebrates, including water balance, social, and parental care behaviors. Functions of oxytocin/vasopressin are often sex-specific for behavior, and it has been suggested that duplication allowed for specialization of function within males and

females. We then experimentally test the relationship between inotocin gene expression and known functions of the duplicates in a subsocial beetle that expresses complex parental care. We find that inotocin is strongly related to water balance in both males and females, corroborating other evidence that water balance was an ancestral function of this gene. Yet, behavioral functions of inotocin were not concordant between the sexes, as inotocin was associated with male, but not female, parental care. Males caring for larvae have higher inotocin than males without larvae, and males that provide more care have more inotocin than less caring males. Together, these results indicate that duplication of an ancestral vasotocin-like neuropeptide allowed for the evolution and elaboration of social and parental behaviors in females.

Abstract ID: 1303

Dissecting the genetic and molecular basis of the evolutionary loss of paternal care in sticklebacks

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Understanding the genetic and molecular basis of complex behavioral traits is an outstanding challenge for modern biology. Here, we capitalize on the recent evolutionary loss of parental care in stickleback fish (*Gasterosteus aculeatus*) to identify the proximate mechanisms underlying parental care. In addition to being an important model for evolution, sticklebacks are a classic model for studying behavior dating back to foundational studies by the early ethologists. Typically, male sticklebacks provide extensive sole paternal care that is necessary for offspring survival. However, there is an unusual ecotype of sticklebacks in Nova Scotia that does not provide care ("whites") and which has diverged recently from a typically caring ecotype ("commons"). To understand proximate molecular mechanisms of this divergence, we examined brain gene expression in reproductive males. We dissected male brains from both ecotypes, across four stages of the reproductive cycle (territorial, nesting, post-spawn, parenting), and measured gene expression in two brain regions harboring nodes important for social behavior, the telencephalon and diencephalon. A large number of genes were significantly differentially expressed between ecotypes and across the reproductive stages, including canonical genes associated with maternal care. Then, a full reciprocal cross of F1 hybrids was generated, phenotyped, and sampled as above to examine *cis*-regulatory divergence. Brain gene expression in hybrids revealed a suite of genes exhibiting allele-specific expression, providing evidence for *cis*-regulatory divergence. Together, these results provide a strong foundation for identifying the genetic and molecular basis of behavioral evolution in this important vertebrate model organism.

Abstract ID: 2471

Evolving new behaviors by tweaking sensory-motor circuits

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How do new social behaviors evolve from pre-existing brain circuitry? Evolving new social behaviors could require adjusting sensory recognition of social stimuli, how that

information is integrated with internal physiological state, or producing novel motor displays. We explored this question in poison frogs (Family Dendrobatidae), where the tadpoles of some species have developed a dance display to beg for food from their mothers. We first determined which sensory modalities tadpoles rely on for maternal recognition and found that tadpoles use olfactory cues for interspecies recognition. We then identified the brain regions and cell types involved in regulating begging behavior, which pointed to a prominent role for dopamine signaling. Pharmacological and cell ablation experiments show that dopamine manipulations produce begging behavior in tadpoles of begging species, but not closely related non-begging species. Our results suggest that tweaking dopamine circuitry can lead to the evolution of novel sensory-motor behaviors.

Symposium: S19. Eco-evolutionary dynamics and feedbacks in invasive species (id: 39)

Abstract ID: 1497

Genome-wide signatures of synergistic epistasis during parallel adaptation in an invading copepod

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The ability of populations to expand their geographic ranges, whether as invaders or climate migrants, presents among the most serious global problems today. However, fundamental mechanisms regarding factors that enable certain populations to rapidly transition to novel habitats remain poorly understood. Recently, populations of the copepod *Eurytemora affinis* complex have invaded freshwater habitats multiple times independently from saline sources. Intriguingly, evolutionary changes during invasions often involved the same loci, with selection often acting on the same SNPs, in wild populations and laboratory selection lines. Most notably, many candidate loci under parallel selection in the invasive populations arose from balanced polymorphisms in the native ranges. In our laboratory evolution experiment, SNP frequencies across loci converged among replicate selection lines far beyond expectations following 10 generations of laboratory selection. Using extensive simulations, we found that this degree of parallelism was consistent with synergistic epistasis among alleles responding in concert across replicate selection lines for this polygenic trait (salinity tolerance). The effect of synergistic epistasis appeared greater than selection from balanced polymorphisms in promoting parallel evolution. Our results were consistent with mechanisms of ion uptake from dilute habitats, requiring the coordinated action of cooperating ion transporter proteins. Most notably, our results suggest that a specific set of ion transporter alleles might be necessary for freshwater adaptation to occur in this system, pointing to a canalized evolutionary pathway. Thus, we find strong support for a novel and potentially widespread mechanism, namely positive epistasis, in promoting this parallel and canalized response. Funding: NSF and ANR

Abstract ID: 2182

The genomics of invasiveness: lessons from the ant *Cardiocondyla obscurior*

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The adaptive potential of introduced species is expected to be low, because their genetic variation is strongly reduced due to the founder effect. However, in a phenomenon referred to as the genetic paradox of invasion, bottlenecked populations of some species often succeed to rapidly adapt to novel habitats. Very little is known about the genomic mechanisms contributing to their success. Here we describe genomic features associated with the invasive, highly inbred ant species *Cardiocondyla obscurior*.
Using population genomics, we characterize genome evolution in six introduced populations showing that recent activity of transposable elements as well as intraspecific introgression between two distinct genetic lineages increase genetic variation. Linkage mapping further revealed a complex genome-wide recombination landscape, shaped by genome structure and incompatible haplotypes, and significantly correlated with transposable element content. Based on these data, we aim to advance our understanding of the molecular mechanisms associated with rapid genome evolution in invasive populations of *C. obscurior*.

Abstract ID: 1560

Genetic signatures of a range expansion in natura: how clones play leapfrog?

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Theoretical population genetics examines how the interplay between demography and dispersal regime shapes genetic diversity along range expansions. Yet it is challenging to test these predictions (such as the surfing phenomenon) in natural populations, in part because of the high stochasticity inherent to the realisation of each colonisation event. Here, we benefit from a remarkable ecological system to disentangle colonization patterns thanks to annual biological replicates[1,2]. Embanked in the Alps, the Durance River valley channels the dispersal of a plant pathogen, the poplar rust fungus. Each year, this species spreads out clonally along the riverbanks. We monitored the epidemics and inferred that dispersal of this pathogen results from a fat-tail kernel. We subsequently tested how this dispersal regime leads to a conservation of genetic diversity, as expected theoretically. We observe clones that play leapfrog from site to site, which prevents a single genotype to surf along the river. Notably, whatever the annual replicate, the range expansion can be split into two phases with different genetic outcomes. Upstream, fast colonization maintained high genetic diversity. Downstream, the colonization wave progressively faltered, diversity eroded, and differentiation increased, as expected under recurrent founder events. Yet the magnitude of these

changes differs from year to year as epidemics differ in intensity. We hence provide, through the study of this remarkable ecological system, direct evidence of the interplay between drift and migration at work.

References:
1 Xhaard etal. 2012 (doi: 10.1111/j.1365-294X.2012.05556.x)
2 Becheler etal. 2016 (doi: 10.1002/ece3.2392)

Abstract ID: 1867

Selection and hybridization interact to shape the outcome of *Helicoverpa* invasion in Brazil.

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The noctuid moth Helicoverpa armigera is among the world's most damaging crop pests, highly polyphagous and resistant to more pesticides than any other species. H. armigera was recently introduced to South America where it hybridized with its American sister species, H. zea, despite near-complete reproductive isolation. An apparent burst of adaptive introgression in 2012-2013 introduced pyrethroid pesticide resistance alleles into H. zea populations. We have generated a time-series whole-genome resequencing dataset of >300 individuals collected at 8 locations in Brazil during a six year period of invasive spread. These data allow us to map the extent of admixture over space and time, identify adaptive introgression at specific loci, and characterise the highly polygenic basis of reproductive isolation between the two species. I discuss the long-term outcome of hybridization between these species, the balance between selection and hybridization, and the extent to which invasive alleles have spread into North America. The use of whole-genome resequencing time-series data has the potential to be employed in many other systems in which invasive species or populations hybridize with natives, paving the way for a deeper understanding of the interplay between hybridization and adaptation during biological invasion.

Abstract ID: 1771

How does sex influence range expansions with evolution of dispersal? A quantitative analysis

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Despite several examples of the impact of evolution of dispersal along range expansions (the most notorious one being the cane-toads invasion in Australia), analyzing the resulting intricate eco-evo dynamics is mathematically challenging. In particular, the interplay between local competition for resources and trait evolution can lead to a spatial sorting phenomenon, where individuals at the front present higher dispersal trait values. Existing theoretical models aiming at analyzing this spatial sorting effect have been focusing on asexual populations, where mutations drive the quantitative dispersal trait's evolution. They successfully derived the long-time acceleration rate of the invasion front in this case. However, identifying such features for sexual populations was lacking, mainly due to the added difficulty of accounting for the effect of segregation on the

dispersal trait's inheritance. In our work ([Dekens and Lavigne, 2021, SIAM Journal of Applied Mathematics]), we circonvent this by using Fisher's infinitesimal model of segregation in a reaction-diffusion model. Our analysis provides an explicit quantitative description of the spatial trait distribution, including main features of the front (position, mean dispersal trait) and of the core of the population, behind the front. It highlights in particular the constraining effects of segregation on the dispersal trait's variance, which results in a significantly slower acceleration than in asexual populations.

Abstract ID: 1375

There and back again: Experimental epidemic waves and eco-evolutionary feedbacks

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Spreading epidemics resemble biological invasions in that eco-evolutionary dynamics can foster the rapid emergence of spatial patterns of trait variation. Similar to organisms at range expansion fronts, parasites at the front of an epidemic wave may evolve higher transmissibility and higher virulence, thus accelerating their rate of spatial spread. However, the opposite prediction may hold if virulence compromises the capacity of infected hosts to disperse. Moreover, little is known about whether such outcomes are modulated by concurrent host evolution, potentially changing eco-evolutionary feedbacks and disease spread.
We investigate the interplay between epidemiology and evolution in interconnected microcosms of the ciliate *Paramecium caudatum* and its bacterial parasite *Holospota undulata.* Two long-term treatments mimic spatially progressing populations, where infected and uninfected hosts at the front reach new patches through active swimming (dispersal treatment) or passively in randomly picked groups (pipetting treatment).
First, we assayed evolved parasites and hosts for differences in traits determining the epidemiological potential (parasite R_0, virulence, resistance) and spatial spread (host dispersal) into linear landscapes. Preliminary results indicate strong parasite effects on spatial host diffusion rates, but also marked spatio-temporal patterns of epidemic waves. We will further present a second assay, comparing these epidemiological dynamics for combinations of evolved parasites and hosts. As simplified abstractions of the real world, such experiments can inform on how different spatial ecological scenarios shape host and parasite trait (co)evolution during an epidemic, and help to assess the impact of such different (co)evolutionary histories on the spatial spread of disease.

Abstract ID: 1228

Complex introduction patterns and population structure of invasive cerambycids in Europe

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The high connectivity by trade increasingly facilitates biological invasions of e.g. the cerambycids *Anoplophora glabripennis* (ALB), *Anoplophora chinensis* (CLB)
and *Aromia bungii* (RLB) that were introduced from Asia into Europe by contamination of

wood packing materials, wooden products or living plants. For ALB, genome-wide SNPs discovered with Genotype-by-sequencing (GBS) were used to infer the introduction patterns into Europe. High population structure and reduced genetic variation revealed founder effects for most infestation sites, indicating multiple independent introductions into Europe. However, signs of secondary human-mediated translocations in a small spatial scale were also confirmed. Some populations indicated admixture, which might stem from multiple introductions from different sources or recurrent introductions from an admixed source population. This could enable the invaders to persist and establish easier, since propagule-pressure and maintained diversity can help to overcome adverse effects of genetic bottlenecks. ALB does not face much adaptive challenges in Europe, because the climate conditions and host trees are comparable with introduction sources from (sub)urban areas in Asia were ALB previously proliferated in the last decades. This preadaptation can also explain, why ALB is not much affected by hostile effects from genetic bottlenecks. The population genomic study of invasive European ALB populations showed very complex introduction patterns into Europe. GBS generated SNPs could furthermore be compared with the closely related invasive CLB to check for introgression in Europe. Furthermore, CLB and RLB outbreaks are currently sampled to be sequenced by GBS from native and invasive ranges to discover source populations.

Abstract ID: 1597

Perspectives on the interplay of ecological and evolutionary processes in species invasions

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Species introductions and invasions will involve a dynamic interplay of ecological and evolutionary processes on concurrent timescales. In this talk, I will present our recent work that considers eco-evolutionary dynamics in invasions from 1) an historical phylogenetic perspective, 2) a contemporary population genetic perspective, and 3) a forward-looking environmental perspective on human modification of ecological and evolutionary landscapes. Considering deeper evolutionary histories, I will discuss alternative phylogenetic models of species invasions, and the potential for the evolutionary history of an invader to interact with the composition of invaded communities, using a case study of global introductions of birds. Focusing in on contemporary dynamics, I will discuss our work on range expansions within invasions, and their affects on both genetic drift and response to selection in an invasive plant (yellow starthistle, *Centaurea solstitialis*). Finally looking forward, I will discuss invasive species evolution across gradients of human urbanization and the need to incorporate human landscape modification into future studies of eco-evolutionary dynamics in invaders. Taken together, these different perspectives will highlight ways in which ecological and evolutionary factors can interact to shape species invasions and their evolutionary outcomes.

Symposium: S20. Unravelling the interplay between plasticity and evolution during rapid global change (id: 941)

Abstract ID: 1690

Plastic *versus* genetic responses to climate change and urbanisation in birds

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Climate change and urbanization represent two of the most significant drivers of global changes across all ecosystems. Organisms can adapt to such changes by shifting their home ranges, or by adjusting their phenotypes via genetic adaptation and/or individual plasticity. We use long-term observations on wild birds, combined with experimental approaches and genomic analyses to tackle the difficult task of deciphering the roles of these two processes in organisms' responses to rapid environmental changes. This talk will present our latest investigations on two very different bird species. First, we quantified phenotypic and genetic trends in timing of spring migration in the long-distant migratory common tern (*Sterna hirundo*) across 27 years. We observed a strong phenotypic advance in arrival date, with birds arriving on average 9.34 days earlier over the study period. Quantitative genetic analyses provided rare evidence for micro-evolution underlying (part of) this bird's adaptive response to climate change. Second we found strong phenotypic divergence in many different traits (morphology, life-history, behaviour) measured in forest *versus* urban great tits (*Parus major*). These phenotypic shifts in cities could be maladaptive since they were never aligned with estimations of natural selection. By exploring the genomic footprints of selection and conducting a common garden experiment we are starting to unravel the interplay between plastic and genetic responses to urbanisation. Understanding the mechanisms by which populations can rapidly adapt to global change is crucial to predict their viability but often requires multiple complementary approaches.

Abstract ID: 2336

Can plasticity and evolution keep pace with climate change? Lessons from urban heat islands

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The rapid rate of warming from climate change threatens population persistence. However, it is an open question whether existing phenotypic plasticity or evolutionary change is sufficient for populations to keep pace with rising temperatures. Urban heat islands represent a promising human-made experiment to study the capacity of plasticity and evolution for adaptive responses to warming. Using common-garden experiments, we measured plastic and evolutionary responses in thermal tolerance to urbanization across several arthropod species, including acorn ants, the common woodland ant, the common woodlouse, and a mycophagous fruit fly. Among these species, we found consistent evolutionary responses of increased heat tolerance and decreased cold tolerance in urban populations. While most populations showed plasticity in response to

increased rearing temperatures, the repeated evolution of greater urban heat tolerance suggests that on its own, plasticity is insufficient to buffer populations to urban heat islands. We next carried out reciprocal-transplant experiments between urban and rural populations of acorn ants and the common woodlouse, which revealed evidence for urban adaptation in both species. For acorn ants, seasonal mortality suggested that adaptation is related to evolutionary divergence in thermal tolerance. Rural ants in urban environments suffered summer mortality, likely due to low heat tolerance, and urban ants in rural environments suffered winter mortality, likely due to reduced cold tolerance. However, for both the ants and woodlice, urban populations were less well-adapted to the novel city environment compared to rural populations in the rural environment, suggesting that species might not keep pace with future warming.

Abstract ID: 1499

The risk of extinction with nonlinear environmental change: models with evolution and plasticity

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Climate change and environmental degradation are placing many species at an elevated extinction risk. To survive in the face of these challenges, migration-limited species must adjust through either phenotypic plasticity or evolutionary adaptation (i.e., evolutionary rescue). Although previous theory on evolutionary rescue assumed the occurrence of linear environmental change, accelerating environmental change may present an even more serious threat. In this work, we model a species inhabiting a changing environment, in which the environmental change may be accelerating or decelerating. This species can either adapt through evolution or adopt advantageous phenotypes through plasticity (within-generational or transgenerational), and thereby avoid extinction. With our model we show that accelerating or decelerating environmental change elevates extinction risk compared to linear environmental change (while controlling for the mean rate of environmental change), unless plasticity is strong enough, or sufficient adaptive genetic variation is available.

Abstract ID: 1198

Experimental evolution of environmental tolerance and plasticity under variable predictability

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Global change affects not only the mean environments, but also the magnitude of environmental fluctuations, as well as their covariance structure through time, potentially reducing their predictability. Phenotypic plasticity may allow rapid responses to short-time environmental fluctuations, but these will only be beneficial when the degree of plasticity matches the level environmental predictability. Measuring population's ability to deal with altered patterns of environmental predictability (or autocorrelation) requires long and expensive field studies. On the other hand, laboratory experiments with microbes allow testing theoretical predictions on plasticity evolution with high replication levels.

I will present results from an evolutionary experiment with the halotolerant microalgae *Dunaliella salina*. We measured the acclimated tolerance surface, mapping population growth against past and current salinities, in 25 populations exposed for more than 200 generations to constant or stochastic salinities with different mean, variance and autocorrelation. We show that tolerance surfaces remained largely conserved, involving constraints on their evolution. However, we evidenced changes in niche position (optimal salinities) and niche breadth in response to environmental mean and variance. The bivariate acclimation surface allowed detecting a reduction of the acclimation effect in unpredictable environments. The latter response can be linked to a change in the major mechanism of osmotic regulation in *Dunaliella salina*, namely the regulation of intracellular glycerol content.

Abstract ID: 1448

Thermal stress, plasticity and selection for head temperature regulation in the World's largest bird

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Organisms inhabiting extreme thermal environments, such as desert birds, have evolved various adaptations to thermoregulate during hot days and cold nights. However, our knowledge of selection acting on thermoregulatory traits and their evolutionary potential is limited, particularly for large organisms experiencing extreme temperature fluctuations. Here we show, using thermal imaging that the featherless neck of the ostrich (*Struthio camelus*) acts as a 'thermal radiator', protecting the head from overheating during hot conditions and conserving heat during cool conditions. We found substantial individual variation in thermal plasticity of the neck to dissipate heat away from the head that was associated with increased egg-laying rates during high ambient temperatures. Combined with low, but significant, heritability estimates of individual thermal profiles, these findings suggest that the ostrich neck functions as an adaptive thermal radiator with evolutionary potential. There were also signatures of past selection, since ostriches originating from more volatile climatic regions and females that incubate during hot daytime conditions exhibited especially high thermal plasticity. Taken together our results indicate that morphological adaptations involved in ostrich thermoregulation, such as the neck, are experiencing ongoing selection and are crucial for successfully reproducing under fluctuating climatic conditions.

Abstract ID: 1467

Variation in phenotypic plasticity in Glanville fritillary butterfly larvae from a latitudinal cline

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Phenotypic plasticity may play a crucial role in the peristence of species under climate change as it allows for a more rapid response to environmental stress than through evolutionary adaptation. Levels of plasticity may be expressed differently between individuals or populations depending on the environment, making it a trait under selection. We used the Glanville fritillary butterfly (*Melitaea cinxia*) larvae originating from a latitudinal cline across its European range to assess whether plasticity in response to thermal condition varies among populations (i.e. are there GxE interactions). For this, we performed a full-factorial common garden experiment where we measured growth rate, mass and fat content in pre-diapause larvae that were reared at four temperatures (25, 28, 31 and 34 °C). Larval growth rate, mass and fat content all increased with rearing temperature and also differed with latitude, indicating genetic differences. Furthermore, we found stronger plastic responses for growth rate and mass in the larvae originating from north compared to those from south, showing that genetic differences for plasticity exist (GxE). As the larvae from higher latitudes experience a shorter growing season with more variable thermal conditions than those from lower latitudes, they may have evolved to take advantage of any increase in temperature. Interestingly, plasticity levels for fat content did vary among the populations, suggesting more canalized response for this trait. Overall, our results suggest a complex interplay between genetic and environmental factors that may impact how species cope with a changing environment.

Abstract ID: 1105

Rapid and transient evolution of local adaptation to seasonal host fruits in an invasive fly

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Adaptive evolution enables a good match between phenotype and environment when the environment is stable for multiple generations, whereas plasticity enables a good match when individuals encounter more than one environment during their life. However, the relative contributions of these two processes remain unclear when environmental heterogeneity is intermediate, with periods of environmental stability over a few generations. With global change the frequency of environmental change is accelerating, creating an urgent need to fill this knowledge gap. Here, we used *Drosophila suzukii* as a model system to evaluate the relative influence of adaptive evolution and plasticity on this match in heterogeneous environments. This species persists throughout the year on a succession of different host fruits, each one being available for only a few generations. Using reciprocal common environment experiments of natural *D. suzukii* populations collected from cherry, strawberry and blackberry, we found that both oviposition preference and offspring performance were higher on medium made with the fruit from which the population originated, than on media made with alternative fruits. This pattern remained after two generations in the laboratory, suggesting that adaptive evolution predominates over plasticity. Our study demonstrates that spatially and temporally variable selection does not prevent the rapid evolution of local adaptation in natural

populations. The speed and strength of adaptation may be facilitated by several mechanisms including a large effective population size and strong selective pressures imposed by host plants.

Abstract ID: 1436

Developmental plasticity and the potential of host shift in the seed beetle

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Diverse aspects of insects' behaviour, physiology, and the relationship between life-history traits are challenged when insects try to expand their host range, exploit alternative food sources and specialise on them. Process that enables phytophagous insects to utilise new food sources, known as host shift, is tightly associated with developmental plasticity and is seldom studied in laboratory settings. Using an experimental evolution approach we simulated the host shift process and observed the evolution of plasticity in seed beetle (*Acanthoscelides obtectus*) laboratory populations that evolved on optimal (common beans) and suboptimal (chickpea) plant hosts for more than 35 years. We have looked into: 1) life-history traits and how the long-term exposure to different hosts affects them; 2) the consequences when insects are exposed to short-term (in a single generation) change of the host plant, and 3) what happens when the host plant is altered each generation, that is, we observed the process of the selection for increased plasticity in a laboratory setting. Prior to life-history assays, populations were in the experiment for 13 generations. We found that long-term host shift to chickpeas decreased plasticity levels for preadult traits compared to bean adapted populations. Simultaneously, fecundity evolved a more plastic response. Groups that were evolving in conditions where plant hosts were alternated each generation had the same plasticity patterns as their ancestral populations, suggesting the need for more time for plastic response to evolve. This research illustrates the importance of phenotypic plasticity in maintaining populations under changing feeding conditions.

Abstract ID: 1300

Environmental response in gene expression and DNA methylation reveals factors influencing adaptation

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Understanding what factors influence plastic and genetic variation is valuable for predicting how organisms respond to changes in the selective environment. Here, using gene expression and DNA methylation as molecular phenotypes, we study environment-induced variation among *Arabidopsis lyrata* plants grown at lowland and alpine field sites. Our results show that gene expression is highly plastic, as many more genes are differentially expressed between the field sites than between populations. The environmentally responsive genes evolve under strong selective constraint – the strength of purifying selection on the coding sequence is high, while the rate of adaptive evolution is low. We find, however, that positive selection on *cis*-regulatory variants has likely contributed to genetically variable environment-responses, but such variants segregate only between distantly related populations. In contrast to gene expression, DNA methylation at genic regions is largely insensitive to the environment, and plastic methylation changes are not associated with differential gene expression. Besides genes, we detect environmental effects at transposable elements (TEs): TEs at the high-altitude field site have higher expression and methylation levels, suggestive of a broad-scale TE activation. Compared to the lowland population, plants native to the alpine environment harbor and excess of recent TE insertions, and we observe that specific TE families are enriched within environmentally responsive genes. In sum, although our results suggest that strong evolutionary constraint at environmentally responsive genes may limit the species' adaptive potential, plastic responses at TEs could rapidly create novel heritable variation that is primed towards environmental adaptation.

Abstract ID: 1994

Temperature-induced recombination rate plasticity in diploid populations of *Arabidopsis arenosa*

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Meiotic recombination rate is one of the key parameters in evolutionary biology, due to its effect on the efficiency of selection and ultimately, the rate of adaptation. While often taken as a static parameter, it is now known that recombination rate can in fact vary between species, populations, individuals, and different genomic regions. Recombination rate can also change in response to environmental factors, especially temperature, and this plasticity may play an important role when adapting to new environments. However, it is not yet clear if recombination rates change in response to a particular environment or in response to perceived stress. To elucidate this, we are characterizing recombination plasticity curves in populations naturally adapted to different environments. We use lineages of diploid *Arabidopsis arenosa* that inhabit geographically adjacent, but climatically very distinct regions – warm, dry Pannonian Basin and temperate, wet Carpathian Mountains. Through genome scan approach we identified several meiotic genes with signatures of diversifying selection in Pannonian lineage, and we hypothesize these signatures might be driven by meiotic adaptations to a warmer habitat. We assess how recombination rate changes under six different temperature treatments in populations representing each lineage, thus providing a rare characterization of temperature-induced recombination plasticity for populations found in different thermal environments. We combine this with pollen and fertility assays to further investigate possible meiotic adaptations to heat and perceived heat stress. This work will provide novel insights into mechanisms through which meiotic processes can be fine-tuned as organisms evolve to adapt to challenging environmental conditions.

Abstract ID: 2343

Rapid evolution in salmon life history induced by direct and indirect human-induced effects

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Identifying the evolutionary impacts of human activities is often challenging because of a lack of temporal data and limited knowledge of the genetic basis of many traits as well as the relative roles of adaptation and plasticity. Age at maturity in Atlantic salmon represents an ideal trait to study contemporary adaptive evolution as it has been associated with a single locus in the vgll3 region and has also strongly changed in recent decades. We conducted a population genetic study utilizing a 40 year data series and identified the drivers of evolution toward maturity at an earlier age in Atlantic salmon through two types of fisheries-induced evolution acting in opposing directions: an indirect effect linked with harvest of a salmon prey species (capelin) at sea (selection against late maturation) and a direct effect due to net fishing in rivers (selection against early maturation). We have also been conducting common garden studies to aimed at better understanding the vgll3-age at maturity association in the absence of environmental variation and if time allows, results of this work will also be presented.

Abstract ID: 1012

Urban evolution of seasonal plasticity of life history and color in Lepidoptera

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Seasonal plasticity relies on cues such as photoperiod to predict future seasonal environmental conditions; however, if anthropogenic changes alter either the cue or the environment, this can create a mismatch between them. Previously adaptive plasticity can become maladaptive unless evolution can correct for these mismatches. In the case of urbanization, these mismatches can arise because the urban heat island effect raises temperatures (changing the seasonal environment) or because light pollution alters photoperiod (changing the cue), and we predict different evolutionary responses to these two changes. In a common garden experiment using *Pieris napi* butterflies from urban and rural environments associated with two Nordic cities, we showed that the photoperiodic reaction norm for diapause induction has evolved in the direction predicted by the urban heat island. Changing diapause is not the only form of seasonal plasticity in this species; they also demonstrate seasonal wing color plasticity. If these plastic responses rely on the same regulatory mechanisms, their evolution could be coupled, but they could instead evolve independently. While the developmental pathway (diapause or direct) is largely a binary decision, melanization can instead be

further fine-tuned within each pathway, giving another option for the evolution of this trait. Using the same common garden experiment, we are testing whether the seasonal plasticity of wing color has evolved in urban environments and how these changes relate to the evolution of diapause induction.

Abstract ID: 1164

Hierarchical plasticity, and selection on plasticity, shape the dynamics of seasonal movement

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Current global changes are rapidly altering patterns of environmental variability. Short-term population responses to resulting perturbations typically primarily reflect plasticity in labile traits that affect fitness, and resulting selection. Such selection can then feed back to drive micro-evolution of plasticity, and hence shape long-term dynamics under new regimes of environmental variability. Yet, our ability to predict resulting population outcomes remains limited by major gaps in conceptualisation and quantification of complex patterns of within- and among-individual variation in phenotypic plasticity arising across hierarchical timescales, and associated forms of selection and underlying additive genetic variation. Here, we present new theoretical developments and empirical results which address the interaction of plasticity and microevolution, focussing on a labile dichotomous trait that directly shapes spatio-seasonal population dynamics: seasonal migration versus residence. We first highlight how distinctive hierarchical patterns of individual variation in expressed phenotypic plasticity, and interactions with micro-evolution, can intrinsically arise in quantitative genetic threshold traits (such as migration versus residence). We then illustrate these points by quantifying phenotypic-scale and liability-scale individual variation, using large-scale longitudinal ring-resight data from a wild bird population. Furthermore, we demonstrate episodes of selection on expressed plasticity, of magnitudes that varied strongly across years and sexes. Finally, we combine these results to show how strong selection altered distributions of individual effects on liability, including additive genetic effects, causing short- and longer-term changes in phenotype frequencies and plasticity. We thereby show how dynamics of plasticity, selection and micro-evolution in an ecologically critical trait can interact to shape population outcomes.

Abstract ID: 1935

Spatial, environmental and genetic contributions to timing of breeding in wild great tits

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Intraspecific variation is necessary for evolutionary change and population resilience. Understanding the causes of individual variation in traits involved with reproductive timing is increasingly important in the face of accelerating global change, especially in systems where reproduction must coincide with seasonal food peaks. Separating genetic and environmental effects on traits is complex, and there has been limited consideration of how small-scale environmental variation might lead to similarities between individuals who occupy similar environments, biasing estimates of heritability. In ecological systems the basic expectation is that places closer together will be more similar, however, environments can often be complex in their spatial structure and it therefore may be important to consider similarity in environments experienced by individuals even when they are not close in space. Here, we use a long-term study of reproductive timing of great tits (*Parus major*) in Wytham Woods, UK, to explore the contributions to variability in a key seasonal timing trait. We use quantitative genetic animal models, with individual phenotype data alongside a pedigree spanning 35 generations, to quantify the relative contributions of genetic and environmental factors to variation in reproductive timing. Our results suggest that accounting for similarity in the environment experienced by individuals may be just as important as considering their spatial proximity, especially in heterogenous environments. Environmental similarity can explain a considerable amount of the variation seen in reproductive timing, leading to decreased estimates of additive genetic heritability, which will in turn effect conclusions about a population's evolutionary potential and resilience.

Symposium: S21. Epigenetics goes wild! Epigenetic diversity and the evolutionary potential of wild populations. (id: 942)

Abstract ID: 2416

Less can be more: Understanding the adaptive role of epigenetics using naturally inbred fish

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Epigenetic variation represents a potential mechanism to generate adaptive responses in the presence of low genetic diversity and could be an alternative source of adaptive plastic phenotypes which may explain the persistence of highly inbred populations in variable environments. Although epigenetic modifications can arise independently from variation in the underlying DNA sequence, the adaptive relevance of the epigenetic variation and its heritability is still unclear and seems to depend to some extent on genetic variation. To what extent epigenetic modifications act independently from genomic variation is key to understanding their potential role in evolution. Inbred organisms provide a uniquely opportunity to detangle genetic from epigenetic variation, but naturally inbred vertebrate models are difficult to find. Mangrove killifishes from the *Kryptolebias*genus are ideal for these studies. *Kryptolebias* marmoratus and *K. hermaphroditus* are the only two known self-fertilising vertebrates, consisting mainly of selfing hermaphrodites, with very few males and high homozygosity. In contrast, *K. ocellatus* seems to reproduce only by outcrossing and tends to have higher genetic diversity. We have analysed genetic and epigenetic (DNA methylation) variation,

behaviour, microbiome composition and response to parasite loads in lab and wild populations of this genus. We have found evidence that DNA methylation patterns depend on the dynamic interaction between the genotype and the environment. Yet, we also found epigenetic parental effects related to the rearing environment which, if maintained, could have long-term evolutionary and act as an evolutionary bet-hedging strategy for species with low genetic diversity under environmental change.

Abstract ID: 1986

Differential methylation and genetic diversity go hand-in-hand in divergent stickleback populations

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Epigenetic mechanisms such as DNA methylation are now thought to comprise an invaluable adaptive toolkit in the early stages of range expansion, especially when genetic diversity is constrained. However, DNA methylation is also known to increase the rate of spontaneous mutations, thus affecting the genetic diversity of a population. Changes in DNA methylation incurred during range expansion may therefore influence sequence evolution. Here, we analysed published BSseq and WGS data from marine and freshwater stickleback fish to examine the relationship between DNA methylation differences and nucleotide diversity in the context of freshwater adaptation. Sites that are differentially methylated between populations have higher underlying nucleotide diversity in both populations, with diversity higher among sites that are hypermethylated in freshwater (methylation gain) than those that are hypomethylated (methylation loss). Strikingly, while nucleotide diversity is generally lower in the freshwater population (as expected from a population bottleneck), this is not the case for hypomethylated sites which instead have elevated nucleotide diversity in freshwater compared to marine. This elevated diversity is associated with a shift in variability of methylation levels and with sites whose methylation levels are environmentally responsive. Subsequently, we show that nucleotide diversity is higher among sites with more variable methylation and also positively correlates with the sensitivity to environmentally induced methylation change. Both suggest that as methylation levels become less tightly controlled, selection against mutations at the sites themselves also becomes relaxed, potentially allowing mutations to accumulate in a population with otherwise restricted genetic diversity.

Abstract ID: 1312

DNA methylation in the wild: stable environmental signature across clones of the wild strawberry

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Epigenetic modifications, such as DNA methylation, are thought to contribute to local adaptation of plant populations. Unlike genetic mutations, environmentally induced epigenetic variants can arise rapidly and generate locally adapted phenotypes, potentially heritable across multiple generations. However, to what extent

environmentally induced epigenetic changes are maintained across generations is still not clear. Using whole genome bisulfite sequencing, we compared epigenetic variation among 21 natural populations of *Fragaria vesca* from field conditions with clones of the same individuals grown for one year in a common garden environment. Epigenetic variation was mostly explained by DNA variation, but also by epigenetic variation related to the original environment of the populations. Many of the environmentally induced epigenetic variants occurred in genes and transposable elements. Our findings suggest that the original environment was associated with an epigenetic signature heritable across multiple clonal generations. They also suggest that environmentally induced epigenetic variants play a key role on gene activity and transposable elements regulation, potentially contributing to local adaptation. We conclude that DNA methylation variation in the wild is common and relevant for plant adaptation.

Abstract ID: 2125

The methylome driven CpG landscape of protein coding DNA in vertebrates

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The consequences of DNA methylation on the DNA base composition of vertebrate genomes is well understood. DNA methylation happens predominantly at cytosines in a CpG context (that is a palindromic sequences stretch where a cytosine is followed by a guanine) and this has a substantial effect on the rate of mutations at these sites. As a consequence there is a genomic dinucleotide composition bias of CpG sites. Most vertebrate genomes are heavily deprived of CpG sites relative to what is expected from nucleotide base composition. Here we summarize the implications of such DNA methylation induced dinucleotide bias on the composition of protein coding DNA, a type of DNA that is exposed to strong selection. We will first show that CpG is the only facultative dinucleotide of the standard genetic code, i.e. that can be avoided when encoding for any amino acid chain if there is no restriction on tRNA availibilty. However, we also show that CpG frequency is actually at higher frequency in protein coding DNA compared to the rest of genome. We will explain this finding by illustrating that a complex interplay of mutation bias, selection on amino acid changes and functional limitations are keeping CpG levels high in protein coding genes. We will also show that genes with extreme CpG content are functionally associated with meiosis and RNA gene expression across vertebrate species. Our results highlight the strong interplay between natural selection, mutational bias and epigenetics and how epigenetic modifications may translate into genetic properties in natural populations.

Abstract ID: 1223

Epigenetic divergence and phenotypic plasticity in the rapid speciation of East African cichlid fish

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In recent years, evidence supporting the role of the epigenome in adaptation and evolution has accumulated. However, the influence of epigenetic mechanisms—particularly chromatin architecture—upon patterns of vertebrate speciation and adaptation remains unclear. Using East African cichlid fish, we interrogate the role of gene regulatory mechanisms in maintaining, and perhaps mediating, phenotypic plasticity and adaptation to novel environments. The African cichlid radiation has gained increased attention in recent years as a model system for plasticity and evolution. Despite displaying an extraordinarily diverse range of morphological, physiological, and coloration phenotypes, these teleosts hold considerably low amounts of genetic diversity between species. As a result, cichlid fishes present an exceptional opportunity to investigate mechanisms of adaptation at the level of epigenetic regulation. To map epigenome divergence across ecomorphological groups within a lake system, we use Cut&Run to characterize the enrichment of four major histone modifications (H3K4me3, H3K27ac, H3K4me1, and H3K27me3) in liver and muscle of Lake Malawi cichlid species (Astatotilapia calliptera, Rhamphochromis longiceps, Maylandia zebra, and Aulonocara stuartgranti). These species represent the diverse range of morphologies and life histories present in Lake Malawi. In this presentation, we describe a genome-wide, comparative study where we find significant divergence in chromatin landscape across a group of closely related fishes. Analysis between species and across data types reveals tissue-specific regulatory patterns coordinating with ecological niche, linking species preferentially by environment. Here we present our findings and their contribution to determining the role of the epigenome in adaptation and diversification.

Abstract ID: 1988

Linking epigenetics and biological conservation: Toward a conservation epigenetics perspective

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Biodiversity conservation is a global issue. Recently several have stressed a need to implement conservationists' toolbox to meet the unprecedented challenges that we are currently witnessing. Genomic tools have revolutionized conservation biology in particular to assess the evolutionary potential of organisms in response to the ongoing global changes. However, the short-term interaction between individuals and their environment is still mostly ignored notably because genetics usually represents the long-term evolutionary background of populations. Moreover, the evolutionary potential relies on functional diversity that is inherited, but the non-genetic molecular mechanisms of inheritance -henceforth well documented in several organisms'- are still little considered. In this context, epigenetic approaches are promising to fill those knowledge and practical gaps. Using recent published results from the literature I will illustrate how epigenetics

can help documenting the ecological structuring of wild populations, and how epigenetic information can be integrated into conservation biology.

Abstract ID: 1322

Does epigenetic diversity contribute to the invasion of Japanese knotweeds?

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Japanese knotweeds (*Reynoutria* ssp.) are invasive in Europe and the USA, and they can impact native biodiversity and cause serious damage to roads and buildings. The source of the European invasion of *R. japonica* is thought to be a single plant introduced by Philipp von Siebold from Japan in the early 1840s, and distributed across Europe. After this, at least two introductions to the USA from both Europe and Asia were identified based on phylogenetic research. Previous work confirmed almost no genetic diversity in the invasive range, therefore, we test the hypothesis that epigenetic variation has contributed to the invasion of new environments in this species. As a first step, we have collected leaves from five individuals at each of 50 USA and 50 European invasive populations, and in 50 native populations from China. In each continent, the sampling took place along a 2000 km latitudinal transect, for a total of 750 samples. We present preliminary analyses of the genetic and epigenetic variation, using GBS and epiGBS, in natural populations of the three continents. We find significant differences in genetic and epigenetic differentiation, and global methylation patterns between invasive and native ranges. We link these results to phenotypic variation, and habitat characteristics.

Abstract ID: 1323

Quantifying the adaptive potential of sea turtles in a warming world via genome-wide DNA methylation

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Understanding what contributes to the evolutionary potential of endangered species is essential for predicting how they will respond to climate change. For endangered species with long-lived, slowly reproducing life histories, it has been proposed that adaptive plasticity underpinned by epigenetic diversity may be particularly relevant for population persistence, as genetic adaptation may be too slow to contend with the unprecedented pace of human-induced environmental change. Sea turtles are such species threatened by global warming, due to their ectothermic physiology and temperature-dependent sex determination (TSD) system, with most populations projected to become almost entirely feminised by the century end. Here, we focused on plastic responses of sea turtles to their thermal environment, using loggerhead sea turtles (*Caretta caretta*) that nest on the Cabo Verde Archipelago (East Atlantic) as a model system. After producing a novel, high-quality reference assembly for this species, we set up a split clutch incubation experiment in field conditions with warm and cool treatment groups, then performed whole genome bisulfite sequencing to compare genome-wide DNA methylation patterns between mothers and their offspring split between the treatment groups. We will report

on regions of interest, including in relation to their TSD system, which have potential conservation implications for the management of sea turtle populations in a rapidly warming world.

Abstract ID: 1687

Convergent DNA methylation changes associated with agriculture in ancient and modern-day humans

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The Neolithic transition from mobile hunting-gathering to sedentism and food production was a major ecological shift for human populations, occurring independently in multiple human populations over the last 10,000 years. How the Neolithic transition affected human physiology and whether it involved convergent epigenetic changes among distinct human populations have remained little understood. Here we tackled these problems using DNA methylation levels estimated from published ancient shotgun genomes produced using UDG-treated aDNA from archaeological bone and teeth samples. We compared 11 such ancient genomes from Upper Paleolithic and early Holocene hunter-gatherer contexts, and 8 ancient genomes from early Holocene Neolithic contexts. Using a variety of approaches, we identified c.100-1000 genes (1%-12%) among approximately 9500 genes showing systematic differences between hunter-gatherer and Neolithic agriculturalist groups. These methylation differences involved small effect sizes but had significant functional associations. We then compared the observed differences with methylation differences estimated between present-day traditional hunter-gatherer and agriculturalist groups in Central Africa, measured in whole blood samples. Intriguingly, hunter-gatherer versus agriculturalist methylation differences we identified in ancient Eurasians were significantly correlated with those in present-day Africa. Ancient and present-day lifestyle-related methylation differences further showed similarity in their functional associations, involving genes with roles in developmental processes. These results suggest unexpected convergence in epigenetic changes driven by agriculturalist lifestyles.

Abstract ID: 1519

Variation in DNA methylation in the great tit (*Parus major*) is largely determined by genetic effects

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As environmental fluctuations become more common, organisms need to rapidly adapt to anthropogenic and ecological changes. Epigenetic modifications - particularly DNA

methylation - potentially provide a proximate mechanism for environmental cues to shape phenotypic responses during development. Studies suggest that changes in DNA methylation allow for lifelong adaptive phenotypic plasticity. If these changes are inherited across generations, this would allow organisms to adapt to environmental change independent of their genotype and facilitate rapid evolutionary change. However, we know relatively little about the proportion of the epigenome that is affected by genetic versus environmental factors, and consequently, the range of functions that could potentially show plastic but heritable responses to environmental changes. To disentangle early rearing effects from common origin effects on DNA methylation, we used a partial cross-foster design in a natural great tit (*Parus major*) population. In this study, we show that most of the variance in DNA methylation is explained by a common origin and not by a common postnatal rearing environment. This indicates that DNA methylation is predominantly affected by genes and the prenatal environment. This was confirmed by a mQTL analysis in which we identified 1747 *cis* and 4803 *trans* SNP-methylation relationships. Our results show that the evolutionary scope for environmentally induced methylation marks independent of the genotype is limited, and that the majority of variation in DNA methylation is determined by genetic factors instead. This has consequences for the expected evolvability of DNA methylation variation in general and environmentally induced variation in DNA methylation specifically.

Symposium: S22. Phenotypic plasticity's importance in evolution: Same old dog or new tricks? (id: 971)

Abstract ID: 1064

How does plasticity influence eco-evolutionary dynamics? Insights from theory-experiment encounters.

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The realization that rapid phenotypic change in the wild often involves a substantial contribution from phenotypic plasticity has fostered considerable interest in recent years for the interplay of plasticity with evolution and demography in novel, changing or fluctuating environments. Theory has produced broad quantitative predictions by relying on simple models that are amenable to analysis and interpretation, but the extent to which these predictions can shed light on empirical patterns largely remains an open question. Some elements of realism missing from models may be of little concern, while others could severely limit their applicability. I will present some of our explorations of these questions using quantitative genetic models of plasticity evolution on the one hand, and laboratory experiments with microalgae under fluctuating salinity on the other hand. My aim will be to illustrate how a fruitful dialogue between theory and empiricism can reinforce our understanding of eco-evolutionary processes, as well as reveal new interesting biology.

Abstract ID: 1071

Anticipatory effects in the filamentous fungi *Neurospora crassa*

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Adaptation of organisms to changing environments often require meaningful phenotypic modifications to match the current conditions. However, getting information about the surroundings during an organism's lifetime could only permit accommodating relatively late developmental modifications. Therefore, it should be advantageous to count on trans-generational cues that provide information about the environment as early as possible to allow development along an optimal trajectory. This transfer of information across generations, known as anticipatory effects, is well documented in animals and plants but not in other eukaryotes as fungi. Understanding anticipatory effects and their evolutionary consequences in fungi is of vital importance as they perform crucial ecosystem functions. In this study, we ask whether anticipatory effects are present in the filamentous fungi *Neurospora crassa* if they are adaptive, and which is the mechanism behind them. We performed a fully factorial reciprocal transplant experiment in which we measured mycelium growth, in a rich and poor environment, of strains that experienced either match or mismatch environment in the previous generation. We found a strong silver spoon effect that lasted for one generation and showed to be adaptive as it increased fitness during competition experiments. The silver spoon effect was also present when the experiment was performed with deletion mutants that lacked key genes in epigenetic processes, suggesting that this parental effect is not orchestrated by epigenetic mechanisms. To further explore the mechanism, we performed RNA-seq on second-generation spores. The gene expression data showed a radical transcription shift that resulted in the suppression of sugars metabolism.

Abstract ID: 2004

The role of *Tribolium castaneum*'s phenotypic plasticity for the rapid evolution of resistance

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Phenotypic plasticity helps shaping adaptive responses and is thus relevant for the evolutionary potential of species. However, plasticity can be costly, so that under stable conditions, fixed strategies would be superior. Assimilation of formerly plastic traits has large potential for adaptation, but it has rarely been studied via experimental evolution, i.e., on a micro-evolutionary time scale. We aimed at elucidating how a highly plastic phenotypic trait, the invertebrate immune memory (priming), affects the evolution of a fixed trait, i.e., resistance to a pathogen. Using *Tribolium castaneum* and *Bacillus thuringiensis*, we performed experimental evolution for 9 generations, in alternating environments, mimicking environmental fluctuations. To determine, if in predictably variable environments, lines that express adaptive plasticity are likely to evolve more rapidly than those expressing maladaptive plasticity, we have set up three experimental treatments. One in which priming always precedes the exposure to bacteria (Matched lines), another in which priming is never followed by the bacterial infection (Unmatched lines), and a Control treatment in which priming is never applied. By the end of the selection experiment, we reveal unexpected trade-offs and intertwined mechanisms leading to the genetic assimilation of the plastic trait in the Matched lines. Coupled with “Common-Garden” experiments, life history trait measurements, RNA-seq and quantitative genetic models, we try to experimentally and theoretically unravel the

underpinnings of the observed rapid loss of plasticity. Our study highlights the importance of long-term experiments with complex patterns of environmental change, testing existing theories about how plasticity helps populations respond to rapid environmental change.

Abstract ID: 1985

De novo evolution of multicellularity via the canalisation of phenotypically plastic cell clumping

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The shift from unicellular organisms to multicellular ones represents a major transition in evolution. Theory expects that the formation of undifferentiated groups (the first step in this transition), relies on the occurrence of rare mutations that are acted upon by subsequent natural selection. Thus, the evolution of multicellularity is expected to be both rare and slow. Here we show that phenotypic plasticity can foster the evolution of multicellularity by avoiding and bypassing the wait for mutational emergence of undifferentiated group formation. Specifically, we first show that highly saline liquid environments can make both Gram-positive and Gram-negative bacteria grow as elongated macroscopic clumps and not as individual planktonic cells. Such clumps tend to be 2-3 cm in length and can comprise several million cells. Such clumping is phenotypically plastic: when transferred to environments with optimal salinity, the clumps disintegrate into individual cells that grow planktonically. Using experimental evolution with *Escherichia coli*, we show that within 300 generations, such clumping can be canalised successfully (the evolved bacteria compulsively grow as macroscopic multicellular clumps without environmental induction, even in optimal salinity environments). Next, we determine the genetic basis of this canalisation and show that the underlying genetic assimilation can be highly repeatable, with most populations enriching mutations linked to cell adhesion. Although most multicellular organisms are eukaryotic, our findings show that owing to phenotypic plasticity, bacteria can also be primed for undifferentiated multicellularity. Finally, condensing our findings into a model, we argue for the importance of phenotypic plasticity in the evolution of multicellularity.

Abstract ID: 2208

Phenotypic plasticity enables the colonization of extreme cave environments

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How organisms adapt to changes in their environment remains one of the major questions in contemporary biology. The colonization of caves is an example of a sudden and drastic environmental change because surface species invade the underground characterized by the constant darkness and food shortage. A subset of colonizers eventually fully adapts to those conditions and develop a series of morphological, neurological, metabolic, and behavioral adaptations. Other colonizers die out or show only partial alterations. In certain cases, the ancestral surface taxon is still extant and

available for comparison with a derived cave form, which enables testing of different hypotheses about the mechanisms of adaptive evolution in these taxa. We hypothesized that phenotypic plasticity must underlie the successful colonization of caves by ancestral surface species. Indeed, we found plastic responses in numerous phenotypes (e.g. body shape, metabolic rate, lipid content) which are associated with cave adaptations as a response to the only common environmental feature of all subsurface habitats – constant darkness. This was true for vertebrates and invertebrates as well as for fully adapted and partially adapted species. We also found non-adaptive plastic responses including in retinal anatomy and pigmentation. Lack of vision and albinism are the most iconic traits present in diverse cave-adapted taxa suggesting that selection against non-adaptive plasticity may be involved in their evolution. Overall, we can conclude that phenotypic plasticity is an important mechanism for the rapid initiation of adaptive changes which may be favored or targeted by natural selection during the evolution of cave-adapted species.

Abstract ID: 1470

Hidden genetic variation in plasticity increases adaptive potential in novel environments in *Senecio*

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If genetic variation in fitness increases when adaptive plasticity fails in novel environments, rapid adaptation could overcome associated fitness declines and allow population persistence through evolutionary rescue. Although plasticity is expected to underlie such increased genetic variance in fitness, this has not been tested empirically. We transplanted cuttings of a Sicilian daisy (Senecio, Asteraceae) within and outside its native range, and quantified genetic variation in fitness, which we related to plasticity in leaf traits and gene expression. Compared to native environments, mean fitness in the novel environment declined by 87%, but was associated with a threefold increase in genetic variation. Fitness in the novel environment was genetically correlated with plasticity: genotypes with greater fitness showed higher plasticity in leaf form, lower plasticity in leaf physiology and more gene underexpression. Surprisingly, genotypes with greater fitness in the novel environment had the lowest fitness at the native site. This means that although genetic variance in plasticity increases the potential for rapid adaptation to novel environments, adaptive plasticity and stabilising selection in native (non-stressful) environments hides such genetic variation in natural populations. Studies of genotypic variation in fitness and plasticity within existing environmental conditions may therefore underestimate the capacity for populations to evolve the new forms of genotypic sensitivity demanded by the environments of coming decades.

Abstract ID: 1679

The role of gene expression plasticity in population response to environmental stressors

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Rapid environmental changes impact the distribution and abundance of species, highlighting the urgency to understand how they will respond. Analysis of differentially expressed genes has elucidated areas of the genome involved in adaptive divergence. However, such studies are hampered by large numbers of genes and limited knowledge of how they work together. Recent methods (termed “pathway analyses”) have emerged that group genes that behave in a coordinated fashion to a factor of interest, aiding in functional annotation and uncovering of biological pathways. Here, we reanalyse a dataset that investigated temperature-induced changes in gene expression in marine-adapted and freshwater-adapted threespine stickleback (*Gasterosteus aculeatus*), using three complementary pathway analyses. We discovered twelve gene modules, six with conserved and six divergent responses between marine and freshwater stickleback when acclimated to 7°C or 22°C. One divergent module was associated with freshwater stickleback-specific response to temperature, while remaining modules showed differences in height of reaction norms. One module enriched for metabolic processes and genes in the oxidative phosphorylation pathway, many of which showed distinct expression differences between freshwater and marine stickleback. It also contained *PPARAa,* a transcription factor that controls metabolic genes and has been implicated as a candidate gene in the adaptive thermal tolerance of several fishes, including stickleback. Pathway analyses uncovered patterns that contribute to a better understanding of both organism-level effects of modified gene expression and the targets of adaptive divergence in response to environmental change.

Abstract ID: 2453

A mechanistic approach to understanding plasticity; a sperm competition example

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Understanding how plasticity itself evolves, what limits or facilitates plasticity, can help us to assess the role of plasticity in evolution. In particular, understanding the genetics of plasticity is required, but reaction norms are likely to be polygenic. Examining the mechanisms underpinning plasticity will help to identify which genes and genomic processes are especially important. It may be that are underlying programmes (or genetic structures) that are permissive of plasticity and heightens the evolvability of responsiveness to different cues. Here I explore an example of very rapid flexible behavioural plasticity, whereby male Drosophila melanogaster fruit flies respond to exposure to rival males. The experimental tractability of fruit flies allows investigation of the processes from sensory inputs to behavioural and physiological outputs, through the genome, proteome, epigenome. Males track their exposure to rival males, matching their reproductive investment in a particular mating to their anticipation of sperm competition. However, the same environmental cue of the presence of a rival male can alter other

traits such as learning ability, stress responses and lifespan. This raises the question of whether these are pleiotropic effects that have hitchhiked along with the sperm response, or whether these traits are independently plastic. For example, the need to be plastic in response to the social environment is implicated in the evolution of cognition more generally. Ultimately, by integrating such studies we could establish whether mechanisms of plasticity are generalizable, and whether 'plasticity' as a trait can be co-opted into mediating responses to novel environmental cues.

Abstract ID: 1492

Not just fitness traits: Changing environments may favor the plasticity of recombination

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The long-discussed evolutionary interplay between genetic adaptation and phenotypic plasticity attracts ever-increasing attention in the context of changing environments. The predominant number of studies focus on the plasticity of fitness-related traits subject to direct selection, while abundant empirical evidence also indicates substantial environmental plasticity of numerous fitness-unrelated traits. This especially holds for variation-affecting processes like recombination, selfing, mutation, or dispersal, which typically do not affect the individual fitness but can still be under sufficiently strong indirect selection given their effect on the population structure in subsequent generations. In a series of theoretical studies, we numerically modeled the evolution of several forms of plastic recombination: with the rate increasing either in an atypical environment or during episodes of strong selection, or upon environmental shifts. We show that alleles conferring these forms of plasticity often outcompete alleles for the best constant recombination rate. Moreover, plastic recombination is not rarely favored even in situations where any constant recombination is rejected, thereby maintaining a non-zero recombination rate in the population. In parallel to the simulations, we also traced microevolutionary changes in both recombination rates and their plasticity, in both laboratory and natural populations of *Drosophila melanogaster*. It turned out that population adaptation to unfavorable environmental conditions may induce indirect selection on increased recombination rate and relaxed crossover interference, and these changes may also be accompanied by milder recombination plasticity. The latter can be viewed as a manifestation of the very profound eco-evolutionary trade-off between adaptation and adaptability, discussed by Darlington (1939) and Gause (1940).

Abstract ID: 1726

'Developmental lines of least resistance' shape the relationship between plasticity and evolution

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Plasticity frequently mirrors evolutionary divergences, a phenomenon often argued to invoke plasticity-led evolution. Here, we investigate potential alternative scenarios that can align plasticity and evolution. Plastic as well as evolutionary changes require modifications of developmental trajectories. Because virtually all developmental systems are biased towards producing certain phenotypes more often than others, such developmental biases have the potential to simultaneously shape the phenotypic effects of both environmental and genetic (e.g., mutational) perturbations. In theory, developmental bias could thus cause an alignment between genetic and environmental effects. Studying dung beetle horns and fly wings, we first investigate how plasticity relates to i) intraspecific variation, ii) the G matrix, iii) population divergence, and iv) macroevolutionary divergence across 60 million years. Next, we test whether the alignment between plasticity and evolutionary responses might be shaped by the developmental architecture of our traits of interest. Combining functional genetics (RNA interference) with geometric morphometrics, our results support the hypothesis that changes in trait shape —whether brought about by environmentally plastic responses, gene knockdowns, or evolutionary divergences— converge along 'developmental lines of least resistance'. That is, plastic and evolutionary changes may align simply because they are products of the same biased developmental system, and not because plasticity leads or precedes evolution.

Abstract ID: 1927

Environmentally-induced variation in lifespan is regulated by cryptic genetic variation n *Drosophila*

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Phenotypic changes in response to environmental change are known as plastic because there are no genetic changes (e.g., new mutations) associated with such rapid phenotypic response. However, the fact that, in many cases, such environmentally-induced phenotypic response differs between individuals suggests an important role for genetic variation in regulating plastic responses. Understanding to what extent the response to environmental change has a genetic basis is fundamentally important to determine the role of plasticity in evolution. Using a large population of outbred *Drosophila melanogaster*, we set up to identify the genetic basis of lifespan in two conditions: control and high sugar diets. In flies, as well as in mice, humans and other species, high-sugar diets modify many phenotypes including a shortening of lifespan. We sequenced over 10,000 individual flies to track genome-wide allele frequency changes over the lifetime of six replicate populations, recording in real time the changes in the genomic composition of each population as flies aged. The high statistical power of this experimental design allowed us to identify thousands of lifespan-associated alleles whose frequency changed between young and old flies. Remarkably, a third of those lifespan-associated alleles appear cryptic in control diet but play an important role in high sugar conditions. Our results show that phenotypic changes driven by

environmental variation within one generation indeed have a genetic basis, suggesting that there is ample opportunity for selection to act on plastic phenotypes.

Abstract ID: 2097

Parallelism and plasticity during adaptation to industrial era mining contamination

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Phenotypic plasticity in ancestral populations is hypothesised to facilitate adaptation in derived populations, but the extent to which ancestral plasticity increases the chances of parallel genetic and phenotypic adaptive changes has not been explored. Generally, the majority of ancestral plasticity in gene expression is reversed over the course of adaptation; a pattern which is often examined transcriptome-wide rather than focusing on those gene that are directly involved in adaptation. Using two lineages of *Silene uniflora* that have independently evolved tolerance to heavy metal contaminated soils ant abandoned industrial mines, we experimentally quantified the contribution of ancestral plasticity to adaptive gene expression evolution. The generally observed pattern of transcriptome wide reversion is driven by the absence of a widespread stress response in *S. uniflora* plants that have evolved zinc tolerance compared to the ancestral, zinc-sensitive plants. We observed that reinforcement of ancestral plasticity has made an important contribution to the degree of plasticity in derived populations and that a third of the constitutive differences between tolerant and sensitive ecotypes have resulted from genetic assimilation of pre-existing ancestral plasticity. The chance that genes are recruited across parallel instances of adaptation is also increased if plasticity is present in the ancestral populations. Despite this, genes with or without ancestral plasticity equally probable to have comparable expression levels in adapted populations. Our experiments show that adaptive parallel evolution is impacted by ancestral plasticity, particularly via genetic assimilation.

Abstract ID: 1392

Density-dependent dispersal promotes female-biased sex allocation in viscous populations

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A surprising result emerging from the theory of sex allocation is that the optimal sex ratio is predicted to be completely independent of the rate of dispersal. This striking invariance result has stimulated a huge amount of theoretical and empirical attention in the social evolution literature. Here, we investigate how phenotypic plasticity, in the form of density-dependent dispersal, shapes patterns of sex allocation in a viscous population setting. Specifically, we find that if individuals are able to adjust their dispersal behaviour according to local population density, then they are favoured to do so, and this drives the evolution of female-biased sex allocation. This result obtains because, whereas under density-independent dispersal population viscosity is associated not only with higher relatedness – which promotes female bias – but also with higher kin-competition – which inhibits female bias – under density-dependent dispersal the kin-competition

consequences of a female-biased sex ratio are entirely abolished. We derive analytical results for a range of group sizes and costs of dispersal, and for haploid, diploid, and haplodiploid modes of inheritance. These results show that population viscosity promotes female-biased sex ratios in the context of density-dependent dispersal, and more generally provide an illustration of how phenotypic plasticity can play a major role in modulating social evolutionary outcomes.

Abstract ID: 2101

Natural selection makes phenotypic plasticity adaptive but constrained by phenotypic integration

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The ability of an organism to modify its phenotype according to environmental conditions is known as phenotypic plasticity and it is expected in organisms adapted to changing habitats. However, different phenotypic traits must covary in order to generate a proper functioning of organisms, which is known as phenotypic integration. How phenotypic integration would constrain the phenotypic plasticity or how phenotypic plasticity would generate disintegration in the phenotype, are questions that have been discussed for decades. We explored this relationship in three ploidy levels of *Erysimum incanum* s.l., where we did measure over 1600 plants across three different environments. We analysed the variation and heritability of phenotypic plasticity. We then characterised the significant selective gradients acting on traits and their plasticities of attributes related to the plant size, flower size and plant reproductive investment. The relationship between phenotypic plasticity and integration was constantly negative. The indirect selection was significantly higher acting on multiple pairs of traits but not on the correlation of their phenotypic plasticities. Similar pattern was found for heritabilities. Natural selection plays an important role making adaptive or maladaptive the phenotypic plasticity, but also consolidating the phenotypic integration by correlated selection and limiting the occurrence of phenotypic plasticity.

Abstract ID: 2174

The primary role of phenotypic plasticity in the face of accelerated environmental change

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The pace of current human-induced environmental change far exceeds the timing of evolutionary processes. This raises a crucial question: how will organisms and species keep up with this rapid eco-evolutionary challenge? Among other consequences, genetic variation in the wild – the 'raw material' of natural selection – is declining; in this context, phenotypic plasticity assumes a central role in enabling populations and species to provide rapid adaptive responses to a changing environment. Although further evidence is needed, there is broad consensus on the increasing relevance of this environment-

induced mechanism in coping with the *tempo* of change in the 'Anthropocene' world, where normal evolutionary rules are suspended, and organisms face an accelerated race for survival. Given the almost entirely anthropogenic nature of today's ecosystems, we suggest that, in order to better frame evolutionarily relevant mechanisms such as phenotypic plasticity, an interdisciplinary view is needed to address the multidimensional inputs that make up the human-natural interaction. In fact, through a 'monumental niche construction process', humans have shaped nearly every ecosystem on Earth, thereby creating an inextricable intertwining of the 'natural' and 'cultural' spheres. It has been argued that even biological responses to anthropogenic climate change, like epigenetic variation or phenotypic plasticity, are influenced, albeit indirectly, by human cultures and worldviews. Such complexity of drivers and impacts needs a plural theoretical framework: collaborating with social sciences and humanities can help the natural sciences explain how humans shape and alter the natural world, thus shedding new light on novel ecological traits and evolutionary adaptations.

Symposium: S23. The evolution and consequences of non-mendelian inheritance (id: 40)

Abstract ID: 2463

Genetic conflicts between sex chromosomes drive expansion and loss of sperm nuclear basic protein genes in *Drosophila*

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Many animal species deploy short, positively charged proteins, called sperm nuclear basic proteins (SNBPs), for tighter packaging of genomes in sperm. SNBPs (protamines) evolve rapidly in mammalian lineages. Their repertoires differ dramatically across animal lineages. Both sperm competition and meiotic drive between sex chromosomes have been proposed as causes of SNBP innovation. We took a phylogenomic approach in *Drosophila* species to investigate SNBP diversification and its underlying causes. Although most SNBP genes evolved rapidly under positive selection, we found that genes important for male fertility in *D. melanogaster* did not. Unexpectedly, however, evolutionarily young SNBP genes are more likely to encode fertility essential functions than ancient, conserved SNBP genes. We found 19 independent amplification events involving seven SNBP genes that occurred preferentially on sex chromosomes in *Drosophila* species. Conversely, we found a dramatic loss of otherwise-conserved SNBP genes in the *montium* group of *Drosophila* species, which coincided with an X-Y chromosomal fusion. Furthermore, we found non-random degeneration or autosomal relocation of SNBP genes that became linked to sex chromosomes via ancient chromosomal fusions. We hypothesize that SNBP genes ancestrally encoded by autosomes suppress meiotic drive, whereas sex-chromosomal SNBP expansions directly participate in meiotic drive. X-Y fusions in the *montium* group render autosomal SNBPs dispensable by making X-versus-Y meiotic drive obsolete or costly. We conclude that although rapid evolution of SNBPs might be a universal phenomenon in animals, this rapid evolution is likely driven by genetic conflicts between sex chromosomes during spermatogenesis in *Drosophila* species.

Abstract ID: 1460

Mitochondrial variant specifically impairs male fertility in seed beetle *Acanthoscelides obtectus*

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Uniparental inheritance of mitochondria leads to asymmetry of mtDNA evolution because selection acts directly on non-neutral mtDNA polymorphisms only through the female lineage. In other words, natural selection will not recognize any mtDNA mutation which is male harming, but neutral, beneficial, or slightly deleterious for females. Ultimately, non-Mendelian inheritance of mitochondria drives the evolution of male-specific mitochondrial mutation loads, an idea known as mother's curse. Naturally occurring mtDNA mutations that impair male fertility, but have no effects on females, have been recognized as an opportunity for the development of the biocontrol of pest species termed Trojan Female Technique (TFT). Namely, females carrying TFT mutations, and their female descendants, could continuously, over multiple generations, produce males that sire fewer offspring than wild-type counterparts. Although the TFT shows promise as a trans-generational, self-sustaining method, its empirical success hinges on the existence of natural TFT mutations that remain uncharacterized in pest insects. In order to identify and test possible TFT candidates for biological control of seed beetle, a common pest in legume storages, three mtDNA haplotypes found in laboratory lines were expressed alongside one outbred nuclear background. We analyzed the effects of specific mitotypes on female and male life history traits, and found a male-only reduction in fertility in one mito-nuclear combination. Specifically, fertility (but not total fecundity and lifespan) of males carrying specific mtDNA variant was reduced by 35% relative to the controls. Our study provides evidence that intergenomic conflict leads to the existence of male-harming mtDNA mutations that segregate within populations.

Abstract ID: 1237

The evolution and genetic mechanism of sex-ratio meiotic drive in *Drosophila affinis*

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Meiotic drivers are selfish genetic elements that promote their own transmission to the gametes. Sex-ratio (SR) meiotic drive occurs when a selfish genetic element on the X chromosome manipulates gametogenesis to prevent the maturation of Y-bearing sperm in males, resulting in the production of predominant female progeny. The spread of SR meiotic drive can affect host genetic diversity, sex chromosome evolution, and even cause host extinction if it reaches high enough frequency. SR meiotic drivers have evolved independently several times, however, the underlying genetic mechanism is only known in few cases. In this study we use a combination of genomics, transcriptomics,

single nucleus RNA-seq (snRNA-seq), and CRISPR-Cas9 to identify the genetic mechanism responsible for the SR meiotic drive in *Drosophila affinis.* We found X chromosome is enriched for differentially expressed (DE) transcripts and that many DE genes had elevated K_a/K_s values between SR and ST. We identified top DE candidate genes, including two X-linked duplicate and testis-specific: encoding a chromosomal protein involved in spermatogenesis (*tHMG2*), and encoding the regulator of chromatin condensation (*Rcc1*). We used CRISPR-Cas9 knockout experiments to test whether these genes were involved in the sex ratio phenotype. Lastly, snRNA-seq analysis recapitulates transcriptional patterns associated with gene expression changes during spermatogenesis between ST and SR testes. Our results suggest the two candidate genes' significant role involving in the drive in this species, providing evidence that rapid evolution of genes disrupting spermatogenesis is important source of intragenomic conflict.

Abstract ID: 1229

Virus-like transposons cross the species barrier driving the evolution of genetic incompatibilities

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Selfish genetic elements (SGEs), such as transposable elements and toxin-antidote elements, might lead to the reduction of gene flow between species, which could play important roles in speciation. At the same time, horizontal gene transfer (HGT) is a mechanism by which different species exchange genetic material bypassing sexual and genetic barriers. Both SGEs and HGT subvert the laws of Mendelian segregation and the interplay between both is not a very explored field.

Here, we identified a mobile toxin-antidote element, msft-1/tlpr-1, which spreads in natural populations of the nematode *C. briggsae*. The toxin's precursor was first horizontally transferred into *C. briggsae* via Mavericks -virus-like transposons- from a distant *Caenorhabditis* nematode. Later on, the toxin was captured by a Mutator-like transposable element (MULE), from which the antidote evolved. Surprisingly, we found that nematode Mavericks are not only equipped with capsid proteins (similar to the one found in virophages) but also fusogens (spike proteins), leading to widespread exchange of cargo proteins between extremely divergent nematode species

Our results show the evolutionary emergence of a mobile toxin-antidote element through the interplay between transposons and horizontal gene transfer.

Abstract ID: 1993

The fate of a suppressed X-linked meiotic driver: experimental evolution in *Drosophila simulans*

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Sex-ratio (SR) meiotic drivers are X-linked selfish genetic elements that promote their own transmission by preventing the production of Y-bearing sperm, which usually lowers male fertility. The spread of SR drivers in populations is expected to trigger the evolution of unlinked drive suppressors, a theoretically predicted co-evolution that has been observed in nature. Once completely suppressed, the drivers are expected either to decline if they still affect the fitness of their carriers, or to evolve randomly and possibly get fixed if the suppressors eliminate their deleterious effects. To explore this issue, we used the Paris *sex-ratio* system of *Drosophila simulans* in which drive results from the joint effect of two elements on the X chromosome: a segmental duplication and a deficient allele of the *HP1D2* gene. We set up six experimental populations starting with 2/3 of X chromosomes carrying both elements (X^{SR}) in a fully suppressing background. We let them evolve independently during almost a hundred generations under strong sexual competition, a condition known to cause the rapid disappearance of unsuppressed Paris X^{SR} in previous experimental populations. In our study, the fate of X^{SR} chromosomes varied among populations, from extinction to their maintenance at a frequency close to the starting one. Our results show that complete suppression can prevent the demise of an otherwise deleterious X^{SR} chromosome, turning a genetic conflict into cooperation between unlinked loci. Observations in natural populations suggest a contrasting fate of the two elements: disappearance of the duplication and maintenance of deficient *HP1D2* alleles.

Abstract ID: 2113

Genomic signatures of ancient asexuality in the oribatid mite *Platynothrus peltifer*

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Despite its various costs, sexual reproduction is the prominent way to produce offspring. In theory, the absence of sex is regarded as an evolutionary dead-end. However, some oribatid mite species escaped their detrimental fate and have evolved and diversified in the absence of sex for millions of years. Identifying mechanisms for the long-term persistence of asexuals will help to untangle the enigma of maintenance of sex in nature. The population and genomic structure of ancient asexuals which enable them to persist are still unknown. Moreover, low input generated a bottleneck for in-depth genomic studies on oribatid mites up until now. We overcame this obstacle and now provide a single individual, haplotype resolved, chromosome-scale genome, and population data of *Platynothrus peltifer*. We look into the population and genomic features to identify singularities that allow for their differentiation and persistence. We found no signs of cryptic sex. Along with differentially expressed genes in the diverged haplotypes, we also found horizontally transferred genes, which were differentially expressed. Further, we detected extensive demographic expansion and recent TE activity. These identified features might contribute to the persistence and evolvability in the absence of sex.

Abstract ID: 1661

Deciphering autopseudogamy of Mesorhabditis nematodes with combined cytology and genomics

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Within the nematode genus Mesorhabditis, several species reproduce by auto-pseudogamy: asexual females produce few sexual males, which are necessary to produce asexual females (doi: 10.1126/science.aau0099). Combining cytological description and genomic analysis, we are exploring the mechanisms of unreduced oocyte production in these species featuring a progressive loss of males and sexuality.
We found that homologous chromosomes pair during meiotic prophase and undergo crossing-overs. Next, although bivalents initially segregate into univalents during meiosis I, anaphase fails to proceed and univalents rearrange for meiosis II. Meiosis II proceeds normally, resulting in diploid oocytes with an assortment of non-sister-chromatids (automixis with central fusion), which recombined during prophase. Given this mechanism, *pseudogamous* females should be homozygous genome wide.
In parallel, we selected one pseudogamous (*M. belari*) and one sexual (*M. spiculigera*) species. We performed whole genome sequencing of the offspring of 10 females sampled at 10 different locations worldwide for each species. We found a low level of linkage disequilibrium in both species, confirming the existence of homologous recombination in *M. belari*. Unexpectedly, we also identified a high level of heterozygosity in both species (1% and 4% for *M. belari* and *M. spiculigera*).
To reconcile our results, we hypothesise that after homologous recombination segregation of sister chromatids is not random: only specific pairs of sister-chromatids, segregate in oocytes. This segregation bias would therefore allow the maintenance of heterozygosity in the long term. To investigate the existence of such a meiotic drive, we are combining genomic analysis with differential chromatid labelling for cytological validations.

Abstract ID: 2052

Constraints and preconditions of clonality and sterility in obtained F1 hybrid loaches (Cobitis)

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Hybridization has a decisive impact on the reproductive outputs and gametogenesis of the hybrid progenies between distant as well as closely related species. Several clonal lineages of hybrid origins arose independently among European spined loaches, but it is not known what triggered their emergence. To test whether certain genetic distance between hybridizing species is required to produce clonally reproducing vs sterile progeny, we crossed eight parental species of different genetic divergence expressed in sequence divergence and morphological differences of karyotypes. We than analysed the gametogeneses of obtained F1 hybrid progeny. The majority of analysed hybrid females were able to produce clonal diploid gametes due to premeiotic endoreplication. However, such a duplication was restricted to a rather small population of their gonial

cells. Only in one type of cross we observed normal pairing of chromosomes in meiosis and formation of haploid oocytes. By contrast, in all F1 hybrid males we identified only non-duplicated pachytene cells with aberrant pairing and no further progression to formation of spermatids. Similar chromosomal mispairing was observed in non-duplicated pachytene cells in hybrid females, but the amount of paired chromosomes was higer than in males. Therefore, chromosomal mispairing in non-duplicated cells lead to hybrid sterility. In particular cases, male sterility is rather caused by undeveloped gonad and lack of transition to meiosis. We conclude that among spined loaches clonality can be easily achieved. Seqeuence divergence of certain genes and chromosomal divergence could play a crucial role in the emergence of clonality as well as hybrid sterility.

Abstract ID: 1676

Meiotic driver homologs in asexual fusarium species

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According to Mendel's law of segregation, in a diploid organism the two copies of a gene are equally likely to be passed on to the next generation. Exceptions to this are, however, common. Recent work into one such exception, namely the spore killing genes (*Spoks*) of *Podospora anserina*, has begun to unravel *how* these genes are able to kill any offspring cell that does not carry them. By genetically transforming *Podospora* with either full or partial copies of the Spoks, the researchers have been able to deconstruct the protein product into a toxin and an anti-toxin domain. Not only do several variants of *Spoks* exist in *P. anserina*, but homologs of these genes in unrelated fungal species abound. Here, I will present my research into the functionality of diverged homologs of the *Spok* genes within the fungal genus *Fusarium,* using yeast genetics. I will show evidence of the conserved function of the toxin and anti-toxin domains, and the apparent separation of these domains in certain *Fusarium* species. The functional conservation of these genes across fungal orders suggests that they play an important role in fungal evolution, and I will propose one mechanism by which they may influence genome evolution in the *Fusarium* genus.

Abstract ID: 1651

Disentangling Verbal Arguments: Intralocus Sexual Conflict in Haplodiploids

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In haplodiploids, (1) alleles spend twice as many generations in females as in males, (2) males are never heterozygous and therefore express recessive alleles, and (3) males sire daughters but not sons. Intralocus sexual conflict therefore operates differently in

haplodiploids than in diploids and shares strong similarities with loci on X (or Z) chromosomes. The common co-occurrence of all three features makes it difficult to pinpoint their respective roles. However, they do not always co-occur in nature, and missing cases can be additionally studied with hypothetical life cycles. We model sexually antagonistic alleles in eight different sex determination systems and find that arguments 1 and 2 promote invasion and fixation of female-beneficial and male-beneficial alleles, respectively; argument 2 also improves prospects for polymorphism. Argument 3 harms the invasion prospects of sexually antagonistic alleles (irrespective of which sex benefits) but promotes fixation should invasion nevertheless occur. Disentangling the features helps to evaluate the validity of previous verbal arguments and yields better-informed predictions about intralocus sexual conflict under different sex determination systems, including hitherto undiscovered ones.

Abstract ID: 2327

Hybrid B chromosome evolution via horizontal gene transfer from bacterial symbiont to insect host

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A supernumerary B chromosome was found in the karyotype of a laboratory strain of the Mediterranean flour moth, *Ephestia kuehniella* (Lepidoptera). In searching for its origin, we used fluorescence *in situ* hybridization with various probes derived from the *E. kuehniella* genome. However, the results were negative, indicating that the B chromosome contains sequences exogenous to the moth genome. Bioinformatic comparison between B-positive and B-negative specimens revealed that the B chromosome comprises sequences derived from an endosymbiotic bacterium *Wolbachia* sp. About 30 *Wolbachia* genes were annotated on the B chromosome, arranged in two clusters repeated in a tandem manner. Despite the prevalence of *Wolbachia* sequences, the element was positive for epigenetic markers of lepidopteran heterochromatin and seemed to be transcriptionally active. We hypothesize that this hybrid chromosome arose by horizontal gene transfer from the *Wolbachia* genome to an existing supernumerary *Ephestia* chromosome followed by expansion of *Wolbachia*-derived DNA. These results are particularly interesting given the recent debate about the non-canonical origin of sex chromosomes in Lepidoptera. Indeed, it was proposed that the lepidopteran W chromosome evolved by domestication of a B chromosome and/or horizontal gene transfer from a parasite or symbiont, acting as a sex-determining trait. In such case, *Wolbachia* sp. would be the perfect candidate, as it is known to manipulate the sex of its host.

Abstract ID: 1335

A killer in hiding: selfish drive by social supergene in silver ants

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Supergenes – large non-recombining genomic regions – control compound adaptive phenotypes, such as alternative colony social organization in ants. Supergenes typically link co-adapted loci but are also prone to accumulate recessive deleterious mutations and selfish genetic elements that distort Mendelian segregation, so that understanding their long-term evolutionary maintenance is challenging. I will present recent advances on the genomic structure, phenotypic effects and evolutionary dynamics of a supergene determining colony queen number in the Alpine silver ant, *Formica selysi*. The derived supergene haplotype (*P*), which is exclusively found in multi-queen colonies, contains three large inversions and 748 genes. The *P* haplotype affects multiple traits at both the individual and colony levels. Strikingly, *P* acts as a maternal-effect killer: all eggs from *MP* queens fail to hatch when they did not inherit *P*. Hence, the haplotype specific to multi-queen colonies contains a selfish genetic element that enhances its own transmission by causing developmental arrest of progeny that do not carry the element. A recent population genetic model revealed that this drive by a selfish supergene destabilizes the polymorphism when mating is random, but that a stable polymorphic equilibrium can be reached when there are high rates of assortative mating by social form. We are currently searching for toxin-antidote elements located on the *P* haplotype, and further investigating the phenotypic effects of the supergene. Overall, this killer hidden in a social supergene shows that in some cases the underlying genetic system plays a direct role in the evolutionary dynamics of complex adaptive phenotypes.

Abstract ID: 991

Paternal genome elimination promotes altruism in viscous populations

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Population viscosity has long been thought to promote the evolution of altruism. However, in the simplest scenarios, the potential for altruism is invariant with respect to dispersal – a surprising result that holds for haploidy, diploidy, and haplodiploidy (arrhenotoky). Here we develop a kin-selection model to investigate how population viscosity affects the potential for altruism in species with male paternal genome elimination (PGE), exploring altruism enacted by both females and males, and both juveniles and adults. We find that: 1) PGE promotes altruistic behaviours relative to the other inheritance systems, and to a degree that depends on the extent of paternal genome expression. 2) Under PGE, dispersal increases the potential for altruism in juveniles and decreases it in adults. 3) The genetics of PGE can lead to striking differences in sex-specific potentials for altruism, even in the absence of any sex-differences in ecology.

Abstract ID: 987

Occasional paternal inheritance of the germline-restricted chromosome in songbirds

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Songbirds have one special accessory chromosome, the so-called germline-restricted chromosome (GRC), which is only present in germline cells and absent from somatic tissues. Earlier work on the zebra finch (*Taeniopygia guttata castanotis*) showed that the GRC is inherited only through the matriline - like the mitochondria - and is eliminated from the sperm during spermatogenesis. Here, we show that the GRC can also be paternally inherited. Confocal microscopy using GRC-specific FISH probes indicated that a considerable fraction of sperm heads (1-19%) in zebra finch ejaculates still contained the GRC. In line with these cytogenetic data, sequencing of ejaculates revealed that males from two families differed strongly and consistently in the number of GRCs in their ejaculates. Examining a captive-bred male hybrid of the two zebra finch subspecies (*T. g. guttata* & *T. g. castanotis*) revealed that the mitochondria originated from a *castanotis* mother, whereas the GRC likely came from a *guttata* father. Moreover, analyzing GRC haplotypes across nine *castanotis* matrilines (estimated to have diverged for up to 250,000y) showed surprisingly little variability among GRCs. This suggests that a single GRC haplotype has spread relatively recently across all examined matrilines. A few diagnostic GRC mutations that arose since this inferred spreading suggest that the GRC has continued to jump across matriline boundaries. Our findings raise the possibility that certain GRC haplotypes could selfishly spread through the population via occasional paternal transmission, thereby outcompeting other GRC haplotypes that were limited to strict maternal inheritance, even if this was partly detrimental to organismal fitness.

Abstract ID: 2019

Gametophytic selection and selective embryo abortion in *Mimulus guttatus*

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Non-Mendelian inheritance is frequently observed in plants and may often be the result of selection during reproduction. In plants, selection can occur during pollen tube elongation (gametophytic selection, or GS), as pollen grains compete for the chance to fertilize a limited number of ovules, and during embryo development (selective embryo abortion, or SEA), as embryos compete for limited maternal resources. GS and SEA are expected to efficiently purge genetic load and accelerate adaptive evolution. However, the prevalence and strength of GS and SEA across the genome is not well understood. We analyzed non-Mendelian segregation ratios resulting from a single autogamous (within-flower) cross of the outcrossing perennial, *Mimulus guttatus*, using models of expected genotypic ratios following GS and SEA. These models take advantage of the ploidy difference between pollen (haploid) and seeds (diploid) to distinguish between possible targets of GS versus SEA. Observed genotypic ratios were compared with the expected ratios using chi-squared tests and the strength of selection at loci fitting the models was quantified. Out of 4,424 mRNA loci exhibiting segregation distortion, 19% fit the SEA model, 3% fit the GS model, and 9% fit both models of transmission ($p < 0.05$). Approximately 45% of loci fitting the GS model exhibited selection coefficients equal to one; selection coefficients were >0.5 for over 60% of loci fitting the SEA model. These results suggest that selection during development is strong and has the potential to accelerate the purging of genetic load in plant populations.

Abstract ID: 1738

Expression and evolution of germline restricted chromosomes in fungus gnats

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Germline restricted chromosomes (GRCs) are a curious biological phenomenon. They are initially present in all cells in an individual but early in development are selectively eliminated from all somatic cells. These chromosomes are present in several animal clades including songbirds, hagfish and several fly lineages, but we know little about how they evolve. GRCs exhibit unusual transmission patterns. In flies in the fungus gnat clade Sciaridae, adults carry two GRCs in germ cells, which exhibit male biased transmission as both are transmitted through sperm but only one GRC is transmitted through eggs. Interestingly, this clade also exhibits a non-Mendelian inheritance system during male meiosis known as paternal genome elimination. Thus, male meiosis in this clade causes non-Mendelian inheritance of not only GRCs but all the chromosomes in the genome. We sequenced the GRCs and found that they are old, exhibiting substantial divergence to homologous regions of the X and autosomes. Additionally, we found that two distinct GRCs are segregating within populations which are substantially divergent from each other, suggesting that GRC transmission patterns may be parent-of-origin-specific. Finally, we are currently examining expression patterns of GRC genes to determine whether they exhibit sex-biased expression and how expression patterns relate to transmission patterns. From these analyses we are gaining a greater understanding of not only how GRCs in fungus gnats initially evolved, but what their current role is in fungus gnat germ cells.

Abstract ID: 1401

The complex story of an old germline-restricted chromosome

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The germline-restricted chromosome (GRC) of songbirds has been found in all the species studied so far including zebra finches and crows. Germline genome data of zebra finch previously showed that the GRC is mainly composed of paralogs from the regular “A chromosomes” and that these were acquired at different chronological moments. Although recent evidence from nightingale germline genomes suggests that the GRC emerged in the common ancestor of zebra finch and nightingales, how this chromosome evolved during early songbird diversification remains mysterious. With the aim of reconstructing GRC long-term evolution across songbirds, here we sequenced 10x Genomics Chromium draft genomes for germline and soma of the same individual from 25 species of Estrildidae and other Passeriformes families, including two

suboscines. After calling testis-specific variants to determine the GRC gene content, we inferred a highly dynamic acquisition and loss of genes by the GRC across the phylogeny, with some punctual dramatic changes. We found only few high-confidence genes that are ancient and widespread like *elavl4* and *cpeb1*, raising the possibility that these are important for the function of this enigmatic chromosome.

Symposium: S24. Progress and prospects in adaptation genomics (id: 935)

Abstract ID: 1285

Adaptation across environmental gradients in Heliconius butterflies

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Environmental gradients pose challenges to organisms, with selection favouring different traits in different locations. This could lead to local adaptation between interconnected demes, despite gene flow between them. Clines in colour-pattern variation in the *Heliconius* butterflies have been studied for many years, and shown to be due to spatially-varying predator-mediated selection, favouring divergent alleles at a few major-effect loci. In this talk, I will present work investigating divergence in quantitative traits in these species. Firstly, we investigate clines in iridescent structural colour. Unlike previously-studied colour-pattern clines, iridescence shows continuous variation, due to continuous variation in scale nanostructures, with very broad geographic clines. Using crosses between populations and gene expression analyses, we identify candidate genes for control of some of this variation. Secondly, we have been working on altitudinal clines, where the butterfly populations show little obvious phenotypic difference, yet we find evidence for morphological, physiological and genetic variation, associated with altitude.

Abstract ID: 1058

Detecting frequency-dependent selection using a genetic marker regression of fitness components

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Frequency-dependent selection (FDS) drives an evolutionary regime that maintains or disrupts polymorphisms. Despite the increasing feasibility of genetic association studies of fitness components, there are few methods to uncover the loci underlying FDS. Based on a simplified model of pairwise genetic interactions, we propose a linear regression that can infer FDS from observed fitness. The key idea behind our method is the inclusion of genotype similarity as a pseudo-trait in the selection gradient analysis. Our

simulations show that the direction of FDS (i.e., negative or positive FDS) can be determined by the regression coefficient of the genotype similarity. These simulated effects of FDS are unlikely to be confounded by over-dominant selection and spatiotemporally varying selection. Reanalysis of *Arabidopsis* and damselfly data could detect known negative FDS, where asymmetric FDS was not significant. A genome-wide association study of the branch number revealed that negative FDS, rather than positive FDS, was enriched among the top-scoring variants in *Arabidopsis thaliana*. On the fifth chromosome of *A. thaliana*, we also found a weak quantitative trait locus attributable to asymmetric positive FDS. These results suggest the wide applicability of our method for both single-locus analysis and association mapping with respect to FDS.

Abstract ID: 1408

Investigating local adaptation at multiple spatial scales: a case study of *Arabis alpina* in the Alps

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Landscape genomic analyses are powerful tools for studying species' local adaptation to their environments, where genetic variation in populations is associated with environmental variables describing local site conditions to detect candidate genes under selection. The development of landscape genomics over the past decade has been spurred by improvements in resolutions of genomic and environmental datasets, increasing the power to search for putative genes under selection and to study local adaptation in non-model organisms. Though Genome–Environment Association (GEA) studies have been successfully applied to numerous species across a diverse array of taxa, a current limitation of these methods lies in that most studies do not fully account for the appropriate spatial scale of environmental predictor variables. Indeed, the scale of predictor variables is known to affect model outcomes and subsequent interpretations of the study organism's adaptation to their natural environments. To address this issue, we investigate the spatial scale of natural selection by implementing multiscale frameworks into evolutionary ecology models. Using a case study from the herbaceous plant *Arabis alpina* collected across four valleys in the western Swiss Alps, we demonstrate how to perform multiscale landscape genomic analyses using multivariate redundancy analyses. In doing so, we investigate the impact of different spatial resolutions of predictor variables on our ability to detect candidate SNPs involved with local adaptation. Our results highlight the importance of using a multiscale framework in landscape genomic studies to obtain a more complete understanding of how the environment is inducing local adaptation in alpine ecosystems.

Abstract ID: 1085

Why do structural variants matter in evolutionary genomics? General framework & two empirical cases

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A significant fraction of genetic diversity lies in structural genomic variation (SV), e.g. chromosomal rearrangements or copy-number variants. Recent technologies provide unprecedent access into SVs, showing their prevalence and their implication in adaptation or diversification. This is opening new prospects in the study of genetic variation and transforming our understanding of the genetic basis of evolutionary changes.
Here, we will reflect on the role of SVs in evolution with examples from the literature and suggest a roadmap to consider more systematically the role and function of SVs in adaptation genomics. We will support these ideas with two empirical studies addressing the role of inversions in adaptation in seaweed flies and the contribution of SVs to Lake Whitefish speciation. Alongside, we present approaches to study SVs at the population-scale. First, we show how we identified and characterized polymorphic chromosomal inversions using low-coverage sequencing of 1,500 *Coelopa frigida* flies in 16 natural populations along a latitudinal gradient and genome assemblies including Hi-C data. Second, I will detail how the combination of long and short reads sequencing helped us account for SVs when studying the genomic architecture of differentiation between the Dwarf and Normal species of *Coregonus clupeaformis.*
The combined evidence presented in this talk underscores that a broadening of our views is needed to better integrate genetic variation beyond SNPs into studies pertaining to adaptive divergence and speciation, and thus paving the way for a more systematic exploration of causal genomic structural variation in evolution.

Abstract ID: 2324

Detection and application of adaptive loci for conservation and management of Atlantic salmon

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How organisms are adapted to their local environment at the genomic level is a key question in evolutionary biology. It is also essential to consider for the management of threatened populations, including many harvested Atlantic salmon (*Salmo salar*) stocks. The species exhibits fine-scale adaptive differentiation and is ideal for studying genetic architectures behind local adaptation. An archive of salmon scales spanning a century provided us with a window to the past, allowing us to compare historical and contemporary adaptive genetic diversity and interpret how human-induced selective

pressures influence the genetic variation of wild populations. Using genome-wide SNP data, we identified candidate loci under local selection in a large wild salmon population. Some of these loci are known to underlie aspects of important life-history variation in salmonids, suggesting they may repeatedly underpin adaptive diversification. Changes in the allele frequencies of the loci may indicate signals of evolutionary responses in these genomic regions. To understand the impact of spatially and temporally varying fishing pressure on these loci over time, we monitored their allele frequency trajectories by studying the genetic composition of salmon harvested in a commercial and recreational fishery between 1928 and 2020. We observed strong temporal changes in the allele frequencies of large-effect loci linked with ecologically important traits, which has potential management implications. We provide an example of using genomic approaches to improve our understanding of adaptive differentiation in wild populations, and using this information to infer, monitor and mitigate human impacts on adaptively important genetic variation in the wild.

Abstract ID: 1339

Metabolomics and other omics point to mechanisms of experimental adaptation to malnutrition

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Most organisms are subjected to periods of nutrient shortage, resulting in natural selection for physiological adaptations that alleviate their consequences. We combined omics tools with experimental evolution to identify candidate pathways involved in adaptation to malnutrition in *Drosophila melanogaster*. We let replicate "Selected" populations have evolved for more than 250 generations on a poor larval diet, with their poor diet adaptation manifested in higher viability and growth rate on the poor diet compared to Control populations. We performed targeted metabolome analysis on larvae raised on poor diet and identified 68 metabolites whose differed between the two selection regimes. Among these metabolites, nine are amino acids, including the three branched chain amino acids, and all are down in Selected populations. Knowing that Selected populations better assimilate proteins from the diet, the reduced amount of these amino acids might suggest that Selected larvae catabolize amino acids more efficiently. In accordance, urate, the nitrogen end product, reaches higher concentrations, suggesting higher deamination rate in Selected larvae. Combining the metabolomics with RNAseq and SNP suggests potential genetic mechanisms while a stable isotope experiment confirms a greater excretion of nitrogen waste in malnutrition-adapted larvae, consistent with increased amino acid catabolism.

Abstract ID: 1121

The distribution of fitness effects of spontaneous mutations in *Chlamydomonas reinhardtii*

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The distribution of fitness effects (DFE) of new mutations describes the relative frequencies of mutations with different sizes of effects on fitness. The DFE is fundamental for many questions in population and quantitative genetics. To study the DFE, we allowed spontaneous mutations to accumulate in replicated mutation accumulation (MA) lines of the single-celled alga *Chlamydomonas reinhardtii* in conditions where natural selection was ineffective. We then determined the locations of the majority of the accumulated mutations using Illumina whole-genome sequencing. We measured changes of the frequencies of these mutations under experimental evolution in large populations derived from crosses between MA lines and their unmutated ancestor where the initial frequencies of the wild type and mutant alleles were 0.5. The frequencies of many mutations changed repeatably among replicated experimental evolution cultures, and, unexpectedly, as many mutations increased in frequency as decreased in frequency. By equating allele frequency changes to selection coefficients, we inferred that the DFE is highly leptokurtic, that is, many mutations have small fitness effects, but the distribution has long tails of beneficial and advantageous mutations, which explain most of the new variation for fitness. A two-sided gamma distribution provides a satisfactory fit to the data. The high frequency of advantageous mutations we observed may reflect the simple experimental evolution laboratory environment. We argue that many of the beneficial mutations we observed would be disadvantageous in a natural environment.

Abstract ID: 1059

Wavelet characterization of spatial pattern in allele frequency

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Characterizing spatial patterns in allele frequencies is fundamental to inference in evolutionary biology because such patterns can inform on underlying evolutionary processes. However, the spatial scales at which changing selection, gene flow, and drift act are often unknown. Many of these processes can operate inconsistently across space (causing non-stationary patterns). We present a wavelet approach to characterize spatial pattern in genotype that helps solve these problems. We show how our approach can characterize spatial patterns in ancestry at multiple spatial scales, i.e. a multi-locus wavelet genetic dissimilarity. We also develop wavelet tests of spatial differentiation in allele frequency and quantitative trait loci (QTL). With simulation we illustrate these methods under a variety of scenarios. We apply our approach to natural populations of *Arabidopsis thaliana* and traditional varieties of *Sorghum bicolor* to identify locally-adapted loci and characterize population structure across scales. We find, for example, that Arabidopsis flowering time QTL show significantly elevated scaled wavelet variance at ~ 300 – 1300 km scales. Wavelet transforms of population genetic data offer a flexible way forward to reveal geographic patterns and causal processes.

Abstract ID: 1189

Rapid adaptation and range expansion in response to agriculture over the last two centuries

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North America has seen a massive increase in cropland use since 1800, accompanied more recently by the intensification of agricultural practices. We studied the impact of these qualitative and quantitative changes in farming on the extent and tempo of evolution in a native plant now pervasive in agricultural habitats, common waterhemp (*Amaranthus tuberculatus),* through genome analysis of present-day and historical individuals from the last two centuries. Despite near panmixia among natural and agricultural environments, numerous loci across the genome showed strong evidence of antagonistic selection. These loci, including alleles coding for resistance to herbicides, have increased in frequency on average by more than 20% over the last ~150 years with nearly all such change occurring since the intensification of agricultural practices in the 1960s (s = 0.027-0.010). Over the same period, we show a clear expansion of southwestern ancestry into the northeastern part of the range, change which predicts contemporary signals of agricultural selection. The intensification of agriculture has thus had extensive impacts on genetic variation for fitness and genome-wide diversity through the interplay of selective and demographic processes, facilitating its success as a 21st-century agricultural weed.

Abstract ID: 1167

The availability of standing genetic variation for rapid adaptation in sticklebacks

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Compared to de novo mutations, standing genetic variation provides a ready-available substrate for rapid adaptation to new or changing environments. The selection-migration balance that maintains differences between divergently adapted populations is likely to play a key role shaping its availability and influencing rates of future adaptive change. Threespine stickleback fish have repeatedly adapted to divergent marine and freshwater environments in the face of ongoing gene-flow and offer an ideal system to study this phenomenon. Parallel adaptation to freshwater environments occurs via reuse of freshwater-adaptive standing genetic variation that is present in the marine population at low frequencies. However, little is known about how this multi-locus adaptive variation is maintained and constrained by a selection-migration balance and the genetic load it places on the marine population. To explore this, we combine empirical studies of standing genetic variation at adaptive loci in 9,000 marine sticklebacks with population genetic simulations. Freshwater-adaptive variants are present as multigeneration introgressed alleles at low frequencies that differ significantly between the two marine populations studied. Individual marine fish “carry” multiple freshwater-adaptive alleles across the genome, potentially facilitating future rapid freshwater adaptation. Using simulations, we explore the cost this freshwater-adaptive genetic variation presents to the marine population. By comparing our data to genomic datasets of globally-diverse

sticklebacks we infer the geographic origins of freshwater-adaptive haplotypes and associations with patterns of hard or soft sweeps in freshwater populations. Combined, we present insight into the origins, availability, and maintenance of standing genetic variation and the evolutionary potential of biodiversity.

Abstract ID: 1656

The Robinson Crusoe experiment: 30 years of adaptation to a lonely island

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Human-introduced populations offer great opportunities to study the genetic basis of evolution in the short term. We present the results of a 30-year local adaptation experiment. Our study organism, the snail *Littorina saxatilis*, shows divergent ecotypes, locally adapted to wave-exposed vs. crab-predation habitats across European shores. Genomic and phenotypic differentiation between ecotypes is well-studied; however, there is no direct evidence that selection caused these differences. In 1992, we collected ~700 Crab ecotype snails and relocated them to an uninhabited, crab-free islet exposed to strong waves. After nearly 30 years, the population remains established on the islet and has diverged morphologically from the parental population. Changes include a reduction in shell size, thickness, and ridges, and an increase in shell patterning, all characteristics of the Wave ecotype. We investigated the genetic basis of local adaptation using genetic markers. Samples included the parental Crab ecotype, the islet, and a nearby Wave ecotype population, were collected in 1992, 2005, 2018, and 2021. As in the phenotypic observations, population genetics analysis indicates divergence of the islet population from the Crab ecotype over time. The signals of divergence are stronger in genomic regions known to differentiate Crab and Wave ecotype in other locations, while other regions remain similar to the parental population, providing strong evidence for selection. Additionally, we show that gene flow from the nearby Wave population may have contributed to rapid adaptation. Our findings demonstrate that adaptive evolution is not necessarily a long-term process but can occur in a few decades.

Abstract ID: 1227

Mapping genomic barriers to gene flow

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The prospect of exploiting information contained in genomic variation to learn about past speciation events has excited speciation researchers for the last decade. This inference problem can be viewed as a particularly challenging, special case of adaptation genomics. In particular, the goal of genomic outlier scans is to detect regions that act as local barriers to gene flow against a noisy genomic background which includes neutral variation, a complex and generally unknown background demography, and selection acting on both globally beneficial and deleterious variation. I will describe genome-wide IM modelling via blockwise likelihoods (gIMble), a statistical framework for disentangling the population genomic signal of local barriers to gene flow from other forms of selection along the genome. I will highlight the advantages and challenges associated with model based scans for past selection using coalescent simulations and example analyses from young sister species pairs of butterfly.

Abstract ID: 1441

Range expansion and its effect on linked neutral genetic diversity

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Range expansions are common in the history of most species. They often consist of serial bottlenecks with subsequent population growth, leading to a progressive loss of genetic diversity along the expansion axis. A consequence of range expansions is the phenomenon of “gene surfing”, where variants located near the expanding front can reach high frequencies or even fix in newly colonized territories. Although gene surfing events have been well characterized for a specific locus, their effects on linked genomic regions and on the overall patterns of genomic diversity have not been explored. In this study, we have simulated the evolution of whole genomes during several types of 1D and 2D range expansions differing by the extent of migration, founder events and recombination. We especially focused on the characterization of local dips of diversity, or “troughs”, taken as a proxy for surfing events. We find that, for a given recombination rate, it is possible to predict the initial evolution of trough density and their average width irrespectively of the expansion condition, once we consider the amount of diversity lost since the beginning of the expansion. Furthermore, when recombination rates vary across the genome, we find that troughs are over-represented in regions of low recombination. Therefore, range expansions can leave genomic signatures often interpreted as evidence of past selective events. Given the generality of our results, they could be used as a null model for species having gone through recent expansions, and thus be helpful to correctly interpret many evolutionary biology studies.

Abstract ID: 1545

Hybridization dynamics and extensive introgression in the *Daphnia longispina* species complex

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Closely related species that have recently come into contact due to ecological or anthropogenic changes can lead to contemporary hybrid zones. Hybrid genomes exhibit varying levels of ancestry from different species that are shaped by recombination and selection. Within the *Daphnia longispina* species complex, a keystone zooplankton taxon in freshwater ecosystems, three species occupy ecologically different niches and have been shown to hybridize. These species are producing resting eggs that accumulate in the sediment over time, thus providing a record of recurrent hybridization events. Here, we analyzed 92 whole genomes from single resting eggs of different ages and live individuals from the water column. We investigated genome-wide variation and introgression in two populations with different ecological conditions. We uncovered recurrent generations of hybridization and introgression and estimated when each hybridization event took place with the junctions approach. Finally, we characterized introgression patterns across the genome to identify regions and genes in hybrid genomes that may be under selection in local populations. These regions could explain the high prevalence of hybrids in these populations and point to underlying differences in ecological conditions. Overall, our study paves the way for a better understanding of ancient and contemporary gene flow and the genomic basis of adaptation in the species complex.

Abstract ID: 1547

Using pool-seq and approximate Bayesian computation to differentiate scenarios of ecotype formation

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A major question in evolutionary biology is how divergent selection can lead to local adaptation in the presence of gene flow. Ecotype formation caused by adaptation to different ecological niches occurs across many taxa, allowing for the study of the interplay between selection and gene flow early in the divergence process. It is often unclear whether ecotype formation occurred multiple times in independent locations with gene flow (parallel origin), or if it happened only once followed by secondary contact (single origin). Demographic modeling and population genomic data can distinguish these scenarios. Pool-sequencing offers a cost-effective strategy to sequence multiple populations, but introduces errors in allele frequencies that can bias downstream analyses. We developed an Approximate Bayesian Computation (ABC) method that explicitly accounts for Pool-sequencing errors (e.g., unequal individual representation).

This method enables the reconstruction of the demographic history through parameter estimation and model comparison. We performed a simulation study and applied our method to Swedish populations of two ecotypes of the marine gastropod *Littorina saxatilis*. Our ABC method is able to distinguish between scenarios of ecotype formation and estimate relevant parameters with typical Pool-sequencing datasets. We report that single origin is the most likely scenario for these populations and that there is evidence for gene flow between divergent ecotypes inhabiting the same location. By uncovering the most likely scenario of ecotype formation, we provide suitable null models for species where ecotypes exist at multiple locations, improving our understanding of the adaptive process.

Abstract ID: 1098

Empirical evidence for positive selection that is not adaptive evolution

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Evidence for positive selection occurring in protein-coding DNA sequence is widespread across different taxa. Positive selection can be a result of adaptive evolution, meaning that individuals have had to adapt to a change in environment or selective pressure. However, current positive selection can also be the result of mutations compensating for deleterious substitutions that have accumulated along lineages, in which case positive selection is non-adaptive and predictable. To evaluate the extent of non-adaptive positive selection, we have combined population-genetics and phylogenetics datasets. We first leveraged phylogenetic codon models which are based on a population-genetics formalism, assuming a non-adaptive fitness landscape. These models estimate the fitness of each of the 20 amino acids for each protein site, given mammalian protein-coding DNA alignments and gene tree topologies. Second, we integrated mammalian divergence data with polymorphic variants found in 29 populations across 7 mammalian genera. For each non-synonymous variant observed at the population level, we predicted its change in fitness from amino-acid fitnesses estimated at the mammalian scale. We found that a large proportion of observed non-synonymous changes are predicted to be positively selected, meaning that the ancestral allele is sub-optimal. These supposedly advantageous variants are indeed showing signs of recent positive selection in all populations. Our work confirms that deleterious substitutions have accumulated across the phylogeny and are currently being compensated for, resulting in widespread positive selection that is not adaptive evolution. This study also shows the leverage obtained by integrating phylogenetic and population genetics on a common formalism.

Abstract ID: 1675

Stabilizing selection promotes the emergence of non-additive variance in gene expression

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The distinction between the additive and non-additive components of genetic trait variance has long been known to be crucial for predicting the potential of contemporary populations to respond to future selection. Yet, we do not know how past evolution influences this potential. Here, we use a quantitative genetic breeding design to delineate the additive and non-additive components of expression variance of 17,656 gene transcripts segregating in the outcrossing plant *Arabidopsis lyrata*. We find that most of the genetic variance in gene expression is from non-additive variance, especially among long genes or genes involved in epigenetic gene regulation. Interestingly, genes with the most non-additive variation not only display a markedly lower rate of synonymous variation, they are also exposed to stronger stabilizing selective forces than genes with high additive variance. This study demonstrates that a genes' potential for future evolution depends on its past history of stabilizing selection.

Abstract ID: 1707

Evolutionary genomics and dynamics of adaptation to complex environments in *Saccharomyces cerevisiae*

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While experimental evolution has been vital for understanding the phenotypic and genomic dynamics of adapting populations, experiments are often done in the context of just one environmental stressor at a time. Natural populations, however, typically experience complex environments in which multiple stressors are acting simultaneously. Interactions between stressors are well-known phenomena, but how such interactions affect the genetic basis of adaptation is poorly understood. In particular, adaptation to one stressor may affect interactions with other stressors, fundamentally changing the adaptive landscape and course of evolution. Here we describe the dynamics of rapid adaptation to increasingly complex environments in populations of the yeast *Saccharomyces cerevisia*e. Initially isogenic populations of yeast were exposed to full factorial combinations of four stressors (salt, low glucose, antifungal, and high heat) for approximately 100 generations. We observed rapid fitness increases in complex environments, mediated by the evolution of trade-offs and interactions between the individual stressors of the complex environments. By combining time-series phenotypic and pool-seq genomic data, we determined: 1) if the fitness effects of simple environments are predictive of combined stressor effects on fitness; 2) if the genetic architecture of adaptation to simple environments is predictive of the genetic architecture of adaptation to complex environments; 3) if adaptation to multiple stressors occurs concurrently or sequentially; and 4) if the order of adaptation or the evolution of trade-offs depends on the genetic architecture of adaptation to the underlying stressors.

Abstract ID: 1769

A lizards' tail: the genomics of island adaption

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Island populations hold a key to understanding rapid speciation and adaption to novel environments. In 1971 scientists did a reciprocal translocation of lizards between two small islands in the Adriatic Sea - Pod Kopište and Pod Mrčaru, harboring *Podarcis siculus* and *Podarcis melisiellensis*, respectively. Ten individuals of each species were translocated between the islands. Thirty-five years later researchers observed only *P. siculus* on both islands. Moreover, they found substantial morphological changes related to dietary shift towards herbivory. This setup provides us with a unique opportunity to explore the genomic basis for rapid genetic adaptation. We collected 45 samples of *P. siculus* from each island and sequenced the genomes to an average of 5X. Based on variation in ~15 million informative SNPs, we estimated an Fst of 0.034 between the two populations. Hints of introgression were seen in the Pod Mrčaru population from the original *P. melisellensis* population. Using ANGSD for window based Fst scan we observed 22 Fst outlier peaks. Among these candidate regions we found evidence for signatures of selection in the neuronal genes SRGAP2 and SIM1. The latter is related to appetite and obesity in mice suggesting a genetic basis for dietary adaptation in the Pod Mrčaru population of *P. siculus*. Our research has thus uncovered the genomic signatures in these lizards that are responsible for a very rapid adaptation to a novel island environment, including a shift in diet. This offers fundamental new knowledge linking genomic and morphological adaptations in islands vertebrates.

Abstract ID: 1991

Natural variation in *Drosophila* shows weak pleiotropic effects

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Pleiotropy describes the phenomenon in which a gene affects multiple phenotypes. The extent of pleiotropy is still disputed, mainly because of issues of inadequate power of analyses. A further challenge is that empirical tests of pleiotropy are restricted to a small subset of all possible phenotypes. To overcome these limitations, we propose a new measurement of pleiotropy that integrates across many phenotypes and multiple generations to improve power. We infer pleiotropy from the fitness cost imposed by frequency changes of pleiotropic loci. Mixing *Drosophila simulans* populations, which adapted independently to the same new environment using different sets of genes, we show that the adaptive frequency changes have been accompanied by measurable fitness costs. Unlike previous studies characterizing the molecular basis of pleiotropy, we show that many loci, each of weak effect, contribute to genome-wide pleiotropy. We propose that the costs of pleiotropy are reduced by the modular architecture of gene expression, which facilitates adaptive gene expression changes with low impact on other functions.

Abstract ID: 2109

Divergent selection, linked deleterious mutations and gene flow: diploid vs hemizygous chromosomes

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Empirical data from diverse taxa indicate that the hemizygous portions of the genome (X/Z chromosomes) evolve more rapidly than their diploid counterparts. Faster-X theory predicts increased rates of adaptive substitutions between isolated species, yet little is known about species experiencing gene flow. Here we investigate how hemizygosity impacts genome-wide patterns of differentiation during adaptive divergence with gene flow, accounting for the impact of deleterious mutations. To quantify this effect we model migration, divergent selection and deleterious mutations using SLiM simulations. For models with divergent selection, we found higher peaks of differentiation in hemizygous than diploid chromosomes, consistent with more efficient selection against maladaptive immigrant alleles due to hemizygosity. Our results predict that background selection (BGS) increases differentiation, but this effect vanishes with increasing migration rates. For recessive and slightly deleterious mutations, we predict diploid chromosomes to be affected by associative overdominance (AOD) at low recombining regions, creating valleys of differentiation. Interestingly, such valleys of differentiation due to AOD are also seen for hemizygous chromosomes, but at a much narrower range of the parameter space. We compare these predictions with genome-wide data from hybridizing haplodiploids (Neodiprion sawflies). Our results indicate that AOD and BGS create heterogeneous genomic patterns, potentially biasing genomic scans to detect divergent selection. In sum, our resulting indicate that selection is more efficient in hemizygous chromosomes, affecting linked variation. Thus, divergent selection with gene flow can lead to higher differentiation at selected and linked variation in hemizygous loci, both in X/Z-chromosomes and haplodiploid species.

Abstract ID: 1155

Identifying the nature of adaptation to micronutrients in modern humans

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Environmental pressures are strong drivers of adaptation and, when variable across a species range, they can lead to local adaptation. Such adaptation has occurred numerous times in human evolution, owing to the highly varied environments humans inhabit across the globe. The level of micronutrients (*e.g.,* Iron, Zinc and Selenium) in the soil, and therefore diet, vary widely around the globe and is a prime example of such environmental variation. Micronutrients play an essential role in human health, with deficiencies compromising key stages of development and increasing the risk of

metabolic, cardiovascular and infectious diseases – making the dietary levels of micronutrients a strong local selective force in humans. Indeed, adaptation to some micronutrients has been identified in humans.
However, there are many genes associated with micronutrient uptake and metabolism, suggesting that adaptation to micronutrients is likely polygenic in nature. Using simulations under realistic demographic histories and integrating tree-recording methods (Relate) and Fst, we demonstrate the power of a gene set approach to identify polygenic local adaptation. We applied these methods to sets of genes associated with 13 micronutrients, in 913 modern humans from 40 worldwide populations. We identify monogenic and polygenic signatures of positive selection in genes associated with the metabolism or uptake of micronutrients at both the local and global scales. These results demonstrate that micronutrient levels have driven adaptation across human history. I will discuss the evidence of polygenic adaptation at the local scale (*e.g.,* Selenium) and the global scale (*e.g*., Zinc) to highlight the diversity of this adaptation.

Symposium: S25. The positives and negatives of whole genome duplication: synthesizing polyploid evolution across organisms and disciplines (id: 969)

Abstract ID: 2465

New genomics perspectives on polyploidy

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In the past two decades, advances in ‘omics technology and analytical methods have dramatically increased the scale of inferences possible about the structure and function of polyploid genomes, both as applied to wild populations and for agricultural improvement.
They have also altered the view that polyploidy is important predominantly in plants, with animal polyploids as rarer exceptions. In 2010, Pamela and Douglas Soltis, Richard Buggs and Jeff Doyle published a thought-provoking paper entitled “What we still don’t know about polyploidy”, after the first decade where genomic-scale analyses became widely accessible. Twelve years later, with continuing advances in genomic technologies, it seems like a good time to revisit how many of these issues have been resolved and where we still need to focus efforts to improve understanding. While there have been exciting advances in uncovering commonalities and variation in terms of genomic consequences of polyploidy across a wide range of systems, there are still areas, such as experimental evidence for adaptive flexibility to respond to environmental change, where genomics alone will not be able to provide conclusive answers. The purpose of this talk will be to review how ‘omics advances have changed views (or not) about polyploidy and suggest areas for future research to fill ongoing gaps in knowledge.

Abstract ID: 2383

Reconciling differences in polyploidy and diversity across the vascular plants

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Polyploidy, or whole-genome duplication, is widely recognized as an important force in the evolution of plants. Ancient genome duplications have driven the re-organization of plant genomes and nearly ⅓ of contemporary flowering plants are of recent polyploid origin. Despite the recognition that polyploidy has been important across plant evolution, there are still many unresolved issues surrounding polyploidy and its role in evolution. Among these issues is reconciling the apparent success of ancient polyploid species with observations that contemporary polyploids have much lower net diversification rates than their diploid relatives. Here, we use phylogenetic simulations to explore the legacy of ancient WGDs with different diversification dynamics of polyploid and diploid species. We will present results from the Brassicaceae on how polyploidy—both recent and ancient—has shaped the diversity in the family. Overall, we will highlight how polyploidy is a potent force capable of impacting plant evolution even millions of years after the initial duplication when lineages have diploidized.

Abstract ID: 2464

Whole genome duplications and the evolution of disease in vertebrates

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Vertebrates emerged from two rounds of whole genome duplication (2R-WGD) about 500 MY ago with teleost fish arising from a subsequent third round of genome duplication (3R-WGD) about 300 MY ago. However, the identification of retained 2R- and 3R-WGD gene duplicates, so-called ohnologs, has remained challenging due to lineage specific genome rearrangements. Our group has identified vertebrate ohnologs using synteny comparison across multiple genomes to enhance statistical power, while taking into account the phylogenetically biased sampling of available species (http://ohnologs.curie.fr). The retention of specific ohnologs is thought to be instrumental in the evolution of vertebrate complexity, development and susceptibility to genetic diseases. In particular, our group has shown that the enhanced retention of "dangerous" ohnologs, prone to dominant deleterious mutations, is a consequence of WGD-induced speciation and the ensuing purifying selection in post-WGD species. This population genetic result has been independently confirmed through data-driven causal inference methods. Similarly, I will discuss how inference methods can analyze the impact of somatic genome duplication in cancer development and resistance to treatment. This occurs as tetraploid cells can exploit their genome redundancy to rapidly evolve resistance strategies under drug treatments. Interestingly, this echoes the long term radiation success of tetraploid species under possible environmental changes.

Abstract ID: 1601

Evolution of diploid and allopolyploid *Camelina* genomes was accompanied by chromosome shattering

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False flax or gold of pleasure (*Camelina sativa*) is an increasingly popular oilseed crop closely related to arabidopsis and canola. Despite the available genome sequence and other genomic resources, the origin and putative parental species of the allohexaploid *C. sativa* (2*n* = 6x = 40) were shrouded in mystery. Until recently, nearly nothing was known about the origin, genome evolution and phylogenetic relationships of the remaining neglected or almost unknown diploid and polyploid *Camelina* species (2*n* = 12, 14, 26, 38 and 40). By employing state-of-the-art tools we established fine-scale comparative cytogenomic maps for all diploid, tetraploid and hexaploid *Camelina* species and elucidated their phylogenetic relationships. We were able to identify the parental genomes of the three known allopolyploid species (*C. microcarpa*, *C. rumelica* and *C. sativa*) and reconstruct the sequence of hybridization events. Besides common chromosomal rearrangements, such as translocations and inversions, chromothripsis-like events generated shattered chromosomes in *Camelina* diploids and polyploids. These complex chromosomal alterations, similar to those associated with several human disorders, have not been reported in a non-model plant species as yet. This study was supported by a research grant from the Czech Science Foundation (grant no. 21-03909S).

Abstract ID: 1178

Rapid parallel adaptation in autopolyploid *Arabidopsis* is dominated by recruitment of shared alleles

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Theory predicts that increased variation provided by doubled chromosome complements (polyploidy) may promote adaptation to novel challenges. Such an example is rapid colonisation of challenging habitats when selection is strong and originally neutral or mildly deleterious alleles standing in polyploid populations may become beneficial. Empirical investigations of adaptation in polyploid plant species are, however, scarce. Importantly, the relative contributions of pre-existing vs *de novo* genomic variation to adaptation are poorly understood, especially in polyploid organisms, which maintain increased variation but also large mutational target size. We assess this in high resolution using autotetraploid *Arabidopsis arenosa*, repeatedly adapted to toxic serpentine soils that exhibit skewed elemental profiles. The island-like distribution of

serpentines provides a uniquely powerful system for studying parallel evolution. Leveraging fivefold replicated serpentine invasions, we assessed selection on SNPs and structural variants (TEs) in 78 resequenced individuals and discovered substantial parallelism in candidate genes involved in ion homeostasis and stress signalling. We further modelled parallel selection and inferred repeated sweeps on a shared pool of variants in nearly all these loci, supporting theoretical expectations. A single, striking exception is represented by TWO PORE CHANNEL 1, which exhibits convergent evolution from independent *de novo* mutations at an identical, otherwise conserved site at the calcium channel selectivity gate. Taken together, this suggests that polyploid populations can rapidly adapt to environmental extremes, calling on both pre-existing variation and novel polymorphisms.

Abstract ID: 1685

Polyploid *Arabidopsis* inherit parental traits *in natura* as shown by deep-learning and soil analyses

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The advantages and disadvantages of polyploidy have long been discussed. In 1971, Ledyard Stebbins hypothesized that polyploids are generalists that can tolerate a wide range of environmental conditions. To test this hypothesis, it is important to quantify traits in naturally fluctuating environments (*in natura*). We studied two environmental responses of the allotetraploid *Arabidopsis kamchatica*—accumulation of anthocyanin and heavy metals. Anthocyanin levels are affected by various stresses. We developed a cost-efficient automatic imaging system to analyze images using deep learning. We validated the estimated amounts of anthocyanin using empirical measurements. We estimated the daily amount of anthocyanin for five months in three seasons. Interestingly, the synthetic polyploid derived from *A. halleri* and *A. lyrata* recapitulated the pattern of natural accessions of *A. kamchatica*. This suggests that *A. kamchatica* inherits the environmental regulation of anthocyanin from the two parental species. Next, we studied soil as a microhabitat because *A. halleri* is characterized by zinc hyperaccumulation, which is a quantitatively measurable adaptive trait that confers tolerance. Natural populations of *A. kamchatica* were found at moderately contaminated microhabitats, e.g., gratings at roadsides and galvanized iron. *A. halleri* exhibited a high level of expression

of heavy-metal-related genes, such as *HMA4*. In *A. kamchatica*, the expression level of *HMA4* was about half that of *A. halleri* consistent with allotetraploidy as permanent heterozygosity. This attenuated response can be a disadvantage in extreme environments. A genome-wide resequencing analysis indicated a different signature of selection between homeologous pairs including *HMA4*, supporting the advantage of merging parental adaptations.

Abstract ID: 1034

Exploring the effects of whole genome duplication on structural variation using pangenomics

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Whole genome duplication (WGD) is the most dramatic mutation a genome can undergo, causing enormous disruption to cellular processes. Paradoxically, many polyploids are successful, frequently invading new niches. In order to survive and thrive, young autopolyploids have undergone rapid evolution of DNA management genes, involved in meiosis and mitosis. Instability in these processes could accelerate generation of structural variants (SVs), increasing the pool of large-scale mutations upon which selection acts. Further, theory predicts increased genetic load at higher ploidies, which may manifest as large effect SV. We investigate this in natural populations of the outcrosser *Arabidopsis arenosa*, which has undergone WGD 20-31k generations ago. Here, we use PacBio and Oxford Nanopore long-read sequencing of five diploid and five autotetraploid *A. arenosa* individuals representing all major lineages across the species range to examine how WGD impacts the landscape of SVs within a species. We construct *de novo* assemblies of each individual, and take a pangenomic approach to detect SVs. We can use this robust catalogue to genotype SVs in an extensively sampled dataset of 660 short read sequenced *A. arenosa* individuals, enabling us to explore the impact of SVs in ecotypic differentiation across a large geographic range in a successful autopolyploid. Combining new approaches with traditional population genomics will allow us to consider both the impact of whole genome duplication on the genomic landscape of SVs, and in turn how they might contribute to the occasional spectacular adaptability of polyploid species.

Abstract ID: 2391

Genomic basis of convergent adaptations to whole genome duplications

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Whole genome duplication (WGD), leading to autopolyploidy is hypothesized to bring multiple adaptive advantages to the organisms. But it is also a traumatic event, transforming cellular landscapes in a single generation. While high evolutionary constraint has been assumed for the conserved processes affected by WGD (such as cell division and cell cycle regulation), reports of nimble evolutionary shifts in these processes have confounded this expectation. My work directly tests this by assessing the

genomic basis of adaptation to WGD in independent adaptation events. The instant meiotic and physiological consequences of WGD necessitate the concerted adjustment of a wide range of core functions, but nevertheless WGD has been repeatedly survived in all kingdoms. Given this repeated adaptation despite obvious challenges, I ask: how do lineages not only survive WGD, but sometimes ultimately thrive? Are the solutions employed constrained or diverse? To answer this, I investigated multiple cases of independent WGDs occurring in plant species separated by millions of years of divergence. I discovered that while WGD does require the adaptation of similar functional processes, the specific genes recruited are often flexible. High degree of gene reuse in adaptation to WGD occurred only in cases of related populations or species which are later "borrowing" their WGD-adaptive alleles via gene flow. In total, my results point to a minimally constrained, polygenic basis for the adaptation following WGD. Based on this, I conclude that there are multiple solutions to WGD-associated challenges, allowing diverse species to establish and succeed as autopolyploids.

Abstract ID: 1746

On the evolutionary implications of neopolyploidization mechanisms in *Nasonia vitripennis*

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Polyploidy has been advantageous in most eukaryotes' evolutionary history, yet neopolyploidization is so detrimental that it is often an evolutionary dead end. Animal polyploidy is difficult to study as there are few means to experimentally induce it, and polyploidized individuals are usually sterile. The hymenopteran *Nasonia vitripennis* is haplodiploid and an exceptional case. Polyploid individuals (diploid males, triploid females) are fertile and can be studied in the long-maintained Whiting Polyploid Line (WPL). Neopolyploids can be generated by RNAi knockdown (KD) of sex determination gene *transformer (tra)* in parental females that then produce diploid males.
I measured cell number and/or size reduction mechanisms by comparing wing cell number, cell size and area among the neopolyploids and the Whiting polyploidy line. Preliminary analysis of WPL shows that they exhibit cell number reduction in their wings as opposed to the *tra* KD line. qRT-PCR analysis of housekeeping genes ak3 and ef1*α* indicates no general gene dosage differences, but a conserved sex-linked dosage compensation pattern. To better understand the differences in gene expression and dosage compensation following polyploidization, we sequenced the full transcriptomes of head and abdomen tissues of *tra* KD and WPL polyploids. Differential expression of candidate genes responsible for mechanistic adjustments (cell size and cell number), and life history traits (memory retention, diapause, pheromone production) were coupled to bioassays to study the implications of neopolyploidization in *Nasonia*.

Abstract ID: 2408

Population genomics of Australian burrowing frogs *Neobatrachus* reveal adaptation to polyploidy

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Polyploidy or whole-genome duplications (WGDs) are characteristic for plants, but they are recognized as important hallmarks in evolutionary history across the whole tree of life, including vertebrates. Polyploids are often associated with extreme environments, which suggests that WGDs can be either adaptive to environmental stress and/or triggered by such. Indeed stress may increase unreduced gamete formation leading to polyploidy, however, the establishment of a polyploid species is restricted by a number of factors such as minority cytotype exclusion, severe population bottleneck, and cell cycle machinery failure. Namely, polyploidy may be adaptive, but you need to adapt to being a polyploid. In order to understand such complex adaptation patterns to external and internal challenges, we study the diploid-tetraploid species complex of Australian burrowing frogs *Neobatrachus*, amphibians living in a desert. Most polyploid vertebrates reproduce asexually, however these Australian burrowing frogs form an interesting exception, with multiple independently originated autotetraploid sexual species. Chromosome-level genome assembly of *N. pictus*, resequencing of 88 individuals across the genus and genome-wide selection scans reveal the first insight into the adaptation to autopolyploidy shown in vertebrates, namely that the synaptonemal complex plays a major role in this process.

Abstract ID: 1060

Identifying subgenomes in non-model organisms using orthology and fossil transposable elements

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In only 5 years, the standard for large genome assemblies has moved from low-quality and fragmented to chromosome-resolved. Despite this advance, high-quality assemblies of non-model polyploid organisms, which often have large genomes and are characterized by high repeat-content, are still rare. In this contribution, I present a practical method to separate subgenomes in an allopolyploid chromosome-resolved assembly for non-model organisms where information on ancestral species is often lacking. This involves: 1) the identification of homeolog chromosomes by identifying orthologs and mapping them to their chromosome location; 2) subgenome characterization by the identification and quantification of transposable elements that were active before the polyploidization event (i.e. when the subgenomes were separated) – termed 'fossil transposable elements'. I apply this method to our recent assembly of the *Scalesia atractyloides* (Asteraceae, Galápagos adaptive radiation) genome, with a size of 3.2 Gbp and with 76% repeat content. After separation of subgenomes, our analysis uncovered large inter-subgenome inversions and similar numbers of genes, isoforms and transposable elements on both subgenomes, indicating a lack of subgenome dominance. I estimated the speciation event to be around 4.2 million years ago, and the polyploidization event to have occurred 3.6 million years ago. The timing of polyploidization is concordant with the geological age of the Galápagos, and I speculate that a lack of subgenome dominance benefits plants' colonization of remote islands, where increased genetic variation is needed to survive and establish.

Abstract ID: 1525

Fixation dynamics of beneficial alleles in prokaryotic polyploid chromosomes and plasmids

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Polyploidy is not limited to eukaryotes; in fact, many prokaryotes carry multiple copies of a replicon -- chromosome or plasmid -- per cell. Predicting the evolution of polyploid prokaryotes is non-trivial since the segregation of replicon copies at cell division leads to daughter cells that are genotypically different from their mother cell. Theoretical models for the allele dynamics on multicopy replicons in prokaryotic populations, however, remain largely lacking. Here, we present a population genetics model for multicopy replicons in prokaryotes and apply the model to study the consequences of polyploidy for the fixation process of a dominant beneficial allele. We find that, depending on the modes of replication and segregation of replicon copies, fixation of the adaptive phenotype may precede fixation of the genotype by many generations. We term this time interval the heterozygosity window and show that it emerges if the replicon copy number is high and selection strong. Replicon ploidy in prokaryotes may thus allow for the maintenance of genetic variation long after phenotypic adaptation has occurred.

Symposium: S26. The biological meaning of SNPs (id: 943)

Abstract ID: 1128

Investigating the genetic architecture of complex traits in Soay sheep

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Understanding the genetic architecture underpinning quantitative traits in wild populations is pivotal to understanding the processes behind trait evolution. The ‘animal model’ is a popular method for estimating quantitative genetic parameters such as heritability and genetic correlation and involves fitting an estimate of relatedness between individuals in the study population. Genotypes at genome-wide markers can be used to estimate relatedness; however relatedness estimates can vary with marker density, potentially affecting results. Increasing density of markers is also expected to increase the power to detect quantitative trait loci (QTL) using genome-wide association. We estimated heritability and performed genome-wide association studies (GWAS) on

five body size traits in an unmanaged population of Soay sheep using two different SNP densities: a dataset of 37,037 genotyped SNPs, and an imputed dataset of 417,373 SNPs. We also partitioned heritability estimates into common SNP- and familial SNP-associated components by fitting both a whole population genetic effect and a family genetic effect using only close relatives. We found that heritability estimates did not differ between the two SNP densities, but the highdensity imputed SNP dataset revealed five new SNP-trait associations that were not found with the lower density dataset. Conditional GWAS analyses after fitting the most significant SNPs revealed two more novel SNP-trait associations. The effect of partitioning heritability estimates differed between traits – the proportion of genetic variance explained by familial SNPs varied between 0-42.6%.

Abstract ID: 2067

Investigating the genetic structure of taxa that form Species complex: a case study of *H. spicatum*

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Species complexes can be defined as a group of closely related organisms with overlapping morphological features, making species boundaries uncertain in these groups. These taxa present an opportunity to study speciation and speciation processes in real-time. Here, we are investigating an Asian paleotropical ginger, *Hedychium spicatum* (Zingiberaceae) that forms a species complex - the Spicatum complex which currently consists of at least six taxonomically distinct species and two putative hybrid forms. The distributional range of *H. spicatum* overlaps with that of other members of the complex and it exhibits interfertility with its sympatric congeners. Thus, we hypothesize that *geographically distinct forms of H. spicatum will show local introgressions with their sympatric congeners.* To test this, we sampled 11 populations of *H. spicatum* from throughout its distributional range, along with sympatric taxa that are part of the complex and the intermediate forms. We are using SNPs extracted via dd-RAD sequencing to test this hypothesis. We used a combination of model based and model free clustering approaches to understand the population structuring of the *H. spicatum* individuals. The population structure was dependent on the de novo assembly pipeline used to get the SNPs and the percentage cut-off used to filter the SNPs. Overall, our results suggested hybridization between spicatum and non-spicatum individuals and that the population structure lacked a clear geographic signature. We suggest that this could be because of multiple dispersals or different reproductive strategies (clonal propagation vs selfing vs outcrossing) adopted by *H. spicatum* in different geographic locations.

Abstract ID: 1305

From variation in a colony to variation in populations: what SNPs tell us about coral biology

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Clonal, colonial corals are animals that can live to be hundreds of years old, appear to be reproductively viable for their entire adult lives, and may or may not senesce or develop cancers. Whether they have embryonic germline segregation is controversial. All of this makes them a pivotal group in which to understand genome maintenance. In addition, they are keystone species that create the structures necessary to support biodiverse coral reef ecosystems, and they are highly threatened and facing strong selective pressures as ocean temperatures rise globally. Studying single nucleotide polymorphisms (SNPs) that occur within branches of a single colony yields somatic mutation rate estimates (on the order of 10^{-7} mutations/bp across the transcriptome, 10^{-6} mutations/bp across the genome), and suggests which DNA repair mechanisms that these animals may employ. In addition, I will show how identifying SNPs in adult corals and the sperm that they produce has led us to a new hypothesis about how germ, stem, and somatic cell lineages develop and mutate over a colony's lifetime. I will also show that the rate of SNPs that occur through somatic mutations in a colony is orders of magnitude lower than the than the rate of SNP differences between colonies of different genotypes with a population. Finally, I will conclude with how studying SNPs is aiding conservation research purposes for corals bred in captivity, by allowing us to test for kinship, selection, and more in coral parents and their sexually produced offspring.

Abstract ID: 1387

The challenge and promise of estimating de novo mutation rates and fates in a non-model primate

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Germline mutations are the raw material for natural selection, driving species evolution and biodiversity. Their evolutionary fate is uncertain, however, given that most de novo mutations (DNMs) will never be fixed at the population level due to purifying selection and/or genetic drift. Though the road from DNM to SNP is a hazardous one, it is of fundamental importance to the field of evolutionary genetics to determine the rate and mechanisms by which this process unfolds across the Tree of Life. DNM rates provide a fossil-free approach for estimating divergence times with the statistically rigorous multispecies coalescent (MSC) model, thus situating speciation events in geological context. There are both operational and theoretical challenges to this exercise, however, as exemplified by our work in the mouse lemur system. These endemic Malagasy primates are morphologically cryptic though remarkably speciose, with unknown mechanisms of reproductive isolation driving their radiation. Using long-read whole-genome sequences from a pedigree, we determined the DNM rate in mouse lemurs to be among the highest calculated for a mammal at 1.52×10^{-8} (95% credible interval: 1.28×10^{-8} to 1.78×10^{-8}) mutations/site/generation. We also conducted an independent analysis of context-dependent substitution types using phylogenetic methods that were consistent with our DNM results. These analyses have increased our understanding of the speciation mechanisms driving this cryptic radiation and show promise for similar insights in other non-model systems.

Symposium: S27. Tandem repeats: their role in molecular evolution and methods (id: 33)

Abstract ID: 2466

Genome-wide analysis of fitness effects of TR mutations and their relevance to human populations

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Short tandem repeats (STRs) comprising repeated sequences of 1-6 bp are one of the largest sources of genetic variation across the tree of life. Due to their rapid mutation rates, STRs provide unique opportunities for modulating complex phenotypes through variation in repeat length. While classical studies have identified key roles of individual STR loci, the advent of improved sequencing technology, high-quality genome assemblies for diverse species, and bioinformatics methods for genome-wide STR analysis now enable more systematic study of STR variation across wide evolutionary ranges. Here, I will discuss new computational methods for performing genome-wide analysis of STR variation, show how those have enabled detailed modeling of mutation and selection processes in humans, rodents, and other species, and present specific examples of effects of STR variation on phenotypes that have been discovered using genome-wide analysis techniques.

Abstract ID: 2419

Uncovering the diverse roles of short tandem repeat variation in colorectal cancer

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Insertions and deletions of repeat motifs are common in short tandem repeat (STR) loci and can affect gene expression levels and protein structures. In cancer, their high mutability can also result in tumor-specific neoantigens, making them promising targets for immune therapies. Although recently developed computational approaches allow for accurate genotyping of STRs from sequencing data, many investigations of STR variation in cancer predate these methods. We therefore suspect that the contribution STRs have to the molecular picture of cancer is currently underestimated. Therefore, we used repeat-specific methods to generate and genotype a panel of over 1.8 million STR loci in colorectal cancer (CRC) patients from The Cancer Genome Atlas. We detected tumor STR variants by comparing repeat lengths between patient-matched healthy and diseased tissue. We then estimated the contribution of these tumor STR variants to gene expression changes in CRC using existing catalogues of STRs known to affect expression. For STR variants in coding regions, we determined the expected changes in protein structure and monitored the generation neoantigens. While a lot of this is still work in progress, we expect our results will provide a better understanding of the diverse roles of STR variation in CRC. Using computational methods specifically designed to analyse STRs, we will demonstrate the importance of this abundant but often bypassed source of variation in cancer. Furthermore, by making our panel of STR loci and their

variation in CRC patients available to the community, we hope to stimulate future investigations into this important topic.

Abstract ID: 2257

Ancient satellite DNA and rapid turnover across passerine birds

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Satellite DNA (satDNA) is among the fastest evolving elements in the genome and is highly abundant in some eukaryotic genomes. Its highly repetitive nature means it is challenging to assemble, and thus underrepresented in most assemblies and often understudied as a result. Birds are an ideal model organism for the study of satDNA and its evolution, since the large amount of available sequenced genomes of this clade allows for dense sampling across the evolutionary timescale and the low number of satDNA families within their satellitomes facilitates their study and comparison between species. Here, we characterize satDNA and its evolution across Passeriformes, an avian clade containing two-thirds of all bird species spanning nearly 50 million years of evolution. With this goal we used both short-read data and long-read assemblies of species representative of over 30 families in this clade to shed light on the evolution of its satellitome. We focused on examining the phylogenetic relationship between satellites common to most species as well as characterizing satellite array structure and location in the genome. We found a unique satellitome in each sampled bird family containing satellites from 3 to 18 different families, and identified differences in the satellite content between male and female individuals suggesting occasional satDNA expansion on the female-specific W chromosome.

Symposium: S28. Beyond transcription: the role of post-transcriptional gene regulation in adaptation and evolution (id: 945)

Abstract ID: 1361

The transcriptional architecture of sexual dimorphism

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Sexual dimorphisms are common across a range of phenotypes and are widely assumed to be the product of different gene expression patterns in males and females. However, while there has been considerable focus on testing the role of expression level change in sex-specific adaptation, other regulatory mechanisms have received less attention. Here, we characterize patterns of alternative splicing across males and females of multiple

avian species to test the link between splicing and sexual dimorphism. We find that patterns of sex-specific alternative splicing have evolved rapidly, likely as a product of sex-specific selection, and that splicing might offer a quick route to phenotypic innovation by circumventing pleiotropic constraints. Next, using simulations, we interrogate comparative approaches to detect signatures of selection across the entire transcriptome. We show that inferring selection on gene expression using data from heterogeneous tissue can lead to false signatures of selection and highlight steps to minimise these sources of bias. Together, our findings demonstrate how diverse patterns of transcriptional regulation can play an important role in phenotypic complexity and offer insight into how best to test for their effects.

Abstract ID: 1159

Molecular mechanisms of adaptation to freshwater in threespine stickleback

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The genetic variants that underlie adaptive phenotypes are being identified in a growing number of cases. However, in most cases, the detailed molecular and developmental mechanisms connecting genotype to phenotype remain a black box. In threespine stickleback (*Gasterosteus aculeatus*), the genes underlying several adaptive phenotypes have been identified. One of these genes is *Ectodysplasin* A (*Eda*), which has pleiotropic effects on the loss of bony lateral plates, changes in lateral line patterning, and changes in schooling behaviour in freshwater stickleback, and is found in an 16kb haplotype that differs between marine and freshwater sticklebacks. In this study, we aimed to gain insights into the developmental pathways and regulatory mechanisms mediating the phenotypic effects of the *Eda* haplotype. By comparing the skin and head kidney transcriptomes of marine sticklebacks that vary only in whether they carry the marine or the freshwater haplotype of *Eda*, we found changes in the expression of hundreds of genes and in the patterns of alternative splicing in dozens of other genes. The genes affected by the *Eda* haplotype include genes involved in ossification processes, BMP signalling and neuronal development, making them strong candidates to mediate the known phenotypic effects of *Eda*. We also uncovered a putative role of the *Eda* haplotype in mediating immune phenotypes. These results also highlighted the relevance of regulatory mechanisms like alternative splicing in adaptation. As a follow-up, we are currently investigating whether alternative splicing has played a broader role in adaptation to freshwater in threespine stickleback.

Abstract ID: 1657

RNA binding proteins in parental genetic conflict: how MBNL3 was co-opted to restrict placental growth in eutherians

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The eutherian placenta is a major site for parental genetic conflict. Here, we identify the X-linked Mbnl3 gene as a novel player in this dispute. Mbnl3 belongs to an RNA binding protein family whose members regulate alternative splicing and other aspects of RNA metabolism in association with cellular differentiation. We find that, in eutherians, Mbnl3 has become specifically expressed in placenta and has undergone accelerated sequence evolution leading to changes in its RNA binding specificities. Although its molecular roles are partly redundant with those of Mbnl2, Mbnl3 has also acquired novel biological functions. In particular, whereas Mbnl2;Mbnl3 double knockout mice display severe placental maturation defects leading to strong histological and functional abnormalities, Mbnl3 knockout alone results in increased placental growth and favors placental and fetal resource allocation during limiting conditions.

Abstract ID: 1345

Intron-mediated induction of phenotypic heterogeneity

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The budding yeast, an otherwise intron-poor species, preserves two sets of ribosomal protein genes that differ primarily in their intron content. Despite recent findings on their role under stress and starvation, understanding the contribution of introns to ribosome regulation remains challenging. In our work, by combining isogrowth profiling with single-cell protein measurements, we show that osmotic stress leads to the bimodal expression of a small ribosomal subunit protein Rps22B, which is mediated by an intron in the 5′ untranslated region of its transcript. The two resulting yeast subpopulations differ in their ability to cope with starvation, where low levels of Rps22B protein result in prolonged survival under sustained starvation, and high levels of Rps22B enable cells to grow faster after transient starvation. Our finding adds regulation of splicing to the mechanisms yeasts employ to induce heterogeneity in the face of changing environment, and suggests that pairs of duplicated ribosomal protein genes serve to resolve the evolutionary conflict between precise expression control and environmental responsiveness.

Symposium: S29. Comparative genomics: a powerful tool for exploring broad evolutionary questions (id: 947)

Abstract ID: 1697

The genetic basis of evolutionary divergence in oceanic island birds:a comparative-genomics approach

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The colonization of oceanic islands by organisms from the mainland has often led to the formation of new species, providing a valuable research model to study processes like evolutionary divergence and local adaptation. The comparison of different taxa that have colonized oceanic islands and have been subjected to similar demographic and selective factors provide the opportunity to study parallel evolution by identifying shared phenotypic and genomic changes. We generated whole genome sequences from mainland and insular counterparts of four passerine species (common chaffinch *Fringilla coelebs*, red-billed chough *Pyrrhocorax pyrrhocorax, house finch Haemorhous mexicanus* and dark-eyed junco *Junco hyemalis)* in order to infer their demographic history and compare the genomic landscapes of differentiation and the factors shaping them. We calculated the relative and absolute differentiation (F_{ST} and d_{xy}, respectively), nucleotide diversity (π), Tajima's D and recombination rate, and also searched for selective sweeps and chromosomal inversions. Phenotypically, insular individuals were larger than their mainland conspecifics, a pattern consistent with the island rule. Upon island colonization, all species showed a marked decrease in effective population size (N_e). Even with similar selective pressures and highly conserved genomic features, we document that the patterns of differentiation were species-specific. The genomic landscapes of each bird species was shaped by different processes, including selective sweeps, chromosomal inversions and recurrent selection.

Abstract ID: 1744

Loss of a muscle enzyme contributed to the evolution of adaptive metabolic traits in hummingbirds

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Hummingbirds are the only birds that evolved true hovering flight, and they have the striking ability to fuel this energy-demanding activity almost entirely with recently-ingested sugars. The genomic underpinnings of these extreme metabolic muscle adaptations are largely unknown. Here, we generated a long-read based chromosome-level assembly of the long-tailed hermit, a member of a sister clade to most other hummingbirds, and performed a genome-wide screen for genes that have been specifically inactivated in the ancestral hummingbird lineage. This screen identified the loss of *FBP2*, a key gluconeogenic enzyme that is active in muscles. Loss of *FBP2* occurred around a time when energy-demanding hovering flight is thought to have evolved in hummingbirds. Using CRISPR-Cas9 to generate a partial *FBP2* knockout in an avian muscle cell line, we show that downregulating *FBP2* upregulates glycolytic flux and mitochondrial respiration, coincident with an increased mitochondria number. Furthermore, genes involved in mitochondrial respiration and organization have upregulated expression in flight muscle of hummingbirds. Together, these results suggest that *FBP2* loss was likely a key step in the evolution of metabolic muscle adaptations required for hovering flight, and illustrate how loss of ancestral genes can contribute to phenotypic adaptations.

Abstract ID: 1611

MI Biodiversity of Antarctic and Subantarctic Ecosystems (BASE): genomics and phylogeography

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The Millennium Institute Biodiversity of Antarctic and Subantarctic Ecosystems (BASE) has started this year as a long-term collaborative project to study the biodiversity in the Southern Ocean, including microorganisms, lichens, plants, marine and terrestrial invertebrates, fishes, seabirds and marine mammals. As the continuity of the Genomic Antarctic Biodiversity (GAB) project, we are generating genomic data to describe geographic patterns of genetic diversity in this region to establish the evolutionary processes driving the diversification of the Antarctic and Subantarctic biota. In the marine realm, the Antarctic Polar Front (APF) acts as a strong biogeographical barrier for numerous taxa, as other boundaries are detected between Antarctica, Subantarctic Islands and South America, that lead to intraspecific genetic differentiation among populations or even divergence between sister taxa. In addition, other boundaries are also detected between the southern tip of South America continent and Malvinas/Falkland Islands, and among Subantarctic Islands such as Kerguelen Islands and Crozet/Marion Islands. The existence or the lack of population structure across these marked boundaries is generally related to the species' life-history traits and ecology. We present here several studies performed by GAB-BASE researchers and involving various models from microorganisms, marine invertebrates, fishes, birds and marine mammals to illustrate how genomics will contribute to assessing the fate of a unique ecosystem in a changing world.

Abstract ID: 1860

Genomes of coronavirus reservoir bats provide insights into immunity changes and viral tolerance

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Bats possess a special immune system that allows them to live with viruses that can be lethal to humans and other mammals. Current research suggests that bats evolved unique antiviral defense systems to dampen immune responses and limit cell damage. However, the underlying genomic and molecular changes that differentiate bats from other mammals are not fully understood. As part of the Bat1K project, we generated state-of-the-art PacBio HiFi genomes of several bat species that are suspected SARS-CoV-2 reservoirs. These genomes improve upon the best existing bat assemblies in terms of contiguity, completeness, and base accuracy. To identify unique changes that differentiate the immune system and virus tolerance of bats from other mammals, we used TOGA to annotate genes and infer orthologs across >100 mammalian genomes. Genome-wide screens for patterns of positive selection showed that selection in immune-related genes is more prevalent in bats compared to other mammals. We identified genes with changes in key residues that may suppress inflammatory responses and enhance antiviral mechanisms. Our work highlights mechanisms that could contribute to viral tolerance in bats.

Abstract ID: 995

A phylogenetic genome-phenome map of complex traits in primates

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The study of the genetic architecture of complex traits and diseases has focused on Genome-Wide Association Studies (GWAS), the search for associations between genetic variation and phenotypic differences across individuals of the same species, usually humans. Large-scale comparative genomics affords the opportunity of focusing on the traits themselves –including their presence and absence– uncovering relevant

and actionable pathways, genes and even individual mutations that have remained undetectable so far. We cataloged measurements for 265 complex primate traits, covering morphology, behavior, ecology, physiology and life-history strategies. We use this resource to perform genome-phenome analysis focusing on the protein-coding genes of 224 different primate species. We track genomic changes building up relevant phenotypes along the primate phylogeny, focusing on convergent amino acid substitutions across primate families and shifts in the rates of protein evolution of the genes under study. This approach allows us to recover thousands of phylogenetic gene-trait associations, both at the level of genes and of individual amino acid changes, improving our knowledge of the genomic basis for traits of evolutionary and biomedical relevance for primates in general and humans in particular.

Abstract ID: 2069

18 years of inbreeding in the wild

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Inbreeding is an important phenomenon across diploid organisms. It leads to increased homozygosity of the genome, thereby enabling the expression of recessive deleterious mutations. In response, some species evolved strategies to avoid matings with close relatives, for example via behavioural avoidance. However, dramatic population declines can increase inbreeding regardless. In some cases, it is possible to avoid the negative effects of inbreeding via genetic resistance, a form of epistasis, dependent on the genetic background of individuals. Until recently, the study of inbreeding was complicated by the need for deep pedigrees to quantify individual levels of inbreeding. Now, modern genomics has enabled the study of inbreeding on a more detailed level. Inbreeding can now be quantified more precisely by analysing long continuous runs of homozygosity, markers of both recent and more distant inbreeding events, in the genome.

We analyse the patterns of inbreeding in a long-term study on free-living wild house mice near Zurich, Switzerland. This population was founded by 12 wild-caught mice from two source populations, one of them with considerable inbreeding signals in the genomes, and was monitored intensively over the years. This population of over 10,000 individuals in total has gradually become more inbred over time. Here, we present first results investigating the traits impacted by inbreeding, the contribution of specific runs of homozygosity to changes in inbreeding-impacted traits, the presence of resistance to inbreeding, and frequency changes of specific homozygous regions over time, such as purging of particularly deleterious alleles.

Abstract ID: 2153

How does *Metarhizium brunneum* maintain diverse ecotypes is as an insect pathogen and root symbiont?

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The genus *Metarhizium* comprises a highly diverse group of insect pathogenic fungi spread worldwide and often found in associations with plants. Variability is present between and within species in phenotypic traits such as virulence, growth, and ability to associate with plants in the rhizosphere. This variability is structured by geography, host range and lifestyle. The fungus *M. brunneum* is a generalist pathogen known to infect insects from at least seven different orders, but also grows symbiotically in plant roots. This variable and versatile lifestyle provides an ideal system for studying ecotype-specific (i.e. entomopathogenicity and plant-mutualism) genome-wide diversity. Here, we present our efforts to understand the underlying genetic variation of *M. brunneum* through intra-specific comparative genomics. First, seven *M. brunneum* isolates spanning much of the known global distribution were sequenced, assembled and compared to study the pan-genomic characteristics of core and accessory genes. Second, this pan-genome is used as reference for studying 24 *M. brunneum* isolates from three land-use types – arable land, grassland and forest – in Switzerland. Among these isolates, there are 12 multilocus genotypes based on 14 microsatellite markers, which we correlate with phenotypic traits of growth rate, virulence and ability to establish association with plants. This comparative phenotypic and genomic analysis sheds light on the evolutionary ecology of *M. brunneum* and how multiple ecotypes likely are maintained in sympatric populations.

Abstract ID: 2467

Evolution on the very fast lane: bacterial genomes as the playgrounds of mobile elements

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Horizontal gene transfer driven by self-mobilizable genetic elements allows the acquisition of complex adaptive traits and their transmission to subsequent generations. Transfer speeds up evolutionary processes as exemplified by the acquisition of virulence traits in emerging infectious agents and by antibiotic resistance in many human pathogens. Mobile genetic elements themselves evolve extremely fast regarding their mechanisms of transfer and especially their gene repertoires. This is partly because transfer is costly and vectors of horizontal transfer compete within genomes where they have their own parasitic mobile elements. As a result, genomes are repositories of multiple immune systems from hosts and from mobile elements that interact in complex ways to drive gene flow in communities. The combination of evolutionary genomics and sequence analysis is now opening up these processes to show how they bring into the genome a constant flux of novel genes that favor the establishment and the invention of novel functions.

Abstract ID: 2386

The silent impact: codon usage bias and protein evolution in bacteria

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Bias in synonymous codon usage has been reported across all kingdoms of life. Evidence across species suggests that codon usage bias is driven by selective pressures, typically for translational efficiency. These selective pressures have been shown to depress the rate at which synonymous sites evolve. We hypothesize that selection on synonymous codon use could also slow the rate of protein evolution if two amino acids have different preferred codons. We test this hypothesis by looking at patterns of protein evolution using polymorphism and substitution data in bacteria. We found that non-synonymous mutations that change from unpreferred to preferred codon are more common than the opposite, but only amongst codons that vary substantially in the level of preference. Overall, selection on codon bias seems to have little influence over non-synonymous polymorphism or substitution patterns.

Abstract ID: 1282

Host control and the evolution of cooperation in host microbiomes

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Humans, and many other animals, are host to dense and diverse bacterial communities which provide many health benefits. It is often suggested that the mutual benefits of the host-symbiont relationship are sufficient to drive the evolution of cooperation. We developed an evolutionary model of the host-microbiota interaction to evaluate this hypothesis. Our model predicts that mutual benefits alone are insufficient to drive the evolution of cooperation. However, cooperation can be rescued if hosts are able to invest in mechanisms that exert control over their symbionts and enforce cooperation, so long as there are constraints on bacterial counter evolution. We test our predictions with genomic data from across the bacterial kingdom and find multiple bacterial traits (the loss of flagella and the maintenance of butyrate production) have evolved as predicted by our model. Moreover, an analysis of symbionts that have retained flagella supports the evolution of host control mechanisms that limit bacterial counter evolution. Our work puts host control mechanisms, such as the immune system, at the heart of microbiome evolution.

Abstract ID: 1288

The evolution of spectrum in antibiotics and bacteriocins

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A key property of many antibiotics is that they will kill or inhibit a diverse range of microbial species. This broad spectrum of activity has its evolutionary roots in ecological competition, whereby bacteria and other microbes use antibiotics to suppress other strains and species. However, many bacteria also use narrow-spectrum toxins, such as

bacteriocins, that principally target conspecifics. Why has such a diversity in spectrum evolved? Here we develop an evolutionary model to understand antimicrobial spectrum. Our first model recapitulates the intuition that broad-spectrum is best, because it enables a microbe to kill a wider diversity of competitors. However, this model neglects an important property of antimicrobials: they are commonly bound, sequestered or degraded by the cells they target. Incorporating this toxin loss reveals a major advantage to narrow-spectrum toxins: they target the strongest ecological competitor and avoid being used up on less important species. Why then would broad-spectrum toxins ever evolve? Our model predicts that broad-spectrum toxins will be favoured by natural selection if a strain is highly abundant and can overpower both its key competitor and other species. We test this prediction by compiling and analysing a database of the regulation of toxins in bacteria and their spectrum. This analysis reveals a strong association between broad-spectrum toxins and density-dependent regulation, indicating that they are indeed used when strains are abundant. Our work provides a rationale for why bacteria commonly evolve narrow-spectrum toxins like bacteriocins and suggests that the evolution of antibiotics proper is a signature of ecological dominance.

Abstract ID: 1426

Strong purifying selection in haploid tissue-specific genes of Scots pine supports masking theory

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Evolutionary expectations for genes expressed in haploid life stages versus genes expressed in diploid differ. Masking theory states that genes expressed in haploid stage will be under more efficient selection. In contrast, selection will be less efficient in genes expressed in diploid stage, where the fitness effects of recessive deleterious or beneficial mutations can be hidden from selection in heterozygous form. This difference can influence several important evolutionary processes as genetic variance, genetic load, and adaptation rate. Masking theory expectations have been confirmed in single cell organisms. However, in more complex organisms as multicelluar plants the effects of haploid selection are not clear-cut. The great majority of haploid selection studies in plants have been carried out using angiosperms' male haploid tissues, with confounding effects of sexual selection, intra-specific competition and haploid selection. Evidence from other plant groups (e.g. the moss *Funaria hygrometrica*) are scarce and results show no support for the Masking theory.
Here we have used Scots pine megagametophyte (maternally-derived seed haploid tissue) and four diploid tissues to test the strength of purifying selection on a set of genes with tissue-specific expression. By using targeted resequencing data of those genes we have obtained the site frequency spectrum and inferred the distribution of fitness effects of new mutations in haploid and diploid tissue-specific genes. Our results show that purifying selection is stronger for genes expressed in the haploid megagametophyte tissue.

Abstract ID: 2413

Testing kin-selection theory with large-scale genomic approaches

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Dynamic evolution in insect societies is different from the irreversible ratchet clicks that produced major evolutionary transitions (MTEs) to caste-differentiated superorganisms, which evolved convergently in the ants, corbiculate bees, vespine wasps and higher termites (1). Hamilton's inclusive fitness theory applies to both trajectories, but societies evolve by conflict reduction while new forms of colonial superorganismality originated by lifetime commitment between a pair of lifetime monogamous parents that precluded conflict up front. The convergent origins of colonial superorganismality are therefore analogous to the origin of metazoan bodies from a lifetime-committed pair of gametes in a zygote. Each MTE to permanent multicellularity or colonial superorganismality is expected to have a unique gene regulatory network (GRN) for obligate germline-soma differentiation and queen-worker reproductive division of labour, which should continue to be expressed and elaborated during adaptive radiation. Metazoan cell differentiation is increasingly studied by single-cell transcriptome sequencing, which has confirmed developmental canalization in meticulous detail. To test analogous predictions for queen-worker differentiation during colony development, we performed massive transcriptome sequencing on brain tissues and whole body samples throughout immature development of individual caste phenotypes in two ant species. This allowed us to partly reconstruct the ancestral reproductive division of labor GRN for the ants, and to show that the ontogeny of caste phenotypes is developmentally canalized.

(1) Boomsma, J.J. (2022). *Domains and Major Transitions of Social Evolution*. Oxford University Press

Abstract ID: 2148

Major changes in domain arrangements are associated with the evolution of termite castes

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Domains as functional protein units and their rearrangements along the phylogeny can shed light on the functional changes of proteomes with the evolution of complex traits like eusociality. It has been hypothesized that, while mainly regulatory changes are expected during the early stages of social evolution, greater functional changes occur in more advanced stages of sociality. Moreover, the functional changes are also expected to occur with the emergence of new phenotypes such as distinct castes. One of the groups of organisms that evolved eusociality is termites. Analyzing the domain rearrangements of three solitary cockroaches and five termites, we observed more rearrangements on the nodes leading to more advanced eusociality compared to the origin of termites. Moreover, the branch of the socially advanced termite Mastotermes natalensis showed the highest amount of rearrangements compared to other termites. Among the new domains that emerged in the origin of termites, we found domains related to metabolic and regulatory processes, insulin expression regulation, and mitochondrial function. Beyond that, the domain rearrangements occurred in genes related to the DNA repair, stress response, and transposon activity indicating the importance of these processes in the evolution of eusociality. Also, we observed a significant enrichment of caste-biased genes among the genes with domain rearrangements in several termite species which could be related to the evolution of termite castes. Preliminary findings suggest different

patterns of selection and methylation for genes with domain rearrangements and altogether show for the first time the importance of domain rearrangements for the emergence of eusociality.

Abstract ID: 1242

The evolutionary significance of horizontal gene transfer in ants

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Bacteria have profoundly influenced animal evolution either as parasites, commensals, or beneficial symbionts. In addition, bacteria have been important sources for new genetic material via horizontal gene transfer (HGT). Specifically in insects, the impact of HGTs on the evolution of phenotypic innovations and environmental adaptations is well documented. However, the extent of HGTs in ants, one of the most successful insect families, remains largely unknown. In this study, we systematically search for HGT in over 160 ant genomes from 12 subfamilies, which were sequenced by the Global Ant Genomics Alliance (GAGA). We uncover that HGTs in ants occurred predominantly from intracellular Enterobacteria and *Wolbachia*, likely due to their intimate association with the germline of the eukaryotic hosts. Among several hundred HGT candidates in 85 species, we find dozens of convergent transfers of *Wolbachia*-derived ankyrin repeat proteins, several cases of ancient HGTs conserved in particular clades of ants, and over 20 expressed and species-specific HGTs, some of which potentially expand the metabolic capacities of the species. Our study builds the foundation for understanding how HGTs affected the evolution of an ecologically dominant and diverse insect family and may furthermore help to understand the evolutionary significance of HGTs in general.

Abstract ID: 1199

The genomics of Heliconiini shows strong selective pressures prior Heliconius' adaptive radiation

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Adaptive radiation is the proliferation of species from a single common ancestor that rapidly diversify into ecologically diverse forms. Within the Heliconiini (Nymphalidae), a tribe of neotropical butterflies, the genus *Heliconius* is known example of sympatric adaptive radiation. Due to its toxicity and Müllerian mimicry, they radiated into the richest species genus of the tribe. This diversity is coincidental with important trait innovations, such as pollen feeding behaviour, a unique feature among Lepidoptera, prolonged reproductive lifespan, and major elaborations of learning and memory centres in the brain. With 63 genome assemblies, we present the most comprehensive genomic resource for the entire tribe of Heliconiini to date. A genome-wise approach was applied to generate a new dated phylogeny, which we use to provide new analyses on incomplete lineage sorting and introgression. We then describe how transposable elements activity affects both genome size and gene structures and estimate how

Heliconiini genomes changed throughout the course of their radiation, inferring evolutionary dynamics of gene expansion/contraction. Finally, molecular signals of adaptive evolution reveal how several basal lineages were affected by strong selective pressures prior to the *Heliconius'* radiation. By doing so we identified candidate genes, pathways, and gene families likely to be responsible for some of the most important innovations we see in these butterflies. Our dataset provides the first tribe-wide quantification of genetic and genomic variation potentially underlying key phenotypical traits, advancing our understanding of the genomic basis of behavioural, physiological and morphological innovation in the context of ecological diversification and speciation.

Symposium: S30. Characterizing genomic landscapes of recombination and their evolution (id: 951)

Abstract ID: 2470

Recombination and its evolution, in vertebrates and beyond

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Recombination is a key component of reproduction and drives genetic diversity in most complex organisms, yet it is also remarkable in its diversity and rapid evolution across species and through time. The work of our group and others on PRDM9 and its evolution allowed us to discover that this gene positions recombination events into hotspot regions in many, though not all, vertebrate species. PRDM9 is also the fastest evolving gene in the mammalian genome. This evolution, twinned with rapid evolution of recombination hotspots themselves, helps drive hybrid sterility, a step towards speciation, and the resulting mechanistic insights offer an explanation of why so many species possess recombination hotspots, despite little conservation in their actual positions. Here, we will present an overview of current knowledge, and describe new work leveraging rapid evolution to identify recombination hotspots from the computational analysis of single genome sequences across diverse phylogenetically related species. We identify recombination hotspots from the present day, back to ancestral "fossils" active many millions of years ago, and across many species, from cats to whales to turtles to the great ape ancestor. We observe (often multiple) complete changes in the landscape of recombination among almost all species through time, offering the potential that PRDM9 may play a widespread role in driving hybrid sterility. Some exceptional species - e.g. birds and whales - show unusual patterns; we also see evidence of changing recombination mechanisms through time, including in feline species. We believe this approach could be expanded further, to allow analysis of this central biological process across much of the tree of life, even in extinct taxa.

Abstract ID: 1587

Historical recombination rate variation in a migratory songbird, the European blackcap

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Recombination influences genetic variability and the efficacy of selection. Bird genomes possess unique properties compared to other vertebrates because they lack the protein PRDM9, a key player in recombination dynamics in most metazoans. Birds show an apparent stasis in the positioning of recombination events, yet recombination rates differ widely across the genome and between different (sub-)species. The causes of recombination rate variation and its impact on evolutionary and behavioural processes remain poorly understood, particularly in natural bird populations. We study recombination dynamics in the European blackcap, an evolutionary model in bird migration research due to its wide repertoire of migratory phenotypes across its range. Analysing whole-genome re-sequencing data of 179 individuals with a composite-likelihood approach that accounts for demography, we (i) characterised recombination rate variation and its association with genomic features along the genome, (ii) assess similarity and divergence of recombination between populations with distinct migratory phenotypes, and (iii) expanded this comparison to an inter-specific level including the Garden warbler as closest sister taxon. Our result revealed variable recombination rates along the genome, which associated positively with nucleotide diversity, GC-content, CpG islands, gene density, and negatively with chromosome size. Recombination rates in *cis*-regulatory regions were significantly elevated. The association with retrotransposons varied according to specific class and location. Recombination patterns between phenotypically distinct populations and between sister species were heterogeneous. We found conserved and non-conserved regions along the genome, leading to the identification of highly divergent genomic regions showing recombination suppression, some of which were identified under background selection.

Abstract ID: 2063

Estimating the rates of crossover and gene conversion from individual genomes

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Recombination can occur either as a result of crossover or gene conversion events. Population genetic methods for inferring the rate of recombination from patterns of linkage disequilibrium generally assume a simple model of recombination that only involves crossover and ignores gene conversion. However, distinguishing the two processes is not only necessary for a complete description of recombination but also essential for understanding the evolutionary consequences of inversions and other genomic partitions in which crossover (but not gene conversion) is reduced. We present heRho, a simple composite likelihood scheme for co-estimating the rate of crossover and gene conversion from individual diploid genomes. The method is based on analytic results for the distance-dependent probability of heterozygous and homozygous states at two loci. We apply heRho to simulations and data from the house mouse Mus musculus castaneus, a well studied model. Our analyses show i) that the rates of crossover and gene conversion can be accurately co-estimated at the level of individual chromosomes

and ii) that previous estimates of the population scaled rate of recombination under a pure crossover model are likely biased.

Abstract ID: 1718

Diversity and determinants of recombination landscapes in flowering plants

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During meiosis, crossover rates are not randomly distributed along chromosomes and therefore they locally influence the creation of novel genotypes and the efficacy of selection. To date, the broad diversity of recombination landscapes among plants has rarely been investigated, undermining the overall understanding of the constraints driving the evolution of crossover frequency and distribution. The determinants that shape the local crossover rate and the diversity of the resulting landscapes among species and chromosomes still need to be assessed in a formal comparative genomic approach. We gathered genetic maps and genomes for 57 flowering plant species, corresponding to 665 chromosomes, for which we estimated large-scale recombination landscapes. Chromosome length drives the basal recombination rate for each species, but within species we were intrigued to notice that the chromosome-wide recombination rate is proportional to the relative size of the chromosome. Moreover, for larger chromosomes, crossovers tend to accumulate at the ends of the chromosome leaving the central regions as recombination-free regions. Based on identified crossover patterns and testable predictions, we proposed a conceptual model explaining the broad-scale distribution of crossovers where both telomeres and centromeres are important. Finally, we qualitatively identified two recurrent crossover patterns among species and highlighted that these patterns globally correspond to the underlying gene distribution. In addition to the positive correlation between recombination and gene density, we argue that crossover patterns are essential for the efficiency of chromosomal genetic shuffling, even though the ultimate evolutionary potential forged by the diversity of recombination landscapes remains an open question.

Abstract ID: 1533

Recombination landscape divergence between domesticated and wild populations of rye

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The genomic landscape of recombination plays an essential role in evolution. Patterns of recombination are highly variable along chromosomes, between sexes, individuals,

populations, and species. In many eukaryotes, recombination rates are elevated in sub-telomeric regions and drastically reduced near centromeres, resulting in large low-recombining (LR) regions. The processes of recombination are influenced by genetic factors, such as different alleles of genes involved in meiosis and chromatin structure, as well as external environmental stimuli like temperature and overall stress. In this work, we focused on the genomic landscapes of recombination in a collection of 916 rye (*Secale cereale*) individuals. By analysing population structure among individuals of different domestication status and geographic origin, we detected high levels of admixture, reflecting the reproductive biology of a self-incompatible, wind-pollinating grass species. We then analysed patterns of recombination in overlapping subpopulations, which revealed substantial variation in the physical size of LR regions, with a tendency for larger LR regions in domesticated subpopulations. Genome-wide association scans (GWAS) for LR region size revealed a major quantitative-trait-locus (QTL) at which, among 18 annotated genes, an ortholog of histone H4 acetyltransferase *ESA1* was located. Rye individuals belonging to domesticated subpopulations showed increased synaptonemal complex length, but no difference in crossover frequency, indicating that only the recombination landscape is different. Furthermore, the genomic region harbouring rye *ScESA1* showed moderate patterns of selection in domesticated subpopulations, suggesting that larger LR regions were indirectly selected for during domestication to achieve more homogeneous populations for agricultural use.

Abstract ID: 1888

Major shifts in the recombination landscape and their consequences for barriers to gene flow

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Major changes to the recombination landscape can arise through structural mutations including chromosome fusions, segmental duplications and inversions. These changes have downstream consequences for evolutionary processes including adaptation and speciation. In this talk I will discuss examples from our research on butterflies of distinct mechanisms that alter the recombination landscape – either conditionally or unconditionally – and their population genetic consequences. In particular I will focus on two contrasting case studies: (1) How a series of ancient chromosome fusions altered the recombination landscape of *Heliconius* butterflies, leading to chromosome-wide reductions in diversity and stronger species barriers on the new fused chromosomes. (2) How a combination of segmental duplications and inversions in *Danaus* butterflies facilitate local adaptation in the face of exceptionally high gene flow, but how ongoing low-level recombination leads to occasional emergence of recombinant alleles that may have enhanced fitness.

Abstract ID: 2406

Genome structure drives the landscape of introgression from selfing into outcrossing *Capsella*

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Introgression between closely related species is widespread in nature, and ancestry derived from introgression is often deleterious. While empirical studies continue to confirm the role of fine-scale recombination in shaping introgressed ancestry through linked selection, recent theoretical work has highlighted this contribution of recombination at different scales. Here we focus on introgression from a recently derived selfing plant, *Capsella rubella,* into the outcrossing *Capsella grandiflora,* with large samples from natural populations. We test the hypothesis that recombination acts on different scales, finding that introgressed ancestry is strongly correlated with fine-scale recombination on fine and broad genomic scales, but that introgressed ancestry also differs substantially beyond this at the level of the chromosome arm. We draw from previous theoretical predictions and use simulations to show that crossovers on short arms have a bigger effect on genomic mixing than crossovers on long arms, leading to our observation of more introgressed ancestry on short chromosome arms beyond what we would expect from differences in recombination rate. We additionally test for the source of selection, focussing on fine-mapped mating system loci and genetic load differences between the species, rooted in expectations about the evolution of mating system. By parsing out the effects of recombination and selection in shaping introgressed ancestry at various scales, this work broadens our understanding of how and when introgressed ancestry is purged, both at the level of the crossover and the fine-scale differences in recombination rate.

Abstract ID: 2000

Evolution of genomic landscape of diversification in peatmosses

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Species accumulate genetic differences with time since their divergence. Variation in distribution of genetic differentiation along the genome has long been interpreted as the result of speciation-with-gene-flow, where divergent selection creates differentiated loci that become impermeable by gene flow. However, an increasing number of studies show that adaptation and speciation may be irrelevant for the evolution of the heterogeneous differentiation landscape that instead originates through indirect effects of selection constrained by intrinsic properties of the genome, such as recombination. These evolutionary models are not incompatible, and their genomic signatures are very difficult to disentangle. Here, we aim to identify which of these models better explain genome evolution during the diversification of peatmosses (*Sphagnum*), a highly diverse, rapidly radiated group of early land plants. Peatmosses have small haploid genomes with fairly conserved size and chromosome numbers. Using low-depth whole-genome sequencing data from populations of 12 species, we describe high correlation of the genomic landscapes of differentiation, divergence and diversity in *Sphagnum*. Our results suggest that peatmoss genome evolution is driven by conserved genomic architecture, leading to similar outcomes of selection in different species, rather than by processes directly related to speciation. We discuss how speciation in peatmosses stem from a complex

interplay between long-term effects of linked selection, incomplete lineage sorting, and genomic architecture, propelled by gene exchange at its earlier stages. Our study supports the growing evidence highlighting the importance of focus on genomic architecture in studies of speciation, especially in non-model organisms.

Abstract ID: 1176

The impact of recombination rate dynamics on signatures of indirect and direct selection

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Recombination is a central evolutionary process that reshuffles combinations of alleles along chromosomes, and as a consequence is expected to influence the efficacy of direct selection via Hill-Robertson interference. Additionally, the indirect effects of selection on neutral genetic diversity are expected to show a negative relationship with recombination rate, as background selection and genetic hitchhiking are stronger when recombination rate is low. However, owing to the limited availability of fine-scale recombination rate estimates across a wide range of species, less is known about the impact of evolutionary changes in recombination rate on genomic signatures of selection. To address this question, we estimate fine-scale recombination rate from patterns of linkage-disequilibrium in two *Ficedula* flycatcher species: taiga flycatcher (*F. albicilla*) and collared flycatcher (*F. albicollis*). This reveals that recombination rate is significantly correlated between the two species, which corresponds with the predicted evolutionary stability of recombination in birds. Nevertheless, lineage-specific patterns occur and allow us to address the impact of recombination dynamics on different measures of selection. We show that lineage-specific recombination rate is strongly correlated with measures of indirect selection, and that the dynamics of recombination rate between species have observable impacts on this relationship. Conversely, measures of direct selection on coding sequences show little to no relationship with recombination rate, even when restricted to genes with stable recombination rate. Thus, using measures of indirect and direct selection that bridge micro- and macro-evolutionary timescales, we demonstrate that the role of recombination rate and its dynamics varies for different measures of selection.

Abstract ID: 1267

The influence of genetic dosage on PRDM9-dependent evolutionary dynamics of meiotic recombination

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Meiosis is an important step in the eukaryotic life cycle during which recombination and proper chromosome segregation takes place. In mammals, recombination is regulated by the Prdm9 gene. This gene, which possesses a double function (recruitment of the double strand break machinery and facilitation of the pairing of homologous chromosomes), induces an intra-genomic Red Queen resulting from the opposition of two antagonistic forces : erosion of the recombination landscape by biased gene

conversion and positive selection on Prdm9. This Red Queen was previously modeled, but without taking into account the role of PRDM9 as a pairing facilitator. Accordingly, I developed a mechanistic model taking into account the dual role of PRDM9. This modeling work gives important insights into the Red Queen mechanism, thus completing previous studies. In particular, it reveals that positive selection of new PRDM9 alleles is due to the reduced symmetrical binding caused by the loss of high affinity binding sites and, on the other hand, it demonstrate the influence of the genetic dosage of PRDM9 on the dynamics of the Red Queen, which can result in negative selection on new PRDM9 alleles entering the population.

Abstract ID: 1851

Reduced selective interference increases experimental adaptive rates in *C. elegans*

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Theory suggests that by reducing selective interference recombination increases adaptive
rates. Here, we use experimental evolution in Caenorhabditis elegans populations with alternative modifiers of the recombination rate landscape to test for adaptation. This nematode
exhibits a wild-type recombination landscape with low recombination rates in chromosomal
centers and high recombination rates chromosomal arms. Loss of function of the rec-1 gene
equalizes recombination rates between centers and arms, without changes in the total recombination map length. Further, in our populations, most fitness loci are located in the chromosomal arms. We challenged C. elegans populations with standing genetic variation but
different rec-1 alleles (wild-type vs. loss-of-function mutant) to a novel environment. After 40
generations of evolution, we measured a fitness-proxy and, during the experiment, patterns of
genome-wide SNP allele frequency change. These data indicate that the wild-type rec-1 allele
increases adaptive rates by decreasing the extent selection interference, thus confirming theoretical expectations.

Symposium: S31. Limits to adaptation: linking evolution, ecology, and genetics (id: 956)

Abstract ID: 2274

Limits to plasmid-driven adaptation of bacterial populations

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Plasmids are a pivotal part of the genetics and evolution of many bacterial species. Especially, plasmids may carry genes coding for beneficial traits and thus contribute to adaptation of bacterial populations to environmental stress. Many types of plasmids can horizontally transfer between cells, even crossing species boundaries, which a priori facilitates the spread of adaptive alleles on plasmids. However, plasmid-driven adaptation is also subject to a range of constraints. Competition between plasmids can limit horizontal transfer; a decline of the plasmid-free population due to environmental stress entails a decrease in the targets for transfer, making it less and less efficient over time; for multicopy plasmids, segregation of plasmid copies at cell division adds an extra-layer of drift, affecting the spread of beneficial mutations. Moreover, at the level of bacterial cells, intra- and inter-species interactions influence the evolutionary dynamics. In this talk, we will present eco-evolutionary models for plasmid-driven adaptation that allow us to quantify the strengths of the various constraints and to disentangle the benefits and limits of horizontal gene transfer. The analysis reveals subtle complexities in the effects of horizontal gene transfer on plasmid-driven evolutionary rescue in the presence of plasmid competition and plasmid costs. We finally discuss a model for the evolution of antibiotic drug resistance in the human gut via transfer of a resistance plasmid from commensal to pathogenic bacteria, accounting for ecological interactions between the two species and antibiotic treatment.

Abstract ID: 2315

A theory of multi-site evolutionary rescue/resistance applied to gene drive suppresion systems

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Evolution of resistance is a major barrier to successful deployment of gene drive systems to suppress natural populations, which could greatly reduce the burden of many vector borne diseases. Multiplexed guide RNAs that require resistance mutations in all target cut sites is a promising anti-resistance strategy, since in principle resistance would only arise in unrealistically large populations. The role of standing variation is poorly understood in this context — at single sites it is well-known population rescue/resistance is more likely to arise from from standing variation than from de novo mutation, though the effect is logarithmically weak (Hermisson & Pennings, 2005). Using novel stochastic Wright-Fisher simulations that accurately model evolution at very large population sizes, we explore this question. Our results highlight the complexity of the mutation-selection-drift balance between haplotypes with complete resistance and those with an incomplete number of resistant alleles. We find this leads to a qualitatively new phenomenon where in the presence of weakly deleterious natural genetic variation the probability of multi-site resistance is very greatly amplified compared to de novo mutation. Although an exact theory of multi-site resistance is difficult for technical reasons, we use heuristic arguments to derive the correct scaling behaviour for the dependence of critical population size on the fitness cost. This theory has broad application to resistance arising in many multi-site evolutionary scenarios including multi-drug resistance to antibiotics, antivirals and cancer treatments, as well as the evolution of vaccine escape mutations in large populations.

Abstract ID: 1621

Snake time machine: investigating constraints on evolution through ancestral protein resurrection

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The repeated evolution of resistance to widespread toxins collectively known as cardiotonic steroids represents one of the clearest examples of natural selection. Numerous plants and animals across the globe are chemically defended by these toxins, which target the vital protein Na+K+ATPase (NKA). In response, many herbivores and predators evolved resistance through target-site insensitivity of NKA. This adaptation has been repeatedly achieved by one or two amino acid substitutions at the same sites in the protein and has demonstrated remarkable patterns of convergence, divergence, and parallelism. Such patterns are expected to be shaped by the degree of pleiotropy (i.e. effect of a mutation on multiple traits) and intramolecular epistasis (i.e. nonadditive interactions between mutant sites in the protein). We evaluate the extent to which these factors constrained the evolution of this adaptation in a group of animals that have repeatedly gained it: snakes. We asked whether substitutions gained over time at other sites in the NKA permitted the adaptive effects of resistance-producing ones or allowed the protein to tolerate any deleterious effects of resistance on its normal function. We answer this question by statistically reconstructing and experimentally resurrecting ancestral snake NKA at key evolutionary steps. We then moved modern resistance-producing substitutions onto the increasingly more ancient genetic backgrounds to measure how their effects on resistance and protein function change. We found compelling evidence that epistasis and pleiotropy were significant constraining factors in the evolution of resistance. Our results help explain the adaptation patterns observed in resistant snakes.

Abstract ID: 1524

Experimental co-evolution reveals demography and selection interact in shaping genetic diversity

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Host-parasite interactions can cause strong demographic fluctuations accompanied by selective sweeps of resistance/infectivity alleles. Both demographic bottlenecks and frequent sweeps reduce the amount of segregating genetic variation and therefore constrain adaption during co-evolution. Recent studies, however, suggest that the interaction of demographic and selective processes may facilitate the rebuild of genetic diversity. Here, we provide direct experimental testing of this hypothesis by disentangling the effect of demography, selection, and of their interaction in a lab-raised host-parasite system. We grew 12 populations of unicellular algae (*Chlorella variabilis*) that experienced either growth followed by constant population sizes (x3), demographic fluctuations (x3), selection through exposure to a virus (x3), or demographic fluctuations together with virus-induced selection (x3). After 50 days, we sampled aliquots from each algal population and conducted whole-genome sequencing. We observed more genetic diversity in populations that jointly experienced selection and demographic fluctuations than in populations where these processes were experimentally separated. Our results strengthen the hypothesis that eco-evolutionary feedbacks promote the rebuild of genetic diversity during host-parasite interactions.

Abstract ID: 1907

Bottlenecks can constrain evolutionary paths

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Population bottlenecks are commonplace in experimental evolution, specifically in serial passaging experiments where microbial populations alternate between growth phases and subsampling. Natural populations also experience such fluctuations caused by seasonality, resource limitation, or host-to-host transmission for pathogens. Yet, how unlimited growth with periodic bottlenecks influence the adaptation of populations is not fully understood.
Here we study theoretically the effects of bottlenecks on the accessibility of evolutionary paths and on the rate of evolution. We model an asexual population evolving on a minimal fitness landscape consisting in two types of beneficial mutations with the documented trade-off between mutation rate and fitness advantage. In the limit of large population sizes and small mutation rates, we show the existence of a unique most likely evolutionary scenario, determined by the size of the wild-type population at the beginning and at the end of each cycle. These two key demographic parameters determine which adaptive paths may be taken by the evolving population by controlling the supply of mutants during growth and the loss of mutations in the bottleneck.
We not only show that bottlenecks act as a deterministic control of evolutionary paths but also that on such a simple landscape, each possible evolutionary scenario can be forced

to occur by tuning demographic parameters. This work clarifies the effects of demographic parameters on adaptation of periodically bottlenecked populations and can guide the design of evolution experiments.

Abstract ID: 1358

Evolutionary rescue in a fluctuating environment

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Microbes evolve in an environment that is never truly constant. For example, this is the case for a population undergoing antibiotic treatment, when the concentration successively goes below and above the minimum inhibitory concentration. Such fluctuations have a non-trivial effect on evolutionary dynamics, especially when the extinction and environmental time scales are similar. Whereas the impact of deterministic changes has been studied, the impact of stochastic changes is not well understood. To investigate this question, we develop a model in which a population evolves in an environment switching successively between two states: one in which it declines toward extinction, the other in which it grows until reaching its equilibrium size. By combining numerical and analytical approaches, we shed light on two regimes delimited by the mean extinction time in the stressing environment. If the duration of each environmental phase is much shorter than this time, the stochastic switches strongly reduce the persistence time of a population and thus its probability to be rescued by a mutation, compared to deterministic ones. The opposite occurs in the second regime, where environmental time scales are larger than those of extinction in the stressing phase. We derive and validate with simulations analytical predictions of the mean extinction time, the probability of rescue, and the appearance time of a successful mutant. Our work takes an important step towards quantifying evolutionary dynamics in fluctuating environments that could, for example, improve our understanding of the evolution of antimicrobial resistance.

Abstract ID: 981

Evolutionary trade-offs between heat and cold tolerance limit responses to fluctuating climates

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The evolutionary potential of species to cope with short-term temperature fluctuations during reproduction is critical to predicting responses to future climate change. Despite this, vertebrate research has focused on reproduction under high or low temperatures in relatively stable temperate climates. Here, we characterize the genetic basis of reproductive thermal tolerance to temperature fluctuations in the ostrich that lives in variable environments in tropical and sub-tropical Africa. Both heat and cold tolerance were under selection and heritable, indicating the potential for evolutionary responses to

mean temperature change. However, we found evidence for a negative, genetic correlation between heat and cold tolerance that should limit the potential for adaptation to fluctuating temperatures. Genetic constraints between heat and cold tolerance appears a crucial, yet underappreciated, factor influencing responses to climate change.

Abstract ID: 1896

Limited host availability disrupts the genetic correlation between virulence and transmission

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Virulence is expected to be linked to parasite fitness via transmission. However, it is not clear whether this relationship is genetically determined, nor whether it holds under different opportunities for transmission. We address this issue in the macro-parasitic spider mite *Tetranychus urticae* on their host, bean. We used inbred lines to disentangle genetic vs non-genetic correlations among traits and varied parasite density and opportunities for transmission. When transmission to uninfected hosts was permitted during the infection period, virulence was positively and genetically correlated to the number of transmitting stages produced. Hence, highly virulent genotypes are expected to produce more transmitting stages during the infection period, having thus higher fitness. Yet, when transmission was restricted to the end of the infection period, we observed a negative relationship between virulence and the number of transmitting stages produced, driven by density dependence, and no genetic correlation between these traits. This suggests that within-host density dependence caused by limited host availability disrupts the genetic correlation between virulence and the production of transmitting stages, hampering selection for higher virulence. Such results may provide a novel explanation as to why limited host availability leads to lower virulence.

Abstract ID: 1536

Unraveling the genetic basis of host specific adaptations in polyphagous butterflies

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Species interactions represent one of the central topics in biological research. However, despite their ecological and economical significance only little is known about the genetic patterns underlying adaptations that allow or limit these interactions. While specialist insects are often strongly adapted to only one host species or family, polyphagous species need to cope with a larger physical and chemical variety of host plants. This diversity can represent a challenge and requires a flexible set of adaptations, since the simultaneous expression of all genes necessary for the utilization of the entire host repertoire would be detrimental and costly. Previous studies rather showed host specific modules of co-expressed genes that differed in their degree of modularity (i.e. overlapping gene expression profiles) among different host plants. To further investigate this host specific gene expression, host switch experiments combined with RNA-

sequencing, and a short-term selection experiment were performed using the polyphagous comma butterfly *(Polygonia c-album).* Besides confirming the presence of host specific gene expression profiles, the selection experiment revealed a performance hierarchy between different host plants that is consistent with physiological trade-offs. Associated expression patterns further elucidated the stability of gene expression modules over multiple generations. Understanding the role of host specific gene expression and evolving modularity in environmental specific adaptations will provide new insights into the mechanisms underlying phylogenetic recurrence and host conservatism. Given the strong resemblance between insect-plant and parasite-host interactions, this will significantly increase our knowledge and the predictability of species interaction dynamics.

Abstract ID: 1008

Sexual dimorphism driven by intersexual resource competition:Why is it rare and where to look for it

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Sexes often differ more obviously in secondary sexual characteristics than in traits that appear naturally selected, despite conceivable benefits to intersexual niche partitioning. The scale of mating competition and spatial variation in resource availability may help predict sexually dimorphic niches or the lack thereof. We investigate why and when dimorphism might fail to evolve even if genetic covariation between the sexes posed no constraint. Our analytical model incorporates the first aspect of spatial interactions (scale of mating competition). It is followed by simulations that explore broader conditions, including multiple resources with habitat heterogeneity, genetic correlations, and non-Gaussian resource-use efficiency functions. Our results show that sexual niche divergence occurs more readily when local mating groups are small and different resources occur reliably across habitats. Polygyny (medium-sized or large mating groups) can diminish the prospects for dimorphism even if no genetic constraints are present. Habitat heterogeneity typically also disfavors niche dimorphism but can also lead to polymorphism within a sex, if it is beneficial to specialize to be very competitive in one habitat, even at a cost to performance in the other. Sexual conflict is usually used to explain dimorphic traits or behaviors. Our models highlight that introducing conflict can also be responsible for sexual monomorphism. Under monogamy, males benefit from specializing to consume other resources than what feeds the female best. Polygyny makes males disregard this female benefit, and both sexes compete for the most profitable resource, leading to overlapping niches.

Abstract ID: 2015

Allometry constrains the evolution of sexual dimorphism in *Drosophila* across 33 million years

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Sexual dimorphism is widely viewed as adaptive, reflecting the evolution of males and females toward divergent fitness optima. However, the evolution of sexual dimorphism may often be limited by the shared genetic architecture of the sexes. We previously showed that cross-sex genetic covariances have the potential to constrain the evolution of sexual dimorphism within a single species of Drosophila, potentially explaining the remarkable evolutionary stasis of Drosophila wings across macro-evolutionary time. Here we investigate whether dimorphism evolution is actually limited. We studied the evolution of sexual size dimorphism, shape dimorphism, and their allometric relationship, in the wings of 82 taxa in the family Drosophilidae that have been diverging for at least 33 million years. We found that shape dimorphism among species was similar, with males characterized by longer, thinner wings than females, but we also found evidence that size and shape dimorphism have adapted to different evolutionary optima in different clades on timescales of about 10 million years. Both within and among species allometry had a key role in limiting dimorphism evolution. Allometry constrained the evolution of shape dimorphism for the two most variable traits we studied, but dimorphism was evolutionary labile in other traits. The keys for disentangling alternative explanations for dimorphism evolution and its limits are studies of natural and sexual selection, together with a deeper understanding of how microevolutionary parameters of evolvability relate to macroevolutionary patterns of divergence.

Abstract ID: 1118

Divergently evolved yeast generate hybrid offspring resilient to a large range of environments

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Natural habitats are rapidly changing due to climate change and globalisation. This can break down mating barriers between species and lead to increased hybridisation rates. How detrimental or beneficial hybridisation is for fitness and adaptation depends on genetic and environmental factors. Here, we use the power of experimental evolution with the model system yeast to investigate at what level of parental divergence the genetic variation gained through hybridisation can assist populations with adaptation, across a large range of stressful environments. We made F1 and F2 'hybrid' crosses between populations evolving in the laboratory for up to 1000 generations at five timepoints of divergence. We compared the fitness of parents and hybrids in 50 stressful, mostly novel, environments. Heterosis in F1 hybrids strongly increased with increasing time since parental divergence (from 19.5% at 100 generations to 66% at 1000 generations), and we found strong parallelism between replicate hybrid populations. Interestingly, the range of stressful environments in which F2 hybrids were more fit than both parents (positive transgression) also significantly increased with parental divergence (from 2.75% to 10.75%), in two of the three crosses. Increasing heterosis and transgression were not explained by the performance of parents in novel environments, which remained largely the same across generations. Our work provides evidence from an evolution experiment that benefits of outbreeding can emerge quickly, only after a few hundred generations of parental divergence *in vitro*, highlighting the important role that hybridisation can play in adaptation to novel environments.

Abstract ID: 1280

Sexual reproduction constrains adaptation in outcrossed populations of *Chlamydomonas reinhardtii*

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Adaptation to novel environments is often constrained by the presence of genetic variation. One way that populations can overcome such constraints is by reshuffling genetic variation through sexual reproduction. Recent experimental studies have repeatedly demonstrated how sexual reproduction may therefore facilitate adaptation. Yet such sexual reproduction may also limit adaptation, if recombination disrupts adaptive allele combinations, thus preventing effective selection in the population. We performed a set of experiments in which we assessed the costs and benefits of sexual reproduction during experimental evolution of the green alga *Chlamydomonas reinhardtii* when subjected to environmental stress. We investigated how the frequency of sexual reproduction, as well as the complexity of the environmental stress affected adaptation in replicated evolving populations. We found that in outcrossed populations, increasing the frequency of sexual reproduction limited the adaptive potential, to the point that the populations experiencing the highest frequency of sexual reproduction showed little sign of adaptation. This negative effect of sexual reproduction occurred however mostly under relatively simple environmental stress. When we changed the environment during experimental evolution from a simple stress (adaptation to one chemical change in the environment) to a more complex stress (three chemical changes in the environment), we observed that sexual reproduction became more advantageous, leading to faster adaptation in the sexually reproducing populations in the complex environments.

Abstract ID: 1531

Polygenic adaptation to a new environment under self–fertilisation

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Many quantitative traits are likely subject to polygenic selection, where many genetic variants influence them. Elucidating the dynamics of polygenic selection is currently a major focus of both theoretical and empirical evolutionary genetics research. The role of the mating system is often overlooked in these studies; it is important to consider it as many natural populations often reproduce uniparentally to some degree. It can fundamentally change the dynamics of polygenic selection by increasing homozygosity within a population, which also weakens the efficacy of recombination. We present results arising from a computational model of a population experiencing different levels of self–fertilisation, as it adapts to an environmental change. Mutations either affect a single

trait, or pleiotropically affect multiple traits. We investigate how self–fertilisation either helps or hinders adaptation to a new environment, and how it affects the distribution of selected mutations throughout the genome. We show that polygenic selection under self-fertilisation does lead to the formation of highly identical haplotype blocks, with the genetic composition being affected by the underlying pleiotropy and presence of background selection. This project demonstrates how the mating system interacts with selected variants present genome-wide to affect adaptation to a changing environment.

Abstract ID: 1625

Short-term adaptation with epistasis from standing variation in recombining populations

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How does standing genetic variation affect polygenic adaptation in recombining populations? Despite a large body of work in quantitative genetics, epistatic (i.e., genetic-background-dependent) and weak additive fitness effects among simultaneously segregating genetic variants are not easily captured experimentally or predicted theoretically. In this study, we simulated adaptation on probabilistic fitness landscapes (of the Rough-Mount-Fuji type) that is driven by standing genetic variation in recombining populations. We observe that high recombination rates facilitate rapid fixation but feature smaller fitness increases as fitness landscapes become larger and more epistatic. This trade-off between fixation time and fitness change is more obvious in large populations. To survey the effect of epistasis on the fixation of directionally selected alleles, we assume that the minor alleles are under positive directional selection. With little epistasis, minor alleles are fixed at high probability due to their direct selective advantage which is not obscured by epistasis. With strong epistasis, minor alleles tend to become fixed only if their initial frequency is high. On the contrary, low-frequency alleles are eliminated more quickly even if they are overall beneficial because genotypes with more intermediate- and high- frequency alleles have a higher marginal fitness. Our study highlights that both recombination rates and starting allele frequencies constrain the adaptive process in a new environment, and that epistasis can speed up adaptation from standing genetic variation by fixing relatively better genotypes.

Abstract ID: 1139

Exploring the limits of thermal tolerance in an Antarctic bacterium

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Global temperatures are gradually increasing as a result of the ongoing climate change. However, climate change is associated with an increase in the frequency and length of extreme heat waves, which cause sudden local high temperatures that can exceed the upper thermal tolerance of organisms. It is not well known whether upper thermal limits

can rapidly evolve, neither if there exist hard physiological limits that constrain their extension. To study the evolvability of upper thermal tolerance we designed an experiment that aimed to facilitate adaptation as much as possible. We used the Antarctic bacterium *Pseudoalteromonas haloplanktis,* a bacterium that lives at temperatures that are several degrees below its upper thermal limit, which can facilitate adaptation to rising temperatures. We challenged 30 populations of *P. haloplanktis* to adapt to gradually increasing temperatures, reaching 30°C, above the ancestor's upper thermal limit. We observed a high degree of parallel evolution among clones adapted to high temperatures. Higher temperatures coincide with the appearance of mutations in the protease Lon, involved in the degradation of mutant and misfolded proteins. However, populations could not grow at temperatures higher than 30°C, suggesting the existence of a hard physiological limit caused by protein misfolding. Our results suggest a low evolutionary potential of upper thermal tolerance, which makes evolutionary rescue very difficult even under the favourable conditions of our experiment. We predict that evolutionary rescue will be even harder in small populations of large individuals living at temperatures close to their upper thermal limits.

Abstract ID: 2302

Condition-dependence modulates sexual conflict and its demographic consequences

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Sexual conflict arises when males evolve traits that improve their mating success but in so doing harm females. By reducing female fitness, male harm can impair recruitment and even lead to population extinction. Current theory on harm is based on the assumption that an individual's phenotype is entirely determined by its genotype. But most sexually selected traits show condition-dependent expression such that individuals in better condition can express more extravagant phenotypes. Here, we develop demographically explicit models of sexual conflict evolution where individuals vary in their condition. We show that condition-dependent expression readily evolves for traits underlying sexual conflict, so that conflict is more intense in populations where individuals are in better condition. This intensified conflict can reduce mean fitness and thus generate a negative association between condition and population size. We find that the impact of condition on demography is particularly deleterious where condition has a genetic basis that coevolves with sexual conflict. This occurs because sexual selection favours alleles that improve condition (the "good genes" effect), producing a feedback between condition and sexual conflict that drives the evolution of intense male harm. More broadly, our results suggest that the good genes effect via sexual interactions leads at best to limited improvements in mean fitness, and may in fact be detrimental if not fatal in the presence of male harm

Symposium: S32. Inferring macroevolutionary patterns from microevolutionary processes: methods and practices (id: 22)

Abstract ID: 1194

Rates of evolution: Interpretation, measurement and microevolutionary models.

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Beyond a few generations evolutionary change rarely resembles a regular trend, but become stochastic with huge variations in both rate and direction. These variations are such that change is often independent of time span, rendering conventional rate measures meaningless. In this talk I discuss the microevolutionary underpinning of this and consider issues in measuring and testing hypotheses about the tempo and mode of evolution.

Abstract ID: 1737

Detecting macroevolutionary signatures of the Bogert effect

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Behavior is one of the major architects of evolution: by behaviorally modifying how they interact with their environments, organisms can influence natural selection, amplifying it in some cases and dampening it in others. Regulatory behaviors (like thermo- and hydroregulation) can buffer organisms from selection and limit physiological evolution, a concept known as the “Bogert effect” or “behavioral inertia”. We illustrate recent progress on the Bogert effect in evolutionary research, and discuss the ecological variables that predict whether and how strongly the phenomenon unfolds. Modern comparative approaches can help put the macroevolutionary implications of behavioral buffering to the test: we describe progress to date, and areas ripe for future investigation. We illustrate, for example, how different model-fitting procedures can be used to test hypotheses about Bogert effect across macroevolutionary scales. Despite many conceptual, empirical, and methodological advances, the macroevolutionary signatures of the Bogert effect remain little explored, leaving wide open many avenues for deeper exploration.

Abstract ID: 1266

Bridging the gap between population genomic and phylogenetic approaches

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The availability of an increasing amount of genetic data has resulted in a boom in molecular evolution studies in recent years and a better elucidation of evolutionary mechanisms such as genetic drift.

The intensity of the genetic drift is inversely proportional to the number of breeders in the population, i.e. the effective size (Ne).
It can impact both short and long term evolutionary processes (estimated respectively from polymorphism and divergence data). The aim of my work is to contrast intraspecific and interspecific data in order to bridge the gap between population genomic and phylogenetic analyses.
In this study, I estimate variations in Ne between species based on genome-wide heterozygosity, correcting for variations in mutation rate (μ), along the mammalian phylogeny in order to study correlations between Ne, ecological traits and molecular traits such as selection intensity (both long term, based on dN/dS, and short-term, based on piN/piS).
For this purpose, I devised a pipeline from the recovery of orthologous gene sequences, ecological and heterozygosity data to Bayesian integrative analysis aiming at reconstructing Ne by a multivariate process (1). I observe that the Ne of very massive animals is much smaller than the Ne of small mammals. I obtain positive corelations between dN/dS and life history traits, consistent with previous analyses (2) and suggestive of a role of Ne. The more direct correlation of traits with heterozygosity and Ne is still under investigation.
1.Brevet, M. & Lartillot, N. (2021)
2.Figuet, E. et al (2016).

Abstract ID: 1351

What controls rates of diversification and diversity across the tree of Life?

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What explains variation in rates of diversification and diversity across the tree of Life and across the globe? To bridge the gap between micro- and macro- in our understanding of speciation requires models that explicitly consider speciation as a process with several sequential steps that take time to complete rather than being instantaneous. Such a model is the protracted speciation model of Etienne & Rosindell (2012). My own contribution has been to analytically explore the implications of this model for our understanding of how the rates of different steps in the speciation cycle should theoretically interact to shape variation in rates of diversification across lineages. Rates of diversification are nonlinear functions of the rates of the steps in the speciation cycle, and may often be most strongly under the control of certain key rate-limiting factors. This explains the apparently paradoxical fact that certain predictors of the rates of steps which are theoretically essential to speciation nevertheless do not correlate with rates of speciation across the tree of Life, because they are relatively not the most rate-limiting. I propose that empiricists should examine models aiming to account for variation in rates of diversification/speciation, with multivariate predictors for the rates of different steps in the speciation cycle, and should test for possible nonlinear and interaction effects. Ultimately we would like to understand which microevolutionary processes are relatively most rate-limiting to the speciation cycle.

Abstract ID: 1816

High investment into reproduction is associated with reduced lifespan in dogs.

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Prominent differences in aging among and within species present an evolutionary puzzle. The theories proposed to explain evolutionary differences in aging are based on the axiom that selection maximizes fitness, not necessarily lifespan. This implies trade-offs between investment into self-maintenance and investment into reproduction, where high investment into growth and current reproduction are associated with short lifespans. Fast growth and large adult size are related with shorter lifespans in the domestic dog, however whether reproduction influences lifespan remains unknown. The domestic dog is a burgeoning model in aging research, in addition it is at the interface between micro and macroevolutionary processes. Here we test the relationship between reproduction and differences in lifespan among dog breeds, controlling simultaneously for shared ancestry and recent gene flow. We found that shared ancestry explains a higher proportion of the among-breed variation in key life history traits, in comparison with recent gene flow. Our results also show that reproductive investment negatively impacts lifespan, and more strongly so in large breeds, an effect that is not merely a correlated response of adult size. These results suggest that basic life history trade-offs are apparent in a domestic animal whose diversity is the result of artificial selection and that among-breed differences in lifespan are due to a combination of size and reproduction.

Abstract ID: 2410

Beyond the M*k* model for studying discrete character evolution on trees

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For more than 20 years the predominant model for the evolution of discrete character evolution on phylogenetic trees has been a simple continuous-time Markov model typically referred to as the (extended) M*k* model. Although mathematically convenient, this model is not particularly well-matched to the microevolutionary processes within phylogenetic lineages that most evolutionary biologists suspect underlie trait evolution in macroevolutionary time. Here, I present several interesting discrete character evolution models that may help to more realistically capture microevolutionary forces in the pattern of macroevolutionary trait data on a phylogeny. I describe how these different models have been implemented in my R package, *phytools*, as well as how they can be applied to study trait correlation, model heterogeneity through time or among lineages, and reconstruct ancestral states.

Abstract ID: 1253

The rock record turns trait evolution into apparent stasis and punctuated equilibrium

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The fossil record allows to trace evolution of morphological traits within lineages over millions of years. Statistical analyses have identified stasis as the dominant mode of trait evolution in the fossil record. However, the microevolutionary processes generating this pattern are still debated.
We combine models on trait evolution and the formation of the rock record to show that trait evolution observed in the fossil record will always appear more similar to stasis and punctuated equilibrium than the underlying evolutionary change in time. Both stratigraphic incompleteness and variability in sediment accumulation generate long stretches of apparent stasis, interrupted by short intervals of apparent increased evolutionary volatility. The extent of these effects differs between depositional environments and changes predictably throughout stratigraphic sections.
Our results demonstrate that reading the rock record at face value will inflate the importance of both stasis and punctuations. Evolutionary change observed in the fossil record is a joint expression of geological and biological processes. We argue that information on the local geological context of fossil time series can be used to disentangle the biasing effects of the rock record from the evolutionary change recorded in the fossil record.

Abstract ID: 1717

The asymmetric brownian motion

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Popular comparative phylogenetic models such as the Brownian Motion, the Ornstein-Ulhenbeck and their derivative, make the hypothesis that at the time of speciation, trait value remains identical between the ancestral and descendant species. This hypothesis contrasts with models of speciation at the micro-evolutionary scale where descendants phenotypic distributions are sub-samples of the ancestral distribution. Various described mechanisms of speciation can lead to a displacement of the ancestral phenotypic mean among descendants as well as an asymmetric inheritance of the ancestral phenotypic variance. In contrast, macro-evolutionary models always assume symmetric and conserved inheritance of the ancestral phenotypic distribution. We propose the Asymmetric Brownian Motion model (ABM) that relaxes the hypothesis of symmetric and conserved inheritance of the ancestral distribution at the time of speciation. Expanding the JIVE framework, it models the evolution of both intra- and inter-specific phenotypic variation. It also allows a continuum of scenarios describing phenotypic distribution inheritance at the time of speciation, from a symmetric and conserved inheritance (both descendants inherit the ancestral distribution) to an asymmetric and displaced inheritance (descendants inherit phenotypic means and variances asymmetrically). The ABM model is a step towards linking micro-evolutionary and macro-evolutionary models of trait evolution. It allows testing the effects of ecological speciation, character

displacement and niche partitioning on trait evolution at the macro-evolutionary scale and also understanding the influence of long-standing processes on recent micro-evolutionary patterns. We present this model as well as its application for understanding the evolution of Darwin finches' beak morphology.

Symposium: S33. Domestication: Fresh insights from ancient genomics (id: 944)

Abstract ID: 1477

Quantifying reproductive isolation between wild and domestic lineages using ancient genomics

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The ubiquity of gene flow between wild and domestic populations has recently been demonstrated in a wide variety of plants and animals using ancient genomics. Many of these studies have shown that domestic populations of different species adsorbed genetic variability from their wild relatives as humans dispersed away from the regions in which domestication took place. Interbreeding, however, can have an homogenising effect - in other words, gene flow could prevent the domestic population from sustaining divergent phenotypes from their wild counterparts. Our knowledge of outcrossing between wild and domestic populations, however, is still rudimentary. Here I will present new results based on pigs, dogs, chickens and cats ancient genomes, that demonstrate how the rate at which domestic species interbreed with their wild counterparts varies dramatically across time, space, and species. Combined with archeological evidence, these results help us to clarify the importance of reproductive isolation during different phases of animal domestication.

Abstract ID: 2045

Ancient dogs and modern tricks: Tracing patterns of selection and trait evolution in ancient dogs

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As the first domesticated species, dogs have existed for more than 11,000 years. Ancient DNA has provided a unique resource to elucidate past demographic processes and selection events, and their legacy on modern dog phenotypic variation. For this study, we analysed admixture and selection patterns on ancestral dog groups across Eurasia and traced the spatiotemporal movement of alleles associated with phenotypic traits using 42 ancient samples and hundreds of modern dog genomes. To account for the genotype uncertainty inherent to low-quality ancient sequences, we implemented a novel approach to impute low coverage genomes utilizing large dog reference panels. We benchmarked this method by down-sampling the coverage of genomes from different ancient dog populations, to evaluate its accuracy for imputing genotypes. We subsequently carried out a series of selection scans, using the programme Ohana, to account for the complex history of canines, characterized by multiple admixture events. Candidate selected regions were detected, putatively driven by changes in the climate and the lifestyle of humans to which dogs adapted to throughout different periods. These were subsequently traced over time using a time-series model of natural selection. For example, selected regions associated with metabolism and diseases were found along the ancestral component shared between ancient and modern Siberian and Greenlandic dogs. Such traits would potentially provide an advantage in the Arctic climate. Our study provides new insights on the evolution of dog phenotypic traits by applying novel approaches that are now within reach, thanks to new methodologies for imputation and demography-aware selection scanning.

Abstract ID: 2384

Genomes of ancient iberian dogs – a story with at least 7,600 years

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Native dogs from Iberia can be grouped into 21 internationally recognized breeds, including local varieties within breeds, and the analysis of genetic markers showed particularities of their diversity. However, the present allele distribution is the consequence of a long and intricate process of evolution. Indisputable evidence for the presence of dogs in Iberia relies on the retrieval of two almost complete dog skeletons dated to the Mesolithic (~7,600 cal BP). The recovery of genomes from ancient specimens combined with data from other research areas such as zooarchaeology, veterinary and history can contribute to the understanding of these processes. We carried out a diachronic genomic study of 14 dog remains collected in the Iberian Peninsula dated from the Mesolithic to the Medieval (Christian) period. Whole-genome shotgun resequencing data were obtained and the endogenous DNA content ranged from 0.25 to 5%. We determined the phylogeny of the maternal lineages and inferred the population structure by means of a principal component analysis and NGSadmix based on genotype likelihoods. We found an over-representation of males in the archaeological record - 10 males versus 4 females. We identified the presence of the major dog maternal haplogroups A, B and C, since early times. We will also discuss the results of the population structure analyses of ancient genomes in the context of 42 reference genomes representative of 10 extant Iberian and African dog breeds, as well as wild Iberian wolves.

Abstract ID: 1574

The complex genomics of Neolithic domestic pigs and European wild boar in Northwest Europe

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Recent research showed that the West Asian genomic fraction in Neolithic domesticated pigs was replaced by European wild boar genomes- a process that took several centuries following their arrival in Europe. Understanding how this genomic turnover unfolded can provide interesting insights into early domestication history. But this phenomenon remains largely unexplored, particularly in Northwest Europe. To address this, we generated 12 complete mitochondrial sequences and 12 whole genome sequences (0.02-6x) from The Netherlands (9, including 3 medium coverage whole genome sequences from a single site), England (1) and Ireland (2) dating from 5500 to 2500 BCE. Together they span the centuries before, during and after the emergence of animal husbandry in Northwest Europe. Results show (1), a Mesolithic European wild boar cluster distinct from the European modern wild boar; (2) a gradual decrease of the Mesolithic wild genomic fraction and the gradual increase of the domesticated genomic fraction; (3) and finally, the occurrence of the black coat color associated with domestication in three morphologically domesticated pigs from Rotterdam dating to c. 3800-3300 BCE, each individual displaying a different variety of the mutation, namely homozygous derived, heterozygous, and homozygous ancestral.

Abstract ID: 1393

Paleogenomics reveals the most ancient breeding of equid hybrids in human history

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Paleogenomics adds an important element to the reconstruction of the evolutionary past of species and individuals. This is well exemplified by our paleogenetic study of Asiatic wild asses (*E. hemionus*) whose relict populations do not represent the past extension and population structure of the species. Indeed, most of the populations/subspecies that have existed in the past are extinct at present. Recently, we could show using paleogenomics of 11,000-, 4500- and 100-year-old specimens that the subspecies *E. hemionus hemippus* has roamed the Levant throughout the Holocene. We also showed that entire equids buried in a Bronze-Age elite cemetery in the northern Levant were F1 hybrids of a wild *E. hemionus hemippus* father and a domesticated *E. africanus asinus* mother. These are the first known human-bred hybrids. Based on archaeozoological, iconographic and documentary evidence, we could attribute these hybrid animals to the “kungas” that are described in Mesopotamian cuneiform tablets. These precious and prestigious equids were used in warfare in Syro-Mesopotamia between powerful city-states, as depicted in the famous 4,500-year-old “Standard of Ur”, a Sumerian mosaic exhibited in the British Museum. Previously, we have also shown through a paleogenomic approach that domestic horses were introduced into southwest Asia only by 2000 BCE, i.e., hundreds of years after the production of kungas. This explains why, despite the considerable technical challenge that the breeding of these hybrids represented for the early Mesopotamian societies, they were produced and used by the belligerent elite until they could be replaced by easy-to-breed domestic horses.

Abstract ID: 1733

Sunflower domestication in space and time

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Where and how many times crop plants were domesticated, how quickly genetic diversity is lost during domestication, and how domestication syndromes are assembled through polygenic evolutionary change are questions of active research and frequent debate. We are addressing these questions with archaeological DNA approaches in the common

sunflower, *Helianthus annuus*. Native American farmers living ~4000-5000 years ago began transforming the common sunflower from a highly branched wild plant with small disks and small seeds into a staple oilseed crop that sports a single large head with large seeds on an unbranched stalk. We have assembled a time series of archaeological samples spanning the domesticated period and obtained endogenous DNA sequences from these samples through whole-genome sequencing and sequence capture approaches, revealing how human cultivation altered sunflower genetic diversity through time. Specifically, our analyses help resolve a controversy about where and how many times sunflower was domesticated, highlight how multiple genetic bottlenecks impacted this crop during its history of cultivation, and uncover intriguing patterns of haplotype turnover that suggest shifts in agricultural practices have occurred over this period. In addition, through targeted resequencing of set of candidate domestication genes we defined through population genomics and transcriptomics approaches with extant germplasm, our archaeological times series is informing the timing and order with which selective sweeps occurred and thus insight into how the sunflower domestication syndrome was assembled by Native American farmers through time.

Abstract ID: 2341

The archaeogenomics of cattle from southwestern Europe and The Maghreb

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The processes of cattle domestication and diversification are not fully understood. Taurine cattle were primarily domesticated in the Fertile Crescent around 10,000 years, whereas zebu cattle originated in the Indus Valley approximately 8000 years. Archaeogenomics data allow us to investigate admixture between domestic animals and wild ancestors, changes within populations over time and depict evolutionary trajectories. Indeed, genomic data collected from ancient cattle showed: a rapid spread of zebu after 4200 years, likely associated with an extensive drought in southwest and central Asia; a distinct strain of aurochs gave origin to cattle in the southern Levant, but an independent domestication of North African cattle could not be confirmed. Our team showed that southwestern European breeds retain high genetic diversity despite the notable geographic distance of this territory from the primary domestication centre. The complex origin of Iberian breeds is reflected in their high diversity in: Y-chromosome haplotypes, including Y1 and Y2 haplogroups and unique patrilines; maternal lineages i.e. common European T3-matrilines, T1-lineages and more distinct Q-haplotypes; and significant gene flow from African taurine cattle. This makes southwestern European breeds a great model for investigating cattle diversification. We will discuss archaeogenomics data generated by our team for specimens from this region to address questions such as: did local aurochs contribute to the gene pool of domestic cattle from southwestern Europe and The Maghreb? To which extent these native cattle represent relics from the past? How were local cattle improved by the human cultures that inhabited this region?

Abstract ID: 2351

Addressing the history of a local cattle breed

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Czech Red cattle (CR) is a historical cattle breed with unclear origin that prevailed in the territory of the Czech lands until the 19th century. The breed is today represented by a limited population, which is included in a conservation programme. Like related breeds of the group of mountain red cattle, e.g., Harz Red cattle and Salers, CR is sometimes reported to be associated with the ancient Celtic cattle, however, historical or archaeological evidence is missing. The availability of data on the genetic structure of the extant population allows to check the continuity of genetic development of the local cattle populations in Modern Age and hopefully also in the Medieval Age. The genome-wide sequencing of the representatives of the extant CR breed was performed with HiSeq X Ten technology with 60 x coverage. The variability in the genes of interest is validated by hybrid resequencing of targeted amplicons using the PacBio RSII technology. This knowledge allows to design the genotyping tests for the traits associated with local cattle evolution, like polledness. The neutral polymorphism in non-coding sequences provides a framework for the detection of changes that might be ascribed to the local adaptation. The mitochondrial DNA polymorphism indicates the import of animals from the Balkan region. No signs of introgression from the aurochs population were detected using mtDNA polymorphism to date. In parallel, DNA isolation procedure from fossil finds is being adapted to investigate their genetic markers in the context of the genomic variability of the extant CR population.

Abstract ID: 1819

Reconstructing the genetic history of the extinct aurochs: structure, demography and genomic legacy

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Taurine cattle (Bos taurus) were domesticated from a small group of their wild progenitors, the aurochs (Bos primigenius), in the Near East approximately 10.5KYA. Through the Holocene, early domestic cattle spread with farming across Europe, Asia, and Africa as part of the Neolithic package. Cattle remain among the most economically important livestock animal today. However, population bottlenecking by domestication and breed formation has left the species with greatly reduced genetic diversity. While the last aurochs cow died in 1627, wild and domestic individuals co-existed for thousands of years and there is genetic evidence of sporadic wild introgression. Little is known about the genetic diversity and structure of the wild population, and the extent local introgression may have influenced the modern taurine genome. Here, we present whole-genome data from a diverse collection of Eurasian aurochs spanning the Late Pleistocene through to the Holocene. These geographically and temporally diverse ancient genomes allow us to explore the structure and diversity of aurochs during the Last Glacial Period when populations likely retreated to local refugia. We investigate how wild populations then reacted to the climatic and anthropomorphic habitat restructuring during the Holocene, resulting in a dramatic collapse of genetic isolation between demes. Finally, we examine the genetic legacy of these extinct populations in modern

domesticates and the potential implications for the domestication process of taurine cattle.

Abstract ID: 1632

Population genetics of ancient Iberian sheep: insights on early European sheep populations

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The advent and expansion of husbandry is one of the most important events in human prehistory. Sheep, as the oldest domestic livestock species, has had a key role in this process. The importance of this species during the expansion and later development of husbandry through Europe, however, is less well understood. To elucidate how this expansion happened we sequenced 14 high-quality genomes (up to 9x) from El Portalón de Cueva Mayor, a cave part of the Atapuerca complex in Northern Iberia from the Neolithic to the Middle Ages. We used an extensive reference panel of modern domestic sheep, feral European mouflons, and wild Asiatic mouflons to analyze how these ancient samples relate to modern breeds. We analyzed the relationship between Neolithic sheep from Iberia and other ancient populations across Eurasia, described how their populations changed after their arrival to the Peninsula and how much this original population has contributed to modern breeds, both in Iberia and other parts of Europe. Furthermore, we investigated the presence of wool-related mutations in our ancient samples to elucidate a potential genetic signature of the secondary product revolution. Our preliminary results suggest population continuity through prehistoric times and similar patterns of genomic contribution sourcing from ancient populations into modern European breeds from Europe, including Iberian breeds. These results highlight the complexity of the demographic history of this domesticate during (pre-)historic times.

Abstract ID: 2192

An archaeogenetic perspective into sheep demographic history by analysing Anatolian Neolithic sheep

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Sheep was one of the first farm animals domesticated during the Neolithic Transition within the area ranging from central Anatolia to northwest Iran. Although

zooarchaeological evidence and genetic data from modern breeds hint at a complex demographic history of sheep, we still know little about its population dynamics since the initial steps of domestication. Genetic studies on present-day breeds provide two major patterns. First, high levels of nuclear and mitochondrial DNA diversity are observed, which may indicate that domestication involved multiple centers, or alternatively a large, heterogenous wild population. Secondly, present-day domestic sheep clusters into two groups; west (Europe) and east (Asia, Africa and Mediterranean Islands) based on genome-wide polymorphism data and proportions of mitochondrial haplogroups. However, it is still not very well understood when and how these patterns emerged. Ancient DNA data from the earliest periods of sheep domestication can help to address these questions. Here we present results from our recent work as well as unpublished ancient whole genomes produced from central and west Anatolian ancient sheep ranging from Epipaleolithic (N=1) to late Pottery Neolithic (N=14) periods. We compared these ancient genomes with the published data from modern breeds as well as ancient genomes from Neolithic and Bronze Age Kyrgyzstan sheep. We show that divergence between West and East appeared early, by 6000 BCE, and that the European and Anatolian sheep gene pools changed significantly since the Neolithic period.

Symposium: S34. How have biomarkers improved our understanding of health and the evolution of senescence? (id: 15)

Abstract ID: 1578

Beauty sleep the marmot way: senescence, hibernation and epigenetic age in yellow-bellied marmots

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Senescence or the deterioration of an individual body with age and its related trade-offs are central to life-history theory. Understanding both the drivers and the consequences of senescence is fundamental to understand evolutionary biology but also to many human applications. Using yellow-bellied marmots, we have been investigating several aspect of senescence in the wild using a long-term study approach (over 60 years), showing: decline with age in mass, reproduction, and survival; impact of sociality on longevity; and transgenerational effects of a female age on its daughter reproduction. More recently integrating new biomarker (DNA methylation) allowed us to ask new or more in-depth questions about the drivers, consequences and mechanisms underlying senescence in a hibernating mammal. We showed that epigenetic ageing is not linear with age and more importantly that it slowed down (and might even reverse) during hibernation. In the talk, I will provide an overview of past ageing research in marmots, give detailed insight and explanation of epigenetic aging with hibernation and discuss the importance of new biomarker for our understanding of marmot senescence and new avenues for our research.

Abstract ID: 1486

Reduced insulin signalling in adulthood protects soma and germline under mutation accumulation

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Central to disposable soma theory of ageing is the assumption that trade-offs between survival and reproduction are ubiquitous. Yet an increasing number of empirical studies now demonstrate that lifespan extension is not always dependent on a cost to fecundity. One of the most compelling examples of apparent cost-free lifespan extension is the downregulation of adulthood nutrient-sensing signalling in *C. elegans* nematodes, using *daf-2* RNAi knockdown in adult worms, making them extremely long-lived and stress-resistant with normal reproduction. We tested whether this apparent absence of a trade-off between survival and reproduction, can be explained by the hidden costs of reduced germline maintenance, leading to a trade-off between parental longevity and offspring fitness. We used a multigenerational mutation accumulation (MA) approach to directly compare extinction rate and fitness decline in replicate *daf-2* RNAi and sham control MA lines after inducing germline mutations using UV irradiation. We tested whether increased investment into somatic maintenance via interference with insulin/IGF-1 signalling (IIS) resulted in increased mutation rate, reduced offspring quality and ultimately, faster extinction of long-lived lines. Contrary to predictions, we found reducing IIS in adulthood improved lineage survival, reproduction and fitness across 40 generations. Our results provide support for the developmental theory of ageing, which maintains that the force of selection on gene expression in major regulatory pathways declines with age and suggest that suboptimal gene expression in adulthood is a major driver of senescence.

Abstract ID: 1206

The bright side of aging, as told by *E. coli*

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Aging is a progressive fitness decline driven by the deterioration of intracellular processes. From an evolutionary perspective, it depends on a clear separation between soma and germline, represented by a parent that retains damage to preserve its offspring. Although this definition seems to exclude unicellular organisms, single-cell microscopy advances have shown that aging is present in algae, yeast, and rod-shaped bacteria. Bacteria were long regarded as “immortal” organisms, but even morphologically symmetric *Escherichia coli* display enough physiological asymmetry to produce an equivalent distinction to that of soma/germline. Upon division, the mother cell retains larger loads of non-genetic damage, generating a rejuvenated daughter. This ubiquitousness of aging raises central questions: What is the advantage of aging for bacteria? Which biomarkers do they have in common with complex organisms? Our work demonstrates that bacterial aging is a deterministic process of damage partitioning, but this process is also highly stochastic. This results in large phenotypic heterogeneity, with genetically identical organisms displaying an array of age-related phenotypes within a single population. When environmental pressures are present, aging plays a protective

role by allowing for the survival of rejuvenated offspring. Moreover, through fluorescence microscopy and microfluidics, we tracked aging biomarkers (*e.g.,* protein repair machinery and SOS response) over generations, quantifying their contribution for the aging phenotype. By following the progression of aging along cell lineages, we show that aging hallmarks are shared between bacteria and complex organisms. Thus, aging represents a deterministic driver of phenotypic heterogeneity that is essential for survival in stressful environments.

Abstract ID: 1418

DNA methylation as biomarker of biological age in non-model species

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The assessment of an individual's biological age can be a vital step towards a better understanding of the ageing process, yet developing a comprehensive biomarker has proven difficult. DNA methylation (DNAm) is a dynamic process that regulates gene expression, plays key roles in cell differentiation and development and changes with age. During recent years, changes in methylation at multiple sites across the genomes of numerous non-model species have generated DNAm scores -describing epigenetic age- that correlate remarkably well with chronological age, provide new insights into the ageing process and promise to help us understand the mechanisms behind it. Such clocks also have ecological, evolutionary as well as conservation applications. However, only a handful of studies published so far include longitudinal samples that have the potential to point to sites that are truly variably methylated with age. I will present an overview of how epigenetic clocks have been used so far to access biological ageing in non-model species, and discuss factors affecting how well epigenetic age predicts chronological age. I will in addition present results from my project which aims to develop an epigenetic clock as a robust predictor of biological age in zebra finches (*Taeniopygia guttata*) using longitudinal blood samples. Utilizing this epigenetic clock we will be able to investigate whether environmental manipulations that have been previously found to affect lifespan– namely developmental conditions, foraging conditions and investment in reproduction- similarly affect DNAm dynamics as well as correlate epigenetic age to other, biologically relevant life history traits.

Abstract ID: 2273

Transposable elements mark tissue specific aging in termite workers

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Within social insect colonies, life spans of nestmates often differ by orders of magnitude, although they share the same genetic background. Queens (and in termites, also kings) can live for decades, while workers often have only months to live. In the termite *Macrotermes bellicosus*, we previously found a high expression of transposable elements (TEs) in old compared to young workers, whereas TEs were not expressed in

queens and kings, regardless of age. At the same time, TE defenses of the piRNA pathway were active in queens and kings but downregulated in old workers. Deregulation of TEs could be a biomarker for senescence in termites. To confirm and expand on these results, we sequenced the genome and re-sequenced old and young workers' DNA and RNA, for two tissues. The most abundant TEs were not highly expressed regardless of age. However, TEs in lower copy numbers were up-regulated in old compared young workers. TE expression differed between heads and fat bodies. Our results suggest that the expression of less abundant TEs might be an aging marker in termites.

Abstract ID: 2012

Life experiences and lifespan: are telomeres an important link?

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Much of the variation in longevity is due to environmental effects, but the mechanisms that underlie this link remain poorly understood. Accumulating evidence suggests that one mechanism and/or biomarker that may be important in this context are telomeres. Telomeres are highly conserved, non-coding sections of DNA that form protective caps at chromosome ends that shorten during cell division and in response to stress exposure and are often predictive of lifespan. In evolutionary ecology, telomeres are increasingly used to better understand and predict the long-term consequences of variation in individual life histories. I will review evidence supporting these ideas and suggest important considerations for future research. Identifying mechanisms and/or biomarkers that can predict the long-term impacts of environmental effects are particularly important in the face of climate change and rising levels of human perturbation.

Abstract ID: 1079

Gut microbiome variation and senescence within a natural vertebrate population

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The vertebrate gut microbiome (GM) can vary substantially across individuals within the same natural population and be dynamic over time, with consequences for host health and fitness. However, although many physical systems are known to decline in function with age, the extent to which the GM of wild animals undergoes senescence is largely unknown. Here, we explore the relationship between host age and GM characteristics using data from the long-term study of a discrete natural population of the Seychelles warbler (*Acrocephalus sechellensis*) on Cousin Island. We identify substantial variation in the diversity and composition of the GM across sampled individuals; this is associated

with various environmental and host factors including breeding season and host sex. Preliminary results also show that GM alpha diversity declines with host age and is significantly lower in senescent individuals that are older than 6 years of age. Differences in the phylogenetic structure of the GM are also significantly associated with host age. Further longitudinal sampling will be needed to unpick whether these effects are observed within individuals (which would indicate senescence) or arise due to selective disappearance. Studies that explore how GM characteristics differ across the lifespan may add to our understanding of the causes and consequences of variation in senescence within natural vertebrate populations.

Abstract ID: 1612

'Old-age-genes' as ageing markers in termites

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Many organisms suffer from an almost universal trade-off between fecundity and longevity. However, queens of social insects (termites, ants, and some bees and wasps) have seemingly overcome this trade-off as they can be highly fecund and at the same time live far longer than their non-reproducing workers. This makes social insects promising models in ageing research, offering to provide new insights into how ageing can be delayed to reach such long lifespans.
We studied ageing in queens of the termite *Cryptotermes secundus* by performing transcriptome analyses of samples covering their whole lifespan of over 10 years. In line with survival analyses, co-expression analyses revealed non-gradual ageing characterized by genes that became differentially expressed only late in life. These 'old-age gene networks' include signs of stress and decline, and reflect processes of physiological turmoil shortly before death. Thus, this set of genes might be used as ageing markers.
We applied these 'old-age genes' in an experiment studying the effect of environmental stress in queens and workers of *C. secundus.* Varying ambient temperature, we studied survival and analysed transcriptomes. Both castes showed lower survival under more constant temperatures. Consistent with these fitness results, we found the 'old-age genes' overrepresented in queens and workers kept under constant temperatures reflecting a high level of stress and ageing in these individuals. We argue that these 'old-age genes' are useful ageing markers to detect signs ageing.

Abstract ID: 1728

Do life history strategies affect within-body mosaics of ageing?

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The disposable soma theory predicts that ageing is a consequence of the investment in reproduction at the expense of self-maintenance. Depending on their pace of life (POL), individuals prioritise either reproduction (fast POL) or self-maintenance (slow POL). A fast POL is associated with a rapid accumulation of physiological damage and early death, and vice versa for a slow POL. To date, it is largely unclear if physiological damage accumulates uniformly across the entire body, or if there are within-body mosaics of ageing, and how life history strategies affect these patterns. Here, we used a combination of biomarkers of somatic integrity (telomere length and oxidative stress), to quantify physiological damage in different tissues of male and female Japanese quail (*Coturnix japonica*) artificially selected for high (fast POL) or low (slow POL) reproductive investment. We found widespread evidence for within-body mosaics of damage accumulation, with marked differences between reproductive and non-reproductive tissues. These patterns were affected by an individual's own POL, but also by the POL of its mating partner. Our study highlights the role of genetic life history variation and indirect partner effects in shaping individual health and ageing trajectories.

Abstract ID: 2184

The ecological and evolutionary role of early-life telomere length in wild house sparrows

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The length of telomeres, the DNA sequences protecting chromosome ends, has been associated with health or fitness in several species. To understand the evolutionary and ecological significance of telomere length (TL) it is important to quantify the relative importance of genetic and environmental variation in TL in wild populations. We measured TL in 2746 house sparrow (*Passer domesticus*) nestlings sampled across 20 years in two island populations. Using an animal model, we showed that there is a small heritable component of early-life TL (h^2 = 0.04). Variation in TL among individuals was mainly driven by environmental (annual) variance, but also by brood and parental effects. We further identified several putative genes underlying TL variation, that have been inferred to be involved in e.g. oxidative stress, growth, development and tumorigenesis in other species. Our populations are known to be affected by inbreeding depression, and using pedigree-based inbreeding estimates, we observed a tendency for inbred nestlings to have shorter telomeres. Using genomic measures of inbreeding we found that inbred nestlings have significantly shorter telomeres. However, early-life TL did not predict later-life survival, but we found a tendency for individuals with shorter telomeres to have higher annual reproductive success. Together, our results show that TL is a heritable, polygenic trait strongly affected by environmental conditions. TL may reveal subtle costs of inbreeding already at early life-history stages. In addition, TL may be a biomarker of individual pace-of-life, with annual reproduction tending to be associated with shorter early-life TL in a free-living bird.

Symposium: S35. The art of microscopic war: interference competition in microbes (id: 9)

Abstract ID: 1659

Antagonism among the abundant Bacteroidales of the human gut microbiota

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The human gut microbiota is one of the densest microbial ecosystems on earth, where microbes engage in numerous competitive interactions. Bacteroidales is the most abundant order of Gram-negative bacteria in the healthy human gut microbiota with most individuals colonized with many diverse species at high density. Many strains of gut Bacteroidales produce antibacterial toxins that are delivered to competing members by both contact-dependent and contact-independent mechanisms. The targeting range of these toxins is varied; some toxins only target strains of the same species, whereas others kill across families. The ecological consequences of these toxins are beginning to be elucidated. We have found that some toxins are potent, killing cells upon engagement with the receptor, whereas the effects of others are dependent on the concentration of toxin, and range from antagonistic to conditionally beneficial. The evolution of resistance by the producing strain differs for each toxin class, and include complete lack of resistance, to the production of immunity proteins, to receptor modification. Several of the genetic loci encoding these antibacterial toxins are on mobile genetic elements that are able to transfer to diverse Bacteroidales species in an individual's gut microbiota, allowing for rapid evolution of antagonistic phenotypes in recipient strains. The latest work from the lab will be presented regarding our current understanding of the evolution and ecology of antibacterial toxin production by this important and abundant order of gut symbionts.

Abstract ID: 1709

The role of antibiotics in Streptomyces interference competition

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Bacteria have evolved a variety of mechanisms to get ahead in the race for resources and space. One of the most important and diverse of these is the secretion of antibiotics. *Streptomyces*, a group of filamentous multicellular bacteria, are the most prolific producers of these compounds, which are used to kill or arrest the growth of competing strains. In our work, we have identified conditions where antibiotics provide significant benefits to producing strains. In addition, we have shown how the metabolic costs of antibiotic production can be reduced by: 1) using social cues to regulate the timing of antibiotic secretion (competition sensing), 2) restricting antibiotic production to only a subset of the colony (division of labour), and 3) integrating these two processes to modulate the fraction of the antibiotic-producing subset. While most studies with *Streptomyces* antibiotics focus on production at the multicellular stage of colony

growth, our recent work has found widespread evidence that spores can also produce inhibitory compounds. These compounds can provide significant fitness benefits by delaying or arresting spore germination of competing strains. Our results highlight the different ways that *Streptomyces* use and regulate antibiotic production throughout their multicellular development, from spores to maturing colonies.

Abstract ID: 1599

Directed evolution of resistance to a bacterial Type VI Secretion System

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Natural microbial communities are characterized by intense competition for nutrients and space. One way for an organism to gain control of these resources is by eliminating nearby competitors. The Type VI Secretion System (T6SS) is a nano-harpoon used by many bacteria to inject toxins into neighboring cells. While much is understood about mechanisms of T6SS-mediated toxicity, little is known about the ways that competitors can defend themselves against this attack, especially in the absence of their own T6SS. Here we use directed evolution to examine the evolution of T6SS resistance, subjecting eight replicate populations of *Escherichia coli* to T6SS attack by *Vibrio cholerae*. Over ~500 generations of competition, the *E. coli* evolved to survive T6SS attack an average of 14-fold better than their ancestor. Whole genome sequencing reveals extensive parallel evolution: *apaH* was mutated in six of the eight replicate populations, while the other two populations each had mutations in both *yejM* and *yjeP*. Synthetic reconstruction of individual and combined mutations demonstrate that *yejM* and *yjeP* are positively epistatic, with *yejM* requiring the mutation in *yejP* to provide a benefit. However, mutations we identified are pleiotropic, reducing cellular growth rates, and increasing susceptibility to antibiotics and elevated pH . These tradeoffs underlie the effectiveness of T6SS as a bacterial weapon, and help us understand how the T6SS shapes the evolution of bacterial interactions.

Abstract ID: 1156

The ecology of strain replacement in bacterial communities

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Bacteria commonly live in dense and diverse communities. Key to understanding these communities is understanding what it takes for a given strain to succeed. Bacteria compete in two main ways: via nutrients (resource competition) and via antibacterial mechanisms (interference competition). While both processes are important, we lack a general understanding of how they work together to define ecological success. Here, we address this with an eco-evolutionary model of bacterial competition. Our model predicts

that resource competition can dominate the outcome of competition whenever a strain attempts to invade a community. This is because invading strains – whether they possess mechanisms of interference competition or not – are unable to grow if a resident strain has depleted resources. However, we further show that this favours metabolic diversification, which co-incidentally empowers interference competition and thereby favours the evolution of interference mechanisms. We tested our predictions with competitions between *Escherichia coli* strains, where we engineer both metabolic overlap and presence or absence of natural antibacterial toxins, known as colicins. As predicted by our modelling, strains only invade when there is metabolic diversity, and it is these conditions that enable displacement of the resident by colicins. We further show that this principle can be used to identify *E. coli* strains that can invade well and, if they are armed with colicins, will displace and replace multidrug-resistant clinical *E. coli* isolates. Our work identifies general principles that shape the composition of bacterial communities and suggest ways to perform targeted replacement of problematic bacteria as a biotherapeutic strategy.

Symposium: S36. Evolution of antibiotic resistance: from lab to clinic (id: 953)

Abstract ID: 2468

Within-patient evolution of plasmid-mediated antimicrobial resistance

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Antimicrobial resistance (AMR) in bacteria is a major threat to public health, and one of the key elements in the spread and evolution of AMR in clinical pathogens is the transfer of conjugative plasmids. The drivers of AMR evolution have been extensively studied *in vitro*, but the evolution of plasmid-mediated AMR *in vivo* remains poorly explored. Here, we tracked the evolution of the clinically-relevant plasmid pOXA-48, which confers resistance to the last-resort antibiotics carbapenems, in a large collection of enterobacterial clones isolated from the gut of hospitalised patients. Combining genomic and experimental approaches, we first characterized plasmid diversity and the genotypic and phenotypic effects of multiple plasmid mutations on a common genetic background. Second, using cutting-edge genomic editing in wild-type multidrug resistant enterobacteria, we dissected three cases of within-patient plasmid-mediated AMR evolution. Our results revealed, for the first time, compensatory evolution of plasmid-associated fitness cost, as well as the evolution of enhanced plasmid-mediated AMR, in bacteria evolving within the gut of hospitalised patients. Crucially, we observed that the evolution of pOXA-48-mediated AMR *in vivo* involves a pivotal trade-off between resistance levels and bacterial fitness.

Abstract ID: 1259

Stochasticity and cooperative effects in the establishment of antibiotic resistance mutations

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The evolution of antibiotic resistance proceeds through the origination and spread of resistance mutations. The establishment of a novel mutant, *i.e.* its rise in frequency to a significant fraction of the population, is stochastic and depends on factors such as drug concentration, nutrient availability and the presence of other bacterial strains. We measure the single-cell establishment probability of four *Escherichia coli* strains expressing β-lactamase alleles with different levels of activity against the antibiotic cefotaxime. We find that concentrations well below the minimal inhibitory concentration (MIC) can substantially hamper establishment. The pattern of establishment suppression is similar in both liquid and agar environments, but the latter shows somewhat higher stochasticity, which is possibly linked to higher variability in the microenvironments on the agar surface. We compute a generalized measure of MIC based on the single-cell establishment probability. Comparison of this expectation with the actual MIC indicates strong cooperative effects for large inoculum sizes, especially for highly resistant mutants. We also quantify the establishment probability of resistant strains in the background of relatively susceptible strains. Surprisingly, we find that the presence of bacteria with very low antibiotic-hydrolyzing activity increase the probability of resistant cells to survive and to grow into colonies due to an active breakdown of the antibiotic. A theoretical model suggests that this observation may be explained by cell filamentation causing delayed lysis. Therefore, the establishment of *de novo* resistance mutants is expected to be enhanced by the presence of susceptible bacteria.

Abstract ID: 1495

Variation of costs of mobile antibiotic resistance genes on their dissemination

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The frequent identification of antibiotic resistance genes (ARGs) in non-pathogenic bacterial strains suggests factors other than antibiotic selection influence their dissemination. One underexplored factor is the possibility that variable basal fitness costs of ARGs could mean that some host strains act as a refuge in the absence of antibiotics. It is generally assumed that ARGs impose costs on their host, but their extent, and how they depend on specific ARGs, host strains, and their interaction, has not been systematically determined. We measured the fitness effect of seven ARGs in each of 12 diverse *Escherichia coli* isolates. Effects depended on the ARG and host strain, and on the interaction between them. For example, bla_{TEM-1} imposed costs ranging from 1.1 - 13% and effects of the *cat* ARG ranged from a cost of 5% to a benefit of 5%. Mechanisms underlying costs are apparently complex in that ARGs with similar activities show different patterns of cost across hosts. By combining a controlled evolution experiment and subsequent genetic manipulations we determined that the cost conferred by the bla_{TEM-1} ARG could be rapidly and repeatedly compensated, most often through mutations in a gene encoded by a naturally occurring plasmid present in the host strain. Our results indicate that some hosts can act as cost-free ARG reservoirs and that even hosts subject to large costs can convert to ARG reservoirs via compensatory evolution. That compensation depended on a naturally occurring plasmid suggests that it may be widespread and transferrable among natural bacterial communities.

Abstract ID: 2235

Eco-evo feedbacks shape the local fitness landscape of an antibiotic degrading enzyme

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The adaptive path that an evolving organism takes is largely dependent on the environment in which it lives. Therefore, environmental changes may alter its adaptive path. This includes changes brought about by the evolving organism itself, which can affect its own fitness landscape, i.e. the relationship between genotype and reproductive success, hence influencing the accessibility and predictability of future adaptive paths. Such interactions between evolutionary processes and ecological properties are referred to as eco-evolutionary feedback loops. To date, there exist few theoretical studies that explore how eco-evo feedbacks impact fitness landscapes, however empirical data is lacking. Here, we take a systematic approach to study the impact of eco-evo feedbacks on the deformability of a local fitness landscape of the antibiotic resistance enzyme TEM-1 β-lactamase towards increased cefotaxime resistance. While TEM-1 β-lactamases readily degrade penicillins, cefotaxime is a poor substrate for TEM-1 but only a few amino acid changes are able to significantly increase its capacity to degrade it. However, in doing so, they make the environment more amenable for sensitive alleles. This can potentially lead to a shift in selective conditions and the fitness landscape topology. By changing the initial cefotaxime concentration and modifying the expression of the β-lactamase, we are able to tune the eco-evo feedback and systematically determine its impact on the local fitness landscape. We demonstrate that increasing the eco-evo feedback increases the deformability of the fitness landscape and, more importantly, limits the number of accessible paths towards the most resistant genotype.

Abstract ID: 2096

Density-associated mutation rate plasticity and the evolution of antimicrobial resistance

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Bacteria live in spatially structured communities, where cells functionally interact with each other and create micro-environments with temporal-environmental variation. Understanding how such environmental variation affects mutation avoidance and DNA repair is essential for understanding the evolution of antimicrobial resistance. Using a high-throughput fluctuation assay, we discovered that microbial populations at lower cell-densities have up to 23-fold higher mutation rates to resistance. This density-associated mutation-rate-plasticity is a genome-wide process that is widespread among

microorganisms, present in all domains of life. In *Escherichia coli* it critically depends on the quorum-sensing gene *luxS* and on a mutation avoidance gene *mutT* (MutT removes oxidised nucleotides). When *E. coli* populations grow anaerobically, or lack all four genes encoding reactive-oxygen-species removing enzymes (*katG*, *katE*, and *ahpCF*), plasticity is absent. To understand how the dynamic interplay between internal cellular processes and external environments drives such plasticity of resistance rates, we recently started to use a more direct approach that allows us to quantify DNA mismatches in a single bacterial cell growing in a spatially structured community. A combination of a super-resolution microscopy and polydimethylsiloxane microfluidics enables us to track single-molecules of various DNA repair proteins. This allows us to determine how the single-cell mutation count depends on the type and distance to neighbouring cells in different environments. Studying *de novo* mutations both in large populations and in individual cells is generating fundamental understanding of how environmentally dependent spontaneous mutations really are. This in turn will enable us to develop sustainable mitigation strategies of antimicrobial resistance.

Abstract ID: 1865

In vitro counter-selection of antibiotic resistance with phage-antibiotic combination therapy

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In the face of antibiotic resistance, treatment options that can effectively clear bacterial infections and weaken selection for resistant superbugs are urgently needed. One therapeutic modality currently being explored is the application of phages, viruses that kill bacteria. However, it remains unclear whether phages are best applied alone or in combination with antibiotics, and how this impacts selection for antibiotic resistance. To address these questions, we studied the population dynamics of *Pseudomonas aeruginosa*, an opportunistic human pathogen, treated *in vitro* with phage DMS3vir and sub-inhibitory concentrations of 8 different antibiotics. The majority of antibiotics antagonized phages and delayed phage epidemics, transiently protecting bacterial populations against phages. We then showed that with tetracycline and gentamycin (two antibiotics with different modes of action), this antagonistic effect requires antibiotic susceptibility, and antibiotic-resistant bacteria are not protected. In turn, this can lead to selection against antibiotic resistance during phage-antibiotic combination treatment: When antibiotic-resistant and susceptible cells grow separately, the phage epidemics is primarily restricted to antibiotic-resistant populations. As a result, antibiotic resistance is counter-selected in the presence of antibiotics. We then used growth on agar to create population structure in a way that mimics more realistically conditions like the structured environment of lungs. Here we observed an intermediate effect, with phage-antibiotic combination leading to weaker selection for antibiotic resistance compared to antibiotics alone, but no counter-selection. We suggest that the timing of treatment is important, and applying phages to populations which have already grown in a structured environment could maximize counter-selection of antibiotic resistance.

Abstract ID: 1537

Population size, mutation bias and the evolution of antibiotic resistance

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Mutations with large fitness benefits and mutations occurring at high rates may both cause parallel evolution, but their relative contribution is expected to depend on population size. We report on evolution experiments showing that small and 100-fold larger bacterial populations evolve resistance to increasing levels of cefotaxime, a β-lactam antibiotic, by using similar numbers, but different types of mutations. Small populations frequently substitute structural variants and loss-of-function point mutations, including the deletion of a low-activity β-lactamase on a plasmid, and evolve modest resistance levels. Large populations more often use point mutations affecting similar targets, including mutations activating the β-lactamase and other gain-of-function mutations, leading to much higher resistance. We hypothesize that structural variants are favored in small populations because of their high rate, whereas stronger clonal interference in large populations leads to the predominant substitution of low-rate, large-benefit point mutations. The hypothesis is confirmed by the temporal ordering of substitution events, as well by the computational inference of rates and effect sizes of different mutation classes from endpoint genotypes. Clonal interference theory is used to quantify the shift from mutation bias to selection as the dominant factor determining mutation choices in populations of increasing size.

Abstract ID: 1000

The bacterial capsule: a gatekeeper of horizontal gene transfer ?

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The high propensity of Klebsiella pneumoniae to acquire and distribute mobile genetic elements throughout the bacterial world is a major challenge in the fight against multidrug resistance. This propensity is modulated by many intra- and extracellular factors, such as the bacterial capsule, a ubiquitous feature of multi-resistant nosocomial pathogens, which is both a virulence factor and a gatekeeper for horizontal gene transfer (HGT). Adding to the complexity, the capsule encoding locus itself continuously evolves though HGT and is highly diverse both genetically and chemically. Our goal is to characterize the interaction between mobile genetic elements and capsules, to shed light on the impact of the cell envelope on gene flow within bacterial species. To do so, we combine comparative genomics with in vitro HGT experiments between artificially swapped serotype mutants. We show that capsule serotype qualitatively shapes phage host range, and thus virion-mediated gene transfer, which is drastically rewired upon serotype swap or capsule inactivation. On the other hand, conjugation efficiency is quantitatively affected by the capsule and its serotypes, which act as a general defense system against conjugative plasmids. These results suggest that cell envelope

composition and spatial hindrance have a major impact on intercellular interactions leading to HGT. Overall, capsules' interaction with mobile genetic elements results in a complex interplay between virulence, phage sensitivity and conjugation rates influencing the evolution of Klebsiella pneumoniae.

Abstract ID: 1703

High potency of sequential therapy with only β-lactam antibiotics

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Evolutionary adaptation is a major source of antibiotic resistance in bacterial pathogens. Evolution-informed therapy aims to constrain resistance by accounting for bacterial evolvability. Sequential treatments with antibiotics that target different bacterial processes were previously shown to limit adaptation through genetic resistance trade-offs and negative hysteresis. Treatment with homogeneous sets of antibiotics is generally viewed to be disadvantageous, as it should rapidly lead to cross-resistance. We challenged this assumption by determining the evolutionary response of Pseudomonas aeruginosa to experimental sequential treatments involving both heterogenous and homogeneous antibiotic sets. To our surprise, we found that fast switching between only β-lactam antibiotics resulted in increased extinction of bacterial populations. We demonstrate that extinction is favored by low rates of spontaneous resistance emergence and low levels of spontaneous cross-resistance among the antibiotics in sequence. The uncovered principles may help to guide the optimized use of available antibiotics in highly potent, evolution-informed treatment designs. As a next step in this direction, we are now assessing the impact of variation in spontaneous resistance rates and in the associated evolutionary trade-offs on evolutionary adaptation to a variety of antibiotics in a diverse Pseudomonas aeruginosa strain panel.

Abstract ID: 1209

Evolution of antibiotic resistance under sequential therapy

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The rapid evolution of antibiotic resistance and the resulting loss in treatment options call for the development of sustainable treatment strategies. Laboratory experiments indicate that alternating antibiotics during treatment restrains the evolution of drug resistance. Evolutionary trade-offs, especially collateral sensitivity, were found to improve the outcome of sequential therapy further. A limitation of these in-vitro evolution experiments is that they do not account for the complex environment of the patient's body. In the body, drugs persist at continuously decreasing concentrations, leading to a temporal overlap of the drugs in a cycling schedule. Drug-drug interactions during these periods of drug overlap might influence the outcome of sequential therapy. To bridge the gap between laboratory experiments and the potential clinical application of the treatment, we set up two models for comparison - a 'lab model' and a pharmacokinetic-

pharmacodynamic 'patient model' that incorporates drug-drug interactions. We aim to identify potential differences in the optimal treatment settings, given the risk of resistance evolution. In the lab model, rapid cycling minimizes the time to extinction across the entire parameter range. In the patient, the picture is more nuanced. While rapid cycling is optimal over large parts of the parameter range, we find that slower cycling can sometimes be better in patient treatment, depending on the drug concentration, the pharmacodynamic drug characteristics, and the interactions between the drugs. As expected, drug-drug interactions mainly affect the outcomes of rapid cycling regimes. In contrast, collateral sensitivity only improves the treatment efficiency if cycling is slow.

Abstract ID: 1842

The effects of antibiotic exposure on the ecology and evolution of *in vitro* gut microbiome models

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Antibiotic exposure is known to affect the ecology and evolution of the human microbiome, often selecting for antibiotic resistance. However, *in vivo* studies lack fine-scale control and replication, and are largely unable to predict or explain outcomes following exposure. Conversely, *in vitro* studies have highlighted how even sub-clinical concentrations of antibiotics promote resistance evolution in individual bacterial populations, but it remains unknown how these results translate to complex natural communities. To bridge this gap, we used human faecal samples to seed microbial cultures, which were then exposed to one of three antibiotics (amoxicillin, ciprofloxacin, or clindamycin) for seven days at sub-clinical concentrations, combining the taxonomic complexity of natural microbiomes with the tractability and power of experimental evolution. 16S rRNA analysis and *in vitro* assays revealed that the effects of antibiotic exposure differed depending on the specific antibiotic and the original faecal community. Exposure to clindamycin selected for antibiotic resistant populations, a distinct community composition, and in some cases decreased diversity compared to untreated controls, while amoxicillin and ciprofloxacin had less clear effects. Of note, many effects of exposure were similar between replicate communities seeded from the same faecal sample and exposed to the same antibiotic, suggesting that the effects of antibiotics on a microbial community are broadly predictable at an individual level. Our results show that very low concentrations of antibiotics affect the ecology and evolution of complex microbial communities, with important implications for antibiotic resistance evolution in human microbiomes and other natural communities in an increasingly antibiotic-saturated world.

Symposium: S37. Microbiomes in the wild: the drivers and evolutionary consequences of microbiome variation (id: 948)

Abstract ID: 1395

The holobiont as an ecosystem: the host perspective

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Symbiosis – “living together” – with microbes contributes to ecological success and is a source of evolutionary innovation. The host and its microbiota form a functional unit called the “holobiont”, which can be regarded as a miniature ecosystem of complex host-microbe and microbe-microbe interactions that result in new functions. It is highly debated how these complex holobionts evolved and are maintained. Holobionts do not occur as isolated units, but are affected by their environment and are embedded in a community of holobionts, in a larger ecosystem. Like a Russian doll. Multiple studies report changes in the microbiome in response to environmental stressors and disease, but have failed to determine causality due to a lack of fundamental understanding of underlying mechanisms of holobiont homeostasis in a changing environment. From the animal perspective, host innate immunity may be the key connector in microbiota-animal-environment interactions and the evolution of symbiosis. When animals emerged, life on Earth had remained exclusively microbial for at least 3 billion years; it seems sensible that animals evolved to “navigate” the microbial world and that (some) microbes mastered exploiting the new available resource. Revealing the mechanisms of interkingdom communications in symbiosis and their evolution represents frontier research, but most investigations have been limited to model organisms. My talk will illustrate how we need a broader taxonomic range of model systems for symbiosis and a more fluid dialog linking the findings from reductionist models to the holistic view provided by studying holobionts in their natural context.

Abstract ID: 2034

Gut microbiota of wild rodents from islands: testing the island biogeography theory

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Given the important services gut microbiota provides its host, it is important to understand the factors driving gut microbiota composition. For example, it is well-documented that gut microbiota can be affected by the host's experience of the environment, such as host diet or exposure to pathogens. Though widely applied to free-living communities, whether the main principles behind island biogeography theory apply to host-associated microbial communities is uncertain. In this study, we examine whether island biogeography theory can explain community diversity and composition in the gut microbiota of a wild rodent, the bank vole (*Myodes glareolus)*, living in an island ecosystem. We captured 363 voles (in 2019 and 2020) from 22 islands and 2 mainland sites in southern Finland and used 16S rRNA gene amplicon sequencing to characterize the gut bacteria communities. We tested whether the diversity and composition of bank vole gut microbiota are associated with 1) the level of island isolation; 2) island size and

3) the distance to the mainland. Although no differences in the alpha diversity of gut microbiota were explained by island features, we found that island size, distance to the mainland, and island isolation were associated with significant changes in gut microbiota community composition. Thus, we demonstrate that some of the principles behind island biogeography theory can apply to host-associated microbial communities.

Abstract ID: 1298

Threespine stickleback gut microbiota divergence associated with repeated shifts in trophic ecology

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The importance of microorganisms for diverse aspects of their hosts' biology has been recognized in a wide range of animals. Yet, it remains largely unknown how host-microbiota interactions facilitate adaptation to ecological niches. Unfortunately, confounding factors such as host phylogeny and the extent of genetic divergence among host lineages often complicate investigations of microbiota dynamics associated with niche shifts. However, many of these confounding factors can be circumvented in study systems where closely related host lineages have independently adapted to similar ecological niches; such systems allow asking whether adaptive changes in host ecology can reliably predict shifts in microbiota composition. Threespine stickleback fish present an excellent system to tackle this question as marine populations repeatedly and recently (< 12,000 years ago) colonized freshwater environments across the Northern hemisphere. Freshwater populations show considerable divergence in trophic ecology, mainly feeding on two types of prey associated with different habitats: littoral invertebrates from the lake sediment (benthic prey) and pelagic zooplankton (limnetic prey). We leverage this repeated divergence along the benthic-limnetic axis and characterized the gut microbiota of 14 lake populations from Vancouver Island, British Columbia. We sought to quantify the relative contributions of host ecology and morphology as well as external environmental factors to patterns of microbiota variation within and across stickleback populations. This data has the potential to improve our understanding of how a host, its gut microbiota, and the environment interact during the adaptation to different ecological niches and how these interactions might shape the evolutionary trajectories of host populations.

Abstract ID: 1247

Alterations to the gut microbiota of a wild juvenile passerine in an urban mosaic

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Urbanisation is a major anthropogenic perturbation presenting novel ecological and evolutionary challenges to wild populations. Symbiotic microorganisms residing in the gastrointestinal tracts of vertebrates have mutual connections with host physiology and respond quickly to environmental alterations. However, the impact of anthropogenic

changes and urbanisation on the gut microbiota remains poorly understood, especially in early development. To address this knowledge gap, we investigated the gut microbiota in juvenile great tits (*Parus major*) reared in artificial nestboxes and in natural cavities in an urban mosaic, employing two distinct frameworks characterising the urban space. Alpha diversity was influenced by cavity-type and the amount of impervious surface surrounding the breeding location and positively correlated with tree cover density. Beta diversity differed between urban and rural sites: these alterations covaried with sound pollution and distance to the city centre. Overall, the microbial communities reflect and are possibly influenced by the heterogeneous environmental modifications that are typical of the urban space. Strikingly, the choice of framework used to define the urban space can influence the outcomes of such ecological studies. Our results open new perspectives to investigate the impact of microbial symbionts on the adaptive capacity of their hosts.

Abstract ID: 1117

Are house mouse genetics affecting the microbiome and antimicrobial resistance in the hybrid zone?

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Antibiotic resistance (AR) is a biological phenomenon emergent at multiple levels of biological organisation and a priority public health problem. AR's selection mechanisms are well understood, while the transmission of antibiotic resistance genes (ARGs) is a comparatively under-researched topic. Notably, the links between molecular, genomic, bacterial community, and host community levels are rarely analysed in an overarching manner. Given the importance of understanding how bacteria carrying ARGs interact in

the microbiome and with the environment of their hosts, we used an amplicon sequencing approach to simultaneously study bacteria and predict ARGs composition in the gut microbiome of house mice (*Mus musculus*) natural populations. We compared gastrointestinal bacterial diversity, composition and abundance across a gradient of pure and hybrid genotypes in the European house mouse hybrid zone between the subspecies *M. m. musculus* and *M. m. domesticus* at different geographical and temporal scales. We detected phenotypes of extreme bacterial abundances due to transgressive segregation in hybrid mice: Some bacterial taxa and overall ARGs have elevated abundance in hybrid genotypes. In contrast, the abundances of other bacteria, but not of any ARGs, are reduced in hybrids compared to parental mice. Our results confirm that host genotype influences the composition of gastrointestinal bacteria. All the above raises the question of whether environmental covariates of the hybrid zone or host genotypes influence the occurrence of ARGs in natural populations of house mice.

Abstract ID: 1719

Dynamics and metagenomics of oral disease in Scandinavian brown bears (*Ursus arctos*)

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Anthropogenic disruptions to the planet's ecosystems impact ecological communities at macro- and micro-scales, including host-associated microbiomes. Here we use a temporal approach to study how human-caused decline of a Scandinavian brown bear (*Ursus arctos*) population has impacted the bear oral microbiome and its potential to cause disease. After nearly being hunted to extinction ca. 100 years ago, Scandinavian brown bears have recovered from a severe population bottleneck. The bottleneck-caused loss of genetic diversity may have impacted the host's ability to regulate its microbiome. Using a collection of 192 museum specimens spanning the last 180 years, we have examined the frequency of oral disease phenotype(s) and characterised the oral microbiome using dental calculus material, which preserves the microbiome signature long after death. We find that the prevalence of oral disease is inversely proportional to host population size. Individuals with dental caries harbour distinct oral microbiomes compared to healthy individuals and have increased abundance of several opportunistic oral pathogens. In addition, the microbial communities impacted by oral disease are functionally enriched in metabolic pathways relating to carbohydrate fermentation and acid production. Through reconstruction of near-complete genomes from disease-associated taxa, we have identified lineages that are distinct from human isolates and contain a set of unique virulence genes while missing others. This work demonstrates how human-driven declines can affect host health through interaction with host-associated microbial communities. Understanding how host-associated microbiomes respond to host-centric or environmental disturbances may be important to predict the impact of ongoing biodiversity crisis.

Abstract ID: 1895

Changes in fish skin microbiota along an eutrophication gradient: a field and transplant approach

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Skin microbiota plays a major role in organism health but understanding the effects of anthropogenic disturbances on host-microbiota interactions remains a challenge. In this study, we tested the effect of eutrophication on freshwater fish using a field approach followed by a reciprocal transplantation experiment across rivers. First, we sampled 17 populations of wild gudgeon *Gobio occitaniae* along an eutrophication gradient and compared their skin microbiota diversity and composition, using a 16s rRNA gene metabarcoding approach. Along the eutrophication gradient, we observed an increase in taxonomic and phylogenetic diversity as well as significant changes in skin microbiota taxonomic composition and beta-diversity. Results also showed a significant shift in Proteobacteria / Bacteroidetes ratio, suggesting environmentally-induced dysbiosis. To experimentally test the effects of eutrophication, we then used a reciprocal transplant experiment approach and compared plastic changes (within 2 weeks) in skin microbiota. Fish transplanted into eutrophic habitats showed an increased alpha diversity and rapid changes in beta-diversity and taxomonic composition. To conclude, our study highlights that eutrophication induces strong variation in microbiota composition and diversity. Our results further show that fish skin microbiota is primarily shaped by environmental factors and also suggest a strong lability in the face of rapid environmental changes. Such alterations in skin microbiota could have potential fitness consequences for hosts and further highlight the need to account for host-microbiome interactions when considering the response of aquatic organisms to eutrophication and other anthropogenic stressors.

Abstract ID: 2255

Exploring the microbial communities associated with the common garden snail

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The common garden snail *Cornu aspersum* is a cosmopolitan agricultural pest. Snails present to their environment a soft skin rich in specialised glandular cells, which are believed to perform essential nutritional and defensive functions. Though overlooked, this skin plays a central role mediating microbial interactions. Here, we explored *C. aspersum*'s cuticular microbiome. Sampling of snails isolated across Europe revealed that *C. aspersum*'s cuticular-associated microbiota is rich in *Erwinia sp.* and in particular *Pseudomonas sp.*. Isolate-level variation in *Pseudomonas* showed that species identity varied with geographical location. Confocal fluorescent microscopy confirmed that bacterial symbionts are resident in cuticular bacteriocytes, arrayed as club-shaped glandular cells throughout the cuticle, and are especially abundant in the anterior portion of the foot and in the mantle. Symbionts could be cured using artificial diet containing high doses of antibiotics, but this was associated with high snail mortality. Provision of antibiotic-resistant *Pseudomonas* symbionts rescued hosts from death, however the extent of colonization was negatively correlated with host growth in surviving individuals. In these gnotobiotic colonisation experiments, we also observed a

significant effect of the symbiont strain on snail growth, and on symbiont colonisation ability. Using RFP-transformed antibiotic-resistant *Pseudomonas* to visualize invasion, we observed competitive exclusion by resident strains even under strong antibiotic selection favouring the invader. Our results suggest that symbiosis in *Cornu aspersum* is widespread, primarily based on diverse strains of *Pseudomonas*, and that one of its likely functions is defensive, mediating mucosal immunity.

Abstract ID: 1971

Disentangling cause and effect in wild microbiome studies

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Understanding the mechanisms by which microbial communities shape the life histories of their hosts remains a major goal, and challenge, in ecology and evolutionary biology. Observational data often yield convincing correlations between microbiome composition and host traits like disease prevalence, or body mass. But whether the microbiome is a causative agent of among-individual trait variation, or simply a passenger riding on the coat tails of host life-history, remains largely undetermined in wild populations. Using data from both amphibians and migratory birds, I will explore how integration of fine-scale ecological data from animal hosts may help to distinguish cause from effect in wild microbiome studies. I also discuss the importance of within-individual longitudinal data for illuminating the strength and direction of feedback loops between ecological processes occurring at the levels of both host and microbiome. Understanding the dynamics of these interactions is likely to yield further insight into the mechanistic role(s) of host-associated microbial communities, and generate novel hypotheses to be tested in both lab and field systems.

Abstract ID: 1861

Vertical transmission of maternal gut microbiota in wild mice

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Vertical (mother-offspring) transmission is one key route by which animals can acquire beneficial symbiotic microbes. While vertical transmission of gut microbes has been studied in laboratory animals, domestic animals and humans, the significance of this transmission pathway in wild mammalian populations is poorly understood. Here, we report findings from a longitudinal dataset of paired mother-offspring faecal samples taken from a wild population of mice (*Apodemus sylvaticus*), for which we also have a rich set of metadata on spatial and social behaviour. By controlling for these and other confounding variables, we identify a clear signal of vertical gut microbiota transmission, that is strongest for immature offspring and declines as offspring age, consistent with findings from other mammalian systems. We further show that vertical transmission is

stronger for some bacterial taxa than others, and that while vertical and horizonal (social) transmission can both have strong impacts on gut microbiota composition, they differ in the phase of life at which they dominate in this system. Overall, our findings demonstrate that vertical maternal transmission has a key role to play in shaping the gut microbiota of wild mice particularly during early life, the biological significance of which requires further study.

Abstract ID: 2130

Microbiome underlying winter adaptations in wild populations of great tits (*Parsus major*)

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Winter poses a key environmental challenge to survival in endotherms. Combination of cold temperatures, limited resources, and short-day lengths present energetic and thermoregulatory challenges that can detrimentally impact fitness in wild populations living at high latitudes. By increasing metabolic rate through thermogenesis and mitochondrial bioenergetics, endothermic animals can adapt to decreasing temperatures by maintaining a stable body temperature, but this is energetically costly. One promising mechanism for regulating energy acquisition and heat production is the gut microbiome (GM). By enabling the host to adapt to rapid environmental perturbations, including cold stress, the GM may contribute to host adaptation. To explore whether the GM can act as a mechanism for winter adaptation, we first studied associations between winter conditions and the GM in two wild populations of great tits (*Parus major*). Large variation in environmental conditions (latitudes, temperature, day length, snow cover) between populations, combined with longitudinal sampling within a season, provides a detailed dataset to test how the GM changes with exposure to cold. To further address the plasticity and causal effects of temperature variation on the GM, we additionally sampled wild-caught individuals in captive conditions kept under either summer or winter temperatures. Secondly, to assess whether temperature-induced changes in the GM are linked to thermoregulation we associated GM composition with biomarkers of thermal physiology including whole-animal metabolism, cold resistance, and mitochondrial function for both the wild and captive populations. Combination of correlative and manipulative methods from wild individuals allows assessment of the role of GM-mediated adaption to environmental changes.

Abstract ID: 1633

Is natural selection driving antimicrobial properties of animal bacterial symbionts?

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Bacteria, which in many cases have pathogenic effects on hosts, may also be part of the animal defensive lines against microbial infections. The beneficial effects of symbiotic bacteria are mediated, indirectly, by enhancing host's immune responses or, directly, by producing antimicrobial substances that prevent pathogenic-microbial infections of hosts. However, different host species exploit different environments and, thus, experience different risks of microbial infection. Consequently, if symbiotic bacteria is somewhat selected by genetically determined host characteristics, we would expect the antimicrobial properties of bacterial symbionts to vary among host species and to be adjusted to risk of infection. Here we have explored this never tested hypothesis, by measuring the antimicrobial ability of the bacterial strains isolated from the uropygial-gland skin of 19 bird species differing in nesting habits and, thus, in risk of microbial infection. In accordance with the predictions, intensity and diversity of antagonistic effects against the indicator strains assayed varied among bird species, with hole- and open-nesters showing the highest and the lowest values, respectively. Since it is broadly accepted that hole-nesters suffer higher risk of microbial infection than open nesters, our results suggest that natural selection has favoured host traits (e.g. uropygial secretion characteristics) that select for antibiotic-producing symbionts at higher risk of infection. We are not aware of alternative hypotheses explaining the non-random variation in antagonistic capacities of microbial symbionts hosted by different bird species. Future research should focus on characterizing symbiotic bacterial communities and detecting coevolutionary processes with particular antibiotic-producing bacteria within-host species.

Abstract ID: 1050

Long-read metagenomics highlights dietary adaptations in the gut microbiome of ant-eating mammals

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In mammals, myrmecophagy (ant and termite consumption) represents a striking example of dietary convergence. This trait evolved independently at least five times in

placentals with myrmecophagous species comprising the aardvark, anteaters, armadillos, pangolins, and aardwolves. Studies of morphological and genomic adaptations linked to this diet have revealed that different adaptive mechanisms were involved between the different myrmecophagous species with potential implications of phylogenetic constraints. The gut microbiome also plays an important role in dietary adaptations as it coevolves with its host and can be influenced by both the host diet and phylogeny. In myrmecophagous species, taxonomic analysis of 16S rRNA sequences has revealed compositional patterns of convergence in the gut microbiota of these species but questions remain regarding the functions carried by those microbial symbionts. In particular whether bacteria participate in the digestion of prey, and more specifically of their chitinous exoskeleton, remains unknown. Using a combination of long- and short-read sequencing we generated 31 gut metagenomes from field-collected fecal samples of nine myrmecophagous and partially myrmecophagous species sampled in French Guiana, South Africa, and the USA. We then applied a genome-resolved metagenomic approach to reconstruct metagenome-assembled genomes (MAGs), assessed their taxonomy, and studied chitin-degrading enzymes. This approach allowed us to retrieve MAGs and identify several chitinase genes, suggesting a potential role of the gut microbiome in prey digestion through complex microbial chitin-degradation pathways.

Abstract ID: 1410

Examining the relationship between the gut microbiota, MHC, and TB resistance in wild meerkats

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Gut microbial symbionts are predicted to protect animals against infectious disease and thereby be under selection. Conversely, pathogens and disease alter the composition of the gut microbiota, challenging the identification of cause and effect. In this study we investigate the three-way interplay between the gut microbiome, MHC genotype, and Tuberculosis exposure and infection using longitudinal data collected from wild meerkats inhabiting the Kalahari in southern Africa. Meerkat TB is a chronic disease caused by *Mycobacterium suricattae* which, after a latent period, culminates in external lesions, weight loss and death. Across the population, most individuals are exposed to the pathogen, yet there is considerable individual variation in TB resistance with only about ~25% of exposed individuals succumbing to the disease. To examine if and how the gut microbiota is involved in TB resistance, we identify gut microbial taxa associated with health and TB disease, and examine how these microbial biomarkers are mediated my MHC genotype and whether their abundances during meerkat development predict later resistance to TB. This study provides a rare example of how the gut microbiota interact with the MHC to mediate pathogen resistance in a wild population.

Abstract ID: 2190

Host-microbiome interactions within an eco-evo perspective: Daphnia and its microbiome as a model.

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In spite of the growing interest in the role of the gut microbiome in host physiology and health, the mechanisms governing its assembly and its effects on the environment are poorly understood. We show that the host genotype and the gut microbiome of *Daphnia* influence the community structure of the surrounding bacterioplankton. When *Daphnia* genotypes were placed in an identical environment, both the gut microbiome and bacterioplankton showed a genotype and diet-dependent taxonomic composition. Overall, the gut microbiome strongly differed from the bacterioplankton in taxonomic composition and was characterized by a lower α-diversity, suggesting a selective rejecting of bacteria from the regional species pool. In microbiome transplant experiments, the assembly of both the gut microbiome andbacterioplankton was strongly affected by the host genotype and the inoculum to which germ-free *Daphnia* were exposed. These results suggests a strong interaction between the host genotype, its gut microbiome and free-living microbial communities. Currently, it is generally assumed that an animal's diet has a strong effect on the animal's gut microbiome, but only a negligible effect on the surrounding environment. However, our results indicate that the diet/microbiome inocula have a small effect on the gut community and a large effect on the community in the surrounding environment. This structuring genotype × microbiome × environment effect affecting host phenotypes is an essential prerequisite that could indicate that microbiomes play an important role in eco-evolutionary processes, especially in the light of stressors and changing climates.

Abstract ID: 1213

Immunogenetic variation shapes the gut microbiome in a natural vertebrate population

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The gut microbiome (GM) can influence many biological processes in the host, impacting its health and survival, but can also be influenced by host's traits. In vertebrates, Major Histocompatibility Complex (MHC) genes play a pivotal role in combating pathogens and are thought to shape the host's GM. Despite this - and the evidenced importance of both GM and MHC variation to individual fitness - few studies have investigated associations between the GM and MHC in wild animals. We characterised MHC class I, MHC class II, and GM variation in individuals within a natural population of Seychelles warblers (*Acrocephalus sechellensis)*. Results show that the presence of specific MHC alleles, but not MHC diversity, influences both the diversity and composition of the GM. Interestingly MHC-I alleles, rather than MHC-II alleles, had the greatest impact on the GM. GM diversity was also positively correlated with genome-wide heterozygosity and varied with

host age and field period. How this GM variation then impact fitness components in the warbler is now being explored. These results suggest that components of the host's immune system play a role in shaping the GM of wild animals, although whether this occurs directly, or indirectly through effects on host health, needs further investigation. Importantly, if immune genes can regulate host health through modulation of the microbiome, then it is plausible that the microbiome could also influence selection on immune genes. As such, host–microbiome coevolution may play a role in maintaining functional immunogenetic variation within natural vertebrate populations.

Abstract ID: 1786

Early life environment has a lasting effect on the gut microbiota of a wild rodent

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Assembly of the vertebrate gut microbiota is the result of numerous host- and environment-mediated processes. There is considerable interest in understanding processes that promote stability of the gut microbiota and the extent to which gut microbiota can vary, for example in response to a change in environment. In this experiment, we aimed to distinguish which of these mechanisms is more important for structuring the gut microbiome of wild bank voles (*Myodes glareolus*). We carried out a reciprocal transplant experiment with longitudinal sampling of faeces, transferring 81 female bank voles (28 recaptured) and their 412 newly born offspring (72 recaptured) between different forest habitats (urban and rural forests) located in Jyväskylä, Finland. Gut microbiota of adult bank voles retained the signal from their site of origin throughout the experiment, with animals that were transferred to a different forest habitat showing little notable change in gut microbiota: specifically, bank voles originating from 'urban forest' had higher alpha diversity and exhibited more inter-individual variation in their gut microbiota than voles originating from 'rural forests', irrespective of the site of transfer. In contrast, the gut microbiota of the offspring was more influenced by the novel site of transfer. Although we found little impact of forest habitat on the alpha diversity on the pup microbiota, their gut bacteria were structured according to the transfer site rather than the maternal site of origin. Our data suggests that the early life environment is a key mechanism that shapes the microbiome of the bank vole in natural populations.

Abstract ID: 1384

Virus-host interaction dynamics in the gut microbiome through the analysis of CRISPR arrays

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The gut microbiome is a complex system whose structure and dynamics is modulated by many diverse factors. Interactions between viruses and microbes are amongst the most relevant and, paradoxically, least well-understood forces driving microbiome dynamics. Such interactions can be monitored through the study of CRISPR-Cas, an adaptive

immune system of bacteria and archaea that collects and stores short fragments of foreign DNA (typically from viruses and plasmids), serving as a record of encounters between prokaryotes and their viruses. Following that idea, we characterized the virus-microbe interaction network in a longitudinal study of human gut microbiome, including 132 subjects sampled every 2 weeks for 1 year. We developed a fully-automated computational workflow that assembles CRISPR-Cas loci from metagenomic samples, identifies and annotates viral and plasmid targets, and quantifies the fluctuations in their abundance. Then, we studied how viral abundances respond to the acquisition of matching sequences in their host's CRISPR arrays. Our analyses revealed rapid and highly correlated fluctuations in the abundance of viruses and their prokaryotic hosts, indicating a strong coupling between the microbiome and the virome that extends at least on a 1-year timescale. Interestingly, despite the strong selective pressure that viruses are assumed to exert on bacterial hosts, the acquisition of CRISPR-based immunity does not generally lead to selective sweeps in the host population, allowing for long-term virus-host coexistence. This study shows a promising way of studying virus-bacteria relationships, not only in the human microbiome, but in other microbial communities for which shotgun metagenomic datasets are available.

Abstract ID: 2367

Spatiotemporal patterns of microbial communities in recirculating aquaculture systems

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Microbial communities influence the growth, development, and welfare of animals, and are intensely studied in evolutionary biology. However, microbial communities in laboratory studies can not accurately capture the complex composition and function of wild microbiomes, while wild microbiomes are difficult to study considering the wealth of confounders. We have identified a promising setting to study a multi-species microbiome-governed system with direct health implications: recirculating aquaculture systems (RAS). RAS allow us to quantify community composition, colonization, and dynamics in a semi-natural, complex and compartmentalized system.
We combine fish health expertise and theoretical ecology and evolution knowledge and use sequencing data from swabs and water samples to a) describe a semi-natural compartmentalized microbiome in time and space, b) quantify the dynamics and repeatability of the establishment of new biofilm and c) quantify dynamics during disease outbreak, treatment, and recovery. Ultimately, we aim to implement mathematical models to derive rules governing microbiome assembly, reaction to disturbance, and succession events.
So far, we have successfully established a variety of methodical approaches and have evaluated different long- and short read data types for aspects of spatiotemporal and taxonomic resolution. We present the results from the pre-trial and the on-going sampling scheme of the main trial, and aim to convince the audience that RAS are a use case where fundamental knowledge about community evolution can be gained from an applied context, and the derived fundamental evolutionary insights in turn have tangible impacts for a growing food industry.

Symposium: S38. Molecular evolution and trade-offs in host-pathogen interactions and host immunity (id: 968)

Abstract ID: 1854

The evolution of powerful yet perilous immune systems

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The mammalian immune system packs serious punch against infection but can also cause serious harm: e.g., COVID-19 has made headline news of the simultaneous power and peril of immune responses. In principle, natural selection leads to exquisite adaptation and therefore cytokine responsiveness that optimally balances benefits of defense against its costs (e.g., immunopathology suffered & resources spent). Principles and tools from evolutionary biology can predict such optima and also help explain when/why individuals exhibit apparently maladaptive immunopathological responses. One example that has received a lot of attention is an evolutionary mismatch: our co-evolutionary history with symbionts such as helminths, malaria, and diverse gut microbes, to help explain cytokine hyper-responsiveness and immunopathology in hosts now living without those symbionts. The impact of hominin demographic history on innate immune responsiveness in modern humans offers another well-studied example. I will outline these but then focus on 2 rarer explanations for mammalian and human susceptibility to immunopathology: the evolutionary legacies of multicellularity and life history strategy. Using empirically-grounded mathematical models, I will illustrate why cellular collectives and constrained pathogen detection systems further explain susceptibility of hosts to overzealous, pathology-inducing cytokine responses. Diverse evolutionary insights thereby complement molecular/cellular mechanistic insights into immunopathology.

Abstract ID: 1062

Expression of the gut parasite, *Crithidia bombi*, reveals networks of infection-relevant genes.

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The trypanosomatid parasite *Crithidia bombi* is a highly prevalent gut parasite of bumblebees. With a striking degree of genotype-by-genotype matching and common coinfection, this host-parasite system has become a model of ecological immunology. While we know a reasonable amount about this interaction and the immunological defences of bumblebees exposed to *C. bombi*, we know comparatively little about the parasite processes that result in successful infection and coinfection. Here we examine the whole transcriptome expression of *C. bombi* during infection and in vitro to identify candidate genes that determine infection and may predict success when competing with other genotypes of *C. bombi*. We revealed 37 up-regulated genes for *C. bombi* of potential importance for infection establishment, some of which are orthologues of known

virulent factors in the human pathogenic trypanosomatid *Leishmania major*. We further examined the co-expression of host and parasite genes to identify interacting networks of genes that may represent the interface of host-parasite conflict and coevolution. Based on these results we are using editing approaches to both visualize infection processes and survey functional roles for these candidate genes that may predict competitive success during coinfection.

Abstract ID: 1081

Tapeworm parasite secreting proteins with antioxidant properties significantly extends host lifespan

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Parasites cause phenotypic changes in their hosts. However, it is often unclear whether these changes are the result of active manipulation of the host, a host defense response, or a side effect of infection that does not benefit the fitness of either party. In this proteomic study, we show that a parasitic cestode that significantly prolongs the life of its intermediate host, a social insect, secretes antioxidant proteins such as thioredoxin peroxidase and superoxidase dismutase into the hemolymph of its host. In fact, more than 6% of all proteins in the ant host hemolymph are of parasitic origin, many of them so novel that we could not find an annotation for them. This contrasts with the proteins identified in the parasite itself, the overwhelming majority of which have a known function, suggesting that the secreted proteins are likely novel and have evolved to function in host manipulation. Not only does the parasite release proteins with life-prolonging functions to the host, but we also find that the host itself, when parasitized, has more proteins with antioxidant functions in its hemolymph. Some of these proteins are the same ones that are enriched in queens, which can live two decades in this species and have a survival rate similar to infected workers. Overall, our study shows how a parasite can extend the lifespan of its host and calls for the identification the underlying molecular mechanisms including unknown proteins.

Abstract ID: 2346

Genomic associations with spatially variable pathogen pressures across island bird populations

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Exploring how pathogens and immune genes covary spatially within and across populations of a single host species can provide insight into mechanisms of host defense and thus mechanisms of adaptation to pathogens. Here, we aimed to test the link between spatial heterogeneity in pathogen infection and genetic variation across endemic populations of Berthelot's pipit (*Anthus berthelotii*). Although similar questions have previously been explored in other host-pathogen systems, we present analyses spanning multiple populations and different archipelagos, using genome-wide data (ddRADseq) and have examined the selective effects of two different pathogens. By applying a population landscape genomics approach (Bayenv), we were able to identify and compare the candidate SNPs associated with avian poxvirus and malaria across the entire range of Berthelot's pipit. Population-level allele frequency variation at these candidate SNPs correlated with population prevalence after controlling for genome-wide divergence due to neutral structure. These sites were located within genes related to metabolism, the complement pathway, the inflammatory response, the stress response, cellular organisation and enzyme pathways. Our results reveal potential genes involved in malaria and pox protection and suggest local adaptation to spatially variable pathogen pressures is an important driver of genetic variation in Berthelot's pipit.

Abstract ID: 1406

How do sick fish sleep? – Sleep of three-spined stickleback upon *Schistocephalus solidus* infection

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Sleep is highly evolutionary conserved across animal taxa and can affect immune system function. Evidence suggests that sleep plays a crucial role in preventing and fighting infections. Additionally, pathogens can also affect sleep of the host. Understanding this bidirectional relation between sleep and immunity therefore requires disentangling the effects of infections on sleep and the effects of sleep on immune function. Here, we investigate the effects of an experimental infection with *Schistocephalus solidus* tapeworms on sleep behavior of three-spined sticklebacks. We estimated sleep by video-recording activity of individual sticklebacks one to four and 29-32 days after exposure to *S. solidus*. We found that infected fish sleep less compared to control fish two-and three-days post exposure. Interestingly, the same infected fish slept significantly more 32 days after exposure. To our surprise, exposed but not infected fish slept less compared to controls after 32 days post exposure. Furthermore, we used Image3C to assess the cellular composition of the immune system taking the head kidney, the main hematopoietic organ of fish. We found an association between immune cell composition and sleep, where granulocytes were significantly increased in exposed fish that sleep less after 32 days. These results provide experimental evidence of an association of the immune response to a macroparasite with sleep behavior of fish and contribute to a better understanding of the immune system-sleep interaction. This establishes a link between complex physiological traits and eco-evolutionary aspects of host parasite interaction.

Abstract ID: 1763

Resistance variation and life-history trait correlations of *Peronospora sparsa* on three *Rubus* hosts

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Most pathogen species are generalists capable of infecting more than one host species. Trade-offs in performance among different hosts are expected to limit the evolution of generalism. Despite the commonness of generalism, variation in resistance and transmission among host species have rarely been studied in wild. I studied field disease severity, transmission dynamics and host resistance variation of downy mildew pathogen *Peronospora sparsa* on its three host plants *Rubus arcticus, R. chamaemorus*, and *R. saxatilis*. In wild and cultivated populations of the three host species, disease severity varied by host species and whether the focal host species grew in shared habitat with other host species. The presence of *R. saxatilis* as an alternative host resulted lower disease severity in *R. arcticus*. To understand how resistance to *P. sparsa* varies among plant species and genotypes, an inoculation experiment was set up using *P. sparsa* strains from different locations and 20 genotypes of the three host species. Significant resistance variation was found among host genotypes but not among host species. When trade-offs for infectivity were tested, high infectivity in one species correlated with high infectivity in another host. However, when pathogen transmission-related life-history correlations were tested, a positive correlation was found in *R. arcticus* but not in *R. saxatilis*. The results suggest that host resistance may shape pathogen life-history evolution with epidemiological consequences in a multi-host pathogen.

Abstract ID: 1754

Deciphering the evolution of the antiviral system via studying the role of MAVS homolog in Cnidaria

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The innate immune system is the frontier defense for animals to survive in their nonstop struggle against viral infections. This continuous condition forced animals to evolve a broad repertoire of innate immune sensors and downstream effector cascades for defense against viruses. Different bilaterian animals rely on different pathways to activate the immune response against these viral infections. This diversity masks the system's ancestral state. To date, the majority of studies on immune systems focused on bilaterian animals. Thus, in this study, we focus on homologs of the vertebrate viral RNA sensors RIG-I-Like Receptors (RLRa and RLRb), and Mitochondrial Antiviral Signaling Protein (MAVS) of the sea anemone *Nematostella vectensis,* representative of Cnidaria, the sister group of Bilateria. We show that the knockdown of *Nematostella* RLRb and MAVS, but not RLRa, leads to a significant decrease in the expression levels of homologs of immune-related genes after microinjection of viral the RNA mimic Polyinosinic:polycytidylic acid (poly I:C). Moreover, biochemical assays and structural predictions suggest MAVS binds RLRb with strong specificity but not RLRa. We believe that the results of this study will give us new insight into the mode of action of RLRs and

MAVS to activate the immune system in cnidarians and reveal whether their mode of action is conserved with their vertebrate homologs. This will shed new light on the immune system in the last common ancestor of cnidarians and bilaterians, which lived roughly 600 million years ago.

Abstract ID: 2073

Selecting for tolerance: Examing the consequences for host and pathogen

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Defence against pathogens can be attributed to a combination of two host strategies, that is resistance and tolerance. Resistance is the ability of the host to limit the pathogen burden. In contrast, tolerance is the ability to limit the damage caused by a given pathogen burden. Unlike resistance, which has a negative effect on pathogen fitness because it reduces replication, tolerance does not directly affect pathogen fitness. As a result, tolerance has been predicted to have a neutral effect on, or even increase, pathogen prevalence in a population, and it has been predicted that it might allow pathogens to be more virulent towards non-tolerant hosts. However, to date, there is little empirical evidence on the evolution of tolerance or on the effects that it will have upon pathogen virulence. We therefore attempted to address this using an experiment where flies were selected over multiple generations for resistance or tolerance to a bacterial pathogen. In this talk I will discuss whether there is a trade-off between host resistance and tolerance defence strategies, whether host selection affects pathogen virulence or replication, and the potential evolutionary and ecological implications of our findings.

Abstract ID: 1981

Coordinated gene expression of hosts and parasites across resistant and tolerant populations

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It is common in nature for parasite resistance to vary dramatically, even between closely related populations to the same parasite. Yet, we are still working to understand the mechanisms that generate this variation. Using the threespine stickleback, *Gasteosteus aculeatus,* and its tapeworm parasite, *Schistocephalus solidus,* we explored how host-parasite interactions shifted in a resistant and tolerant population and how this influenced parasite-parasite interactions that arise with coinfection. Using gene expression of both hosts and parasites, we found that in the resistant population, fish had baseline upregulation of immune pathways before infection and when infected, expressed genes linked to a resistance phenotype (peritoneal fibrosis). Tolerant populations, on the other hand, upregulated metabolic pathways and suppressed immune pathways when infected. Analysis of tapeworm gene expression revealed that pathways linked to secreted glycoproteins used to manipulate host immunity were less expressed in

resistant populations, especially in hosts with a strong fibrosis response. Interactions between tapeworms arising from coinfection were more pronounced in the tolerant population compared to the resistant population for both fish hosts and tapeworms. By building trans-species gene coexpression networks using gene expression data from fish and tapeworms, we are gaining additional insight into the genes and pathways that underly host-parasite interactions and coevolution in this system.

Abstract ID: 1539

Transgenerational evolution of immunity in an invertebrate-yeast system

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Parasites impose different selection regimes onto their hosts, which respond in return by increasing their resistance, i.e., reducing the infection rate, or their tolerance, i.e., altering epidemiologically related life-history traits. Parasite challenge may impact the challenged generation as well as their offspring, a mechanism known from invertebrates as transgenerational immune priming (TGIP). Based on previous studies of TGIP in the *Daphnia-Pasteuria* system, we exposed two parental generations of the water flea *Daphnia magna* to a high infectious dose of the horizontally transmitted parasitic yeast *Metschnikowia bicuspidata* in a fully cross-factorial experiment, and recorded life-history traits in the offspring generation. Our susceptibility assays revealed no impact of parental exposure on offspring resistance. Nonetheless, different life-history traits were altered, with maternally primed animals producing more offspring than the unprimed ones, supporting the “environmental matching hypothesis”. We also found evidence of strong grandmaternal effects in early life-history traits, which likely affect offspring fitness. In a second experiment, we exposed young and older parental *Daphnia* to a low infectious dose of the same parasite and recorded resistance and tolerance in the offspring generation. We found that offspring originating from older mothers were more resistant to the parasite than those coming from younger mothers, while maternal parasite exposure had a marginal effect. Multiple tolerance related traits, however, were affected by both maternal age and maternal treatment. Our findings increase our knowledge regarding TGIP responses in invertebrates and show that TGIP is not a consistent mechanism even within the same species.

Abstract ID: 1619

Amputations and antimicrobial wound care of infected wounds in ant societies

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Animals developed different behavioural adaptations to combat infections. Ants typically use the metapleural gland to combat pathogens, but some ant genera have lost this gland in their evolutionary history. Here we compare the strategies to combat infected wounds between two species, one having a metapleural gland and the other having no metapleural gland. By treating infected wounds with antimicrobial compounds secreted

from the metapleural gland the ant *Megaponera analis* efffectively reduces mortality by 90%. We identified in the metapleural gland secretions of *M. analis* over 121 chemical compounds and 41 proteins, almost half of which have an antimicrobial effect. All *Camponotus* species do not have a metapleural gland. Remarkably, we observed that workers of several *Camponotus* species amputate an infected leg by biting it off at its base, thereby reducing mortality by 80% without the need of antimicrobial compounds. Overall, our study reveals two highly effective behavioral adaptations to identify and treat festering infections of open wounds in ants. The prophylactic and therapeutic use of antimicrobial secretions to counteract infection in *M. analis* mirrors modern medical procedures for dirty wounds, while the amputation behaviour of *Camponotus* mirrors medical procedures of a pre-antibiotic era. Thereby demonstrating convergence in the solutions that evolved to mediate infected injuries across human and insect societies.

Abstract ID: 2177

CRISPR, herd immunity and transduction allow bacteria to speed up adaptation by recombination

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Unlike most eukaryotes, bacteria reproduce by binary fission, which is devoid of recombination. Recombination is known to be able to speed up adaptation by bringing beneficial alleles, initially present on different chromosomes, together. In a clonal bacterial population, the beneficial alleles, arising in different individuals, compete with each other in a process called clonal interference, which slows down adaptation. Although bacteria lack recombination as it occurs in eukaryotes, they can occasionally exchange genetic information directly between individuals in a process called horizontal gene transfer (HGT). Yet, remains largely unclear, how much does HGT affect evolutionary dynamics within bacterial populations. We experimentally determined that in bacterial populations of *Escherichia coli*, CRISPR-based herd immunity can lead to coexistence of CRISPR+ (resistant) and CRISPR– (susceptible) strains and the P1 phage in the population. As the P1 phage is capable of generalised transduction and the resistant strain is protected from lysis by the phage, transduction leads to a continuous gene flow from the susceptible to the resistant strain. This enables recombination of two different beneficial loci encoding for antibiotic resistance to appear on the same background and thus circumvents clonal interference. In our system, this rate is one to two orders of magnitude higher than the rate at which a functionally similar mutation can arise *de novo*. We thus show that a combination of CRISPR-based herd immunity and transduction can substantially limit clonal interference and aid bacterial adaptation by frequent chromosomal recombination.

Abstract ID: 1946

What can integrative studies of songbird immunity tell us about tolerance and virulence evolution?

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Host immune systems protect hosts from pathogens but can also contribute substantially to host disease severity, and thus mortality. While some host populations have rapidly evolved resistance to novel pathogens, the evolution of host tolerance (reductions in per-pathogen morbidity and mortality) may be strongly favored in systems where host inflammation underlies disease-induced mortality. Using a tractable songbird-pathogen system, we asked how both host responses and pathogen virulence might evolve in systems where host disease is mediated by inflammatory responses. First, using a space-for-time approach to understand host evolution following pathogen invasion, we inoculated house finches from seven populations spanning the USA with one of two strains of a novel bacterial pathogen (*Mycoplasma gallisepticum*) that stimulates severe conjunctival inflammation. Host populations earlier on the pathogen's invasion front showed evidence for rapid evolution of tolerance (mild conjunctivitis despite high pathogen loads) relative to populations with no (Hawaii) or very recent (Arizona) pathogen invasion, which showed severe conjunctivitis at similar loads. RNAseq data showed associations between population tolerance and "silencing" of immune response pathways present in populations more evolutionarily-naïve to *M. gallisepticum*. To understand inflammation benefits for pathogens, we used transferrable UV powder to show that host tissue inflammation favors virulent *M. gallisepticum* strains by increasing the ability of a given unit pathogen to transmit to flockmates. Together, our results suggest the possibility of an evolutionary arms race with respect to host inflammation, and more broadly, emphasize the role of understanding immune mechanisms of disease for predicting evolutionary responses of hosts and pathogens.

Abstract ID: 2138

Patterns of adaptation following serial infection of a specialist fungal pathogen in a novel host

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The genus *Metarhizium* comprises a set of diverse insect-pathogenic fungi that exhibit a wide spectrum of host ranges. Within this genus, *M. acridum* is a specialist pathogen that infects orthopteran insects and is currently used in environmentally friendly biological control of locust pests. Although this species exhibits a global distribution across tropical and sub-tropical regions, much of the current genotypic and phenotypic characterization is based on only two isolates. To increase our understanding of how evolutionary factors and genomic diversity drive host colonization, we first expand current knowledge of intra-specific variation by establishing a reference-quality pangenome of *M. acridum* based on six assembled genomes of isolates from four continents. We find that 7,242 of the 10,177 gene clusters (71%) are shared among all isolates (core genome), and used enrichment analysis to determine the functional differences between the core and accessory regions. Using this foundational genomic dataset, we then selected three isolates displaying divergent genotypic and virulence profiles for a serial passage experiment to investigate how standing genetic variation in a pathogen contributes or constrains the ability to colonize novel hosts. We passaged *M. acridum* through three host environments for five generations: *Locusta migratoria* grasshoppers, representing the natural host; *Tenebrio molitor* beetles, representing the novel host; and sabouraud dextrose agar media

representing an experimental control. We observe clear changes in fungal growth and virulence following serial passaging, and use our studies to reveal how standing genetic variation and the pan-genomic structure of a specialist pathogen influence patterns of early adaptation.

Abstract ID: 1720

Genomics and transcriptomics of D. melanogaster adaptation against oral bacterial infection

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When confronted with pathogens, *Drosophila melanogaster* deploys well-described immune responses that encompass behavioural, developmental and physiological facets. Notwithstanding studies about how specific genes or uncontextualized variants contribute to these responses, knowledge gaps remain on how evolution can shape them. To address this, we selected an outbred population of *D. melanogaster* against oral infection with its natural pathogen *Pseudomonas entomophila*. After 10 generations of selection, almost 100% of the population had higher survival upon infection and this phenotype was maintained, even under relaxed selection, for over 80 generations.

To understand the genetic basis of such rapid adaptation, we performed Pool-Sequencing of Control and Evolved populations at different generations. Subsequently, under relaxed selection, we additionally performed RNA-Seq at different timepoints throughout infection, both of whole-body and of gut-specific samples.

Our results showed distinct differential gene expression profiles between local and whole-body responses, but we identified overlaps of individual candidate genes across timepoints, evidencing the integrative way in which selection shaped defences against *P. entomophila*. Additionally, we linked underlying genomic changes with consequent gene expression patterns by comparing the main candidates from Pool-Seq with the ones from both transcriptomic approaches and concluding that there were common targets between them.

Finally, we validated the key genes from our multiple approaches using RNAi knockdowns and assessed their contribution to the adapted population's phenotype. We pinpoint gut permeability and a tighter regulation of immune effectors as the main mechanisms that responded to selection and thus contributed to the overall increased survival upon oral bacterial infection.

Abstract ID: 1663

Intrinsic and extrinsic early life effects shape responses to infection in European shags.

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Environmental conditions can play a key role in shaping responses to infection. Conditions may vary both temporally and spatially, leading to differences in parasite exposure and the resources available to respond. These effects may have immediate impacts on host tolerance or resistance, or carry-over to influence parasitism in later life. Furthermore, the strength and timing of environmental impacts may vary with intrinsic factors, such as sex. Here we show, in a long term population study of European shags, that gastrointestinal nematode parasite burden is influenced by differences in current and early-life conditions, but the relative importance of these differs between the sexes. Burdens increased across the season in both chicks (of both sexes) and adult females. However, in adult males, the year, and time of hatching within the year, impacted on later-life burdens. Specifically, late-hatched males and males born in productive years had lower burdens as adults, suggesting that early life may shape behaviour or physiology, impacting subsequent infection. We also find evidence that these effects may be linked to immune variation with sex differences in immune cell profiles present in early life, and current and early-life effects on adult immunity. Our results highlight that the sexes may differ in their sensitivity to environmental impacts on parasitism and the timescale over which these play out. Incorporating the impact of seasonality and sex specific responses to parasitism is crucial if we are to understand how predicted environmental shifts could impact disease dynamics.

Abstract ID: 2008

Trade-offs in immunity in the metal hyperaccumulator *Noccaea caerulescens*

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Metal hyperaccumulating plants are able to accumulate exceptionally high concentrations of heavy metals in their shoots to levels that would be toxic to most other plant species. This trait has evolved independently multiple times in the plant kingdom. Although our understanding of the molecular mechanisms involved in metal uptake and tolerance has improved, not much is known about the processes that have led to the evolution of metal hyperaccumulation in plants. Recent studies have provided new insight into the ecological and evolutionary significance of this trait by showing that the metal hyperaccumulating plant *Noccaea caerulescens* can use high concentrations of accumulated metals to defend itself against attack by pathogenic microorganisms. Interestingly, infected *N. caerulescens* plants show none of the inducible defence responses that are used by most plants to provide protection against infection, which suggests that it relies on accumulated metal for disease resistance. The fact that these plants have evolved the ability to uptake and store metals in their shoot tissue, but have in turn lost defences common to most plants suggests a trade-off in expressing both traits. We studied the evolutionary, ecological and functional processes involved in the gain of metal hyperaccumulation and loss of other defensive traits in *N. caerulescens*. Genes involved in the trade-off were identified and analysed using a combined phenotyping and transcriptomics strategy. Our results provide new insights into the evolution and ecology of metal hyperaccumulation and contribute to the understanding of how plant adaptation to biotic and abiotic stress may be connected.

Abstract ID: 1640

The causes of pathogen-mediated balancing selection

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Immune genes are often highly polymorphic, with signatures of balancing selection. Antagonistic coevolution with pathogens, driven by negative frequency-dependent selection (NFDS), has long been considered an important cause of such balancing selection. However, it is difficult to disentangle NFDS from other types of pathogen-mediated balancing selection, such as heterozygote advantage or varying selection due to environmental heterogeneity in pathogen abundance. Consequently, conclusive evidence for NFDS is rare, in particular in vertebrates. In a recent study we focused on MHC genes (which encode cell surface proteins involved in adaptive immunity) and tested a critical assumption specific to NFDS, namely that there is a host genotype-by-pathogen genotype interaction (G*G). We studied a wild rodent population (bank voles) naturally infected with the tick-transmitted bacterium *Borrelia afzelii* and tested for G*G between MHC class II and *B. afzelii* strain. One MHC allele was involved in a G*G, such that voles carrying the allele had higher prevalence of two strains and lower prevalence of one strain than individuals without the allele. G*G involving immune genes have also been demonstrated in some studies of humans. I review patterns of G*G found so far in vertebrates and discuss whether these G*G are sufficient to drive NFDS.

Abstract ID: 1258

What can we learn from typing MHC genes and haplotypes from 22,000 chickens?

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Chickens are generally not considered non-model organisms by evolutionary biologists nor model organisms by the biomedical community. However, there are estimated 80 billion chickens alive each year, with many diverse populations including wild junglefowl, but mainly commercial meat and egg-laying birds. For examining infectious disease, commercial and backyard chickens combine many of the best features of humans and biomedical models like mice, with vast populations carefully monitored, but with the opportunity to bring field strains of pathogens into the lab where they can be studied by direct experiments with inbred lines and outbred populations of chickens. Moreover, some central gene systems for adaptive immunity in chickens, including the major histocompatibility complex (MHC), are much simpler than that in typical mammals, resulting in strong genetic associations of the MHC with economically-important diseases. The simple expression patterns of chicken MHC class I genes allowed the discovery of a hierarchy from promiscuous generalists to fastidious specialists that was overlooked in the more complex MHC of mammals. To further understand the

importance of chicken MHC loci, alleles and haplotypes, we developed a polymerase chain reaction-next generation sequencing (PCR-NGS) protocol that determines the sequence of exons which encode the peptide-binding region of all classical class I and class II B genes, and a bioinformatics pipeline that robustly identifies alleles and haplotypes. Typing over 22,000 samples from commercial, fancy and African chickens, we have identified some 500 alleles and 200 haplotypes, and related them to disease resistance and susceptibility in commercial and African chickens.

Abstract ID: 1598

MHC diversity does not confer fitness advantage in an urban bird

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Genes of the major histocompatibility complex (MHC) encode key molecules of vertebrate acquired immune system, which are directly responsible for pathogen recognition. In general, high individual MHC diversity is expected to increase fitness by broadening the spectrum of pathogens recognized (heterozygote advantage hypothesis). Alternatively, individuals with optimal (intermediate) rather than maximum diversity of the MHC could achieve the highest fitness because of inherent costs associated with expressing diverse MHC alleles (optimality hypothesis). To test these hypotheses, we examined associations between MHC class I and class II diversity and fitness-related traits in an urban population of the Eurasian coot Fulica atra. Contrary to our expectations, high diversity of MHC genes (both class I and II) was associated with lower condition, weaker ornamental expression, later onset of breeding and smaller clutches. Although we found no support for associations of MHC diversity with hatching or reproductive success, our results suggest that the costs of expressing many MHC alleles outweighed any benefits associated with a diverse MHC repertoire. We speculate that this pattern could be driven by relatively low diversity of urban pathogen communities.

Abstract ID: 1655

Repeatability and transgenerational relative expression of MHC-I genes in the great reed warbler

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MHC molecules are key components of adaptive immunity and are encoded by the MHC multigene family. The number of MHC genes have greatly expanded in birds of the order Passeriformes, but the functional relevance of this high MHC-I diversity is unknown. We therefore set out to study the expression of MHC-I in the long distant migratory great reed warbler (*Acrocephalus arundinaceus*) using a unique family dataset from a long-term monitored wild population breeding in southern Sweden. Our study design enabled us to measure relative MHC-I gene expression between years within individuals and also transgenerational within families. Overall, the majority of the MHC-I alleles was expressed but their relative expression varied greatly between the MHC-I alleles. The relative expression of MHC-I alleles did not differ between samples collected in

successive breeding seasons in adult birds. Finally, we compared transgenerational MHC-I relative expression pattern within families between parents and chicks. The most highly expressed alleles in the parents were also found highly expressed in the chicks. The relative expression pattern of MHC-I alleles suggests that one or two MHC-I genes are highly expressed in all individuals and that the relative expression of MHC-I genes is most likely inherited. This study is the first, to our knowledge, to look at the repeatability and the inheritance pattern of MHC-I relative expression in a wild passerine population and constitute a major step forward in understanding the evolution of MHC-I gene diversity in birds.

Abstract ID: 2246

Influence of major histocompatibility complex genes on the reproductive success of wild barn owl

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The genetic variation at the genes of the major histocompatibility complex (MHC) is well known to differently protect against pathogens and generate differences in survival across individuals. A less studied pathway through which MHC variation could influence fitness is by inducing differences in reproductive success among individuals. We use a 23-year dataset of a wild barn owl (*Tyto alba*) population to investigate the relative contribution of each parent's MHC-I and MHC-II composition on their reproductive success. This species is suited to test such associations given their monogamous behaviour and biparental investment. Specifically, we tested whether clutch size and fledging success are mediated by the combination of parental MHC functional divergence and supertypes. We found no evidence that parental MHC is related to the clutch size. The fledging success was negatively associated with the MHC-I functional divergence of the father and by the interaction of the presence of supertype 2 of MHC-II DAB1 of the parents. The fledging success decreased by 25% when only the mother carried compared to when neither parent carried it, suggesting that fathers invest differently on the brood depending on the female's MHC. We speculate that selection on MHC is driven by phenotypic effects on parental fitness. Our results show a correlative link between parental MHC and reproductive success and highlight the importance of investigating both MHC classes and several reproductive proxies. Further studies are needed to understand the exact mechanisms driving this pattern and whether it is a result of mate recognition and sexual preference.

Abstract ID: 1882

MHC class II proteins mediate susceptibility and resistance to coronavirus infections in bats

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Cryptic species diversity might mask functional differences in ecologically important traits, such as those related to disease resistance. Bats of the diverse Sub-Saharan *Hipposideros* species complex differ in susceptibility to coronavirus infections. The best understood genetic basis of resistance are the genes of the Major Histocompatibility complex (MHC), and differences at the MHC are one possible reason for asymmetrical infection probabilities among closely related species. In this cross-sectional study we assigned 2,396 bats to their respective species using mtDNA cytochrome *b* gene and investigated asymmetries in infections with three Coronaviruses (CoVs: CoV-229E, SARS-like CoV-2B and a more basal CoV-2B). We identified the allelic and functional (i.e., supertype) diversity at the MHC DRB class II for a subset of 569 bats, and linked the presence of certain MHC supertypes to CoV infections. All four *Hipposideros* species share much of the existent functional MHC diversity, but the prevalence of the three CoVs is highest in the most numerous and ubiquitous species. At least one MHC supertype shared amongst all species, ST12, was consistently linked to susceptibility with CoV-229E, a virus with recent common ancestry with the human coronavirus (HCoV-229E). The same MHC supertype was connected to resistance to the SARS-like CoV-2B. Bats with ST12 also had fewer co-infections, underscoring the supertype's pleiotropic effect, and body mass when infected with CoV-229E. Maintaining functional genetic diversity in hosts, reservoirs and vectors may become the most effective tool to prevent future cross-species spillover of diseases with zoonotic potential.

Abstract ID: 1883

MHC and sex bias: shaping of the systemic T cell repertoire in three-spined stickleback fish

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The T cell receptor (TCR) diversity necessary for the recognition of a broad antigen spectrum is determined by the interaction between T cell receptors (TCRs) and cognate ligands presented by major histocompatibility complex (MHC) molecules during T cell selection in the thymus. Evolution might have favored an optimal diversity in the copy number-variable MHC, defined by a trade-off between the benefits of presenting a larger number of foreign antigens and the disadvantage of a limited mature T cell repertoire following negative thymic selection, due to presentation of a larger number of self-

antigens. However, our understanding of how the initial T cell repertoire is shaped is still very limited.
Three-spined sticklebacks have a completely functional adaptive immune system and exhibit a natural level of diversity at the MHC. The small size of this wild fish allows an easier estimate of the systemic TCR diversity for each individual, ideal in eco-immunological studies. We have developed a cDNA-based 5'RACE protocol with unique molecular identifiers and a stickleback TCRß gene reference library.
By characterizing the systemic TCRß repertoire diversity among male and female naive lab bred individuals belonging to different families and harboring copy number-variable MHC genotypes ranging from low to high diversity, we have directly tested the association between gender, MHC, and naive TCR diversity. Our results contribute to the understanding of the T cell selection process and the balance between the recognition of pathogenic vs self antigens during the evolution of the vertebrate adaptive immune system.

Abstract ID: 1925

Trade-offs constraining MHC gene number expansion: beyond simple TCR depletion hypothesis

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The major histocompatibility complex (MHC) genes encode proteins crucial for the adaptive immunity of vertebrates. Co-evolutionary dynamics between hosts and pathogens generate and maintain huge allelic polymorphism of MHC, yet, individuals possess only a few functional MHC loci. Thus, paradoxically, individuals can use only a fraction of the adaptive diversity present at the population level. T-cell receptor (TCR) depletion hypothesis posits that this limitation results from an evolutionary trade-off between pathogen recognition and self-tolerance, as increased MHC diversity might enhance negative selection and deletion of T cells, leading to a depletion of TCR repertoires. The generality of this long-standing hypothesis was recently challenged, in a test correlating an intra-individual MHC diversity with total TCR repertoires in a laboratory population of bank voles, supporting its predictions for MHC class I but not class II. Here we expand beyond immunogenetics and look into how diversity of each MHC class influences both numbers and TCR repertoire size of the responding T cell subsets. We found that an average MHC class I diversity correlated with highest numbers of cytotoxic $CD8^+$ T cells, but no relationship was found for MHC class II diversity and either helper $CD4^+$ or regulatory $CD4^+Foxp3^+$ T cells. We will further examine TCR repertoire sizes of corresponding T cell subsets. Also, an overall proportion of T cells among all

lymphocytes was highest in bank voles with average MHC gene numbers, supporting not only T cell depletion model, but also a more general model of immunogenetic optimality.

Abstract ID: 1413

Adaptive immune response selects for increased body size

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The emergence of adaptive immunity, which is pathogen-specific and enables immunological memory, is considered a major evolutionary innovation of vertebrates. Proteins of the Major Histocompatibility Complex (MHC) initiate the adaptive immune response by presenting pathogen-derived antigenic peptides to T cells. MHC genes are characterized by extraordinary polymorphism, the result of balancing selection driven by host-pathogen coevolution. However, the effect of these processes on the evolution of host life-histories remains unknown. Here, we model how host MHC–pathogen coevolution—and its concomitant impact on host mortality—can affect the evolution of host life-histories, as represented by body size at maturity. Life histories were compared in scenarios with and without adaptive immune response under equal mortality rates. We show that host-pathogen coevolutionary dynamics select for postponed maturation and increased body size; the Red Queen process generates linkage disequilibrium between immunocompetent MHC alleles and the maturation-postponing alleles of physically unlinked genes that determine body size at maturation. Particularly large body size was attained when pathogens mutated slowly, thus allowing the advantage of resistant MHC alleles to last over multiple generations. Our work suggests that the adaptive immune response, mediated by polymorphic MHC genes, may drive the evolution of host body size. This form of adaptive immunity may have thus predisposed vertebrates to evolve large body size and exhibit the macroevolutionary patterns of increasing body size over time that have been detected in comparative studies.

Abstract ID: 1434

Evolution of germline repair and mutation rates under strong pathogen selection

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Infection and costly inflammatory responses are major regulators of mutation susceptibility, imposing challenging threats on health. Cytotoxic intermediates arising in many inflammatory diseases not only inflict DNA damage but also affect DNA repair pathways, thereby increasing the overall deleterious mutation rate. Interestingly, if they are unrepaired germline mutations and can be transmitted to subsequent generations,

they can elevate the costs of pathogen resistance mechanisms, with major implications to adaptation against infections and disease. In the present work, we tested this hypothesis by using *Tribolium castaneum* females infected with heat-killed/live *Bacillus thuringiensis* cells. We analysed their germline maintenance by estimating their failure to repair DNA damage in mutagenized sperm post-fertilization. Both immune activation and live infection compromised the female germline DNA repair, causing them to transmit a higher rate of deleterious mutations to their grand-offspring (reducing fitness by 50%). Can they evolve to reduce such fitness costs? Indeed, using experimentally evolved *Tribolium* lines under strong pathogen selection (~17 generations), we found that evolved lines passed on a lesser mutation load to subsequent generations. Overall, in addition to revealing mutation transmission as a novel cost of immunity, our results suggest rapid evolution of germline repair to mitigate such costs under long-term pathogen selection.

Abstract ID: 1048

A game-theoretical description of defense and counter defense in host-pathogen interactions

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Host-pathogen interactions consist of an attack by the pathogen, frequently a defense by the host and possibly a counter-defense by the pathogen. Here, we present a game-theoretical view of such interactions. We consider a game where the host and pathogen are players and defense or counter-defense are taken as their strategies. Specifically, the host may or may not produce a toxin to protect against the pathogen's attack. The pathogen can choose between two strategies to counteract the defense: producing or not producing an enzyme degrading the toxin. We consider that the host and pathogen must also incur a cost for toxin or enzyme production. We consider both the sequential and non-sequential versions of the game and determine the Nash equilibria. Our work reveals that a paradox occurs in this interplay: If the inactivating enzyme is very efficient, the toxin becomes useless. If the toxin is no longer produced, the enzyme becomes useless, so that production of the toxin becomes useful again. The question arises: does this lead to an oscillatory change in strategies or instead to a steady state that is attained as a trade-off, in which both species produce an optimal amount of toxin and enzyme, respectively? We tackle that question using payoff matrices with three strategies: no, partial and full (counter-)defense. Under certain conditions, we obtain 'partial (counter-)defense' strategies as Nash equilibria in this game, implying that producing a moderate amount of toxin and enzyme is the best choice for the organisms.

Abstract ID: 1200

Host immunity adaptation to SIV across chimpanzee populations

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Central and eastern chimpanzees are naturally infected with Simian Immunodeficiency Virus (SIV). While infection causes fitness effects, it is not typically associated with the immunodeficiency that characterises AIDS in humans—caused by the zoonotic transmission of chimpanzee SIV that gave rise to HIV and one of the deadliest pandemics in history. Chimpanzees have been infected for tens of thousands of years and evolved to reduce SIV pathogenicity. To understand how these adaptations arose we investigated signatures of natural selection in population genomic datasets. The ancestor of central and eastern chimpanzees, which was first infected by SIV, shows evidence of adaptation in SIV/HIV Viral Interacting Proteins (VIPs), likely because disrupting SIV physical interactions was critical upon zoonotic transmission. Subsequent adaptations in central and eastern chimpanzees appear in genes involved in SIV/HIV cell entry and SIV-related immune response, respectively, reflecting a shift in strategy probably to account for host-pathogen co-evolution as chimpanzees became semi-natural hosts. Integrating candidate genes across populations shows evidence of selection in numerous steps of the biological pathway responsible for T-helper cell differentiation, including *CD4* and proteins that SIV/HIV use to infect and control host cells. This pathway is active only in the CD4+ cells that SIV/HIV infect, and it plays a crucial role in shaping the immune response to efficiently control viruses. Our results confirm the importance of SIV as a selective force, shed light on host strategies to reduce SIV's pathogenicity, and demonstrate the potential of population genomics to understand these processes.

Symposium: S39. Mechanisms of host-symbiont coevolution: from genotype to phenotype (id: 967)

Abstract ID: 2469

Lousy and wormy tales: endless search for sympatric speciation via host-parasite co-evolution

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Parasites and other symbiotic organisms comprise a major component of global biodiversity. Historically, evolution via host specificity was believed one of the major factors driving the differentiation of parasitic populations, thus, it should represent a significant mode of speciation globally. From the geographical point of view, most free-living species are expected to speciate in allo- or parapatry, whereas the evolution via host specialisation represents an example of sympatric, ecological speciation, which is otherwise rare to find in nature. Frequent co-occurrence of lineages of parasites differing in their host specificity could indicate their possible adaptive and sympatric evolutionary origin. Particularly, ectoparasites like lice, possessing a direct life cycle with no free-living stage and only a single host during their life cycle, provide promising models for such ecological speciation research. On the contrary, the differentiation patterns in parasites with complex life cycles, such as tapeworms, are expected to be less straightforward, due to their free-living stages and the necessity to adapt to multiple hosts. Using examples of several ecto- and endo-parasite taxa, I show that the interaction between hosts and parasites is convoluted through their shared history and requires detailed studies of biogeography, population genetics, and "omics" approaches to be understood

properly. Whereas the narrow level of host-specificity in sympatric lineages of *Polyplax serrata* lice parasitising several *Apodemus* mouse species is shown to have originated in allopatry, a possible sympatric origin of two host-adapted races is suggested for *Ligula intestinalis* tapeworms parasitising fish as one of their hosts.

Abstract ID: 2321

Drivers of highly specialized bird-haemosporidian associations in African sky islands

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Fragmented Afromontane environments (sky islands) host unique and vulnerable communities of organisms whose mutual interactions are poorly known. To increase our knowledge of host-parasite associations between Afromontane bird hosts and haemosporidian blood parasites (genera *Haemoproteus* and *Plasmodium*) we test several host- and parasite- centric hypotheses that were previously utilized to explain host-parasite associations in the temperate region. The hypotheses were tested using more than 1,300 bird samples from two Afromontane sites in the Cameroon volcanic line (the Bamenda Highlands and Mt. Cameroon). While the sites differ considerably in the number of parasite lineages and total parasite prevalence, we find highly specific hots-parasite interactions characterized by limited sharing of hosts and parasites at both sites. Intriguingly, some of the parasite lineages are generalists on a global scale but demonstrate more specialized associations in our study system. We also find significant phylogenetic congruence of hosts and parasites, suggesting that closely related parasite lineages infect phylogenetically related hosts. The influence of the tested factors (e.g., host abundance, body size, evolutionary distinctiveness, foraging strata) on parasite prevalence and lineage diversity of the two-parasite genera vary considerably and our findings differ notably from findings from temperate regions. Parasite diversity and specificity in these sky islands also differ notably from patterns observed on “true” (oceanic) islands. The unique dynamics of fragmentation and isolation of montane habitats that restrict migration between isolated sky islands could be driving these highly specialized interactions in Afromontane environments.

Abstract ID: 1708

How does the presence of a male killing parasite influence host dispersal strategy?

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The African Monarch butterfly (*Danaus chrysippus*) and its endosymbiont *Spiroplasma sp* form a host-parasite system where the so-called male killer transmits vertically from host mothers to their offspring. Parasitized male offspring die in early stages of development, while parasitized female offspring develop into adults that are phenotypically indistinguishable from their uninfected conspecifics. Because a fully infected population produces no males, parasites can cause local extinction — but infected populations may be rescued by a flux of male immigrants and/or healthy female immigrants (who are able to produce males). Infected female dispersal, in turn, brings the parasite to new habitat patches. In our study, we aim to understand which host dispersal strategies impact the spread and persistence of a male killer. Further, we model the idea that the parasite's own interests may be better served at a different dispersal rate than its host's, which opens the door to parasites manipulating host dispersal traits. We determine how (potentially sex-specific) host dispersal influences the spread and prevalence of male killers in a population, including a scenario where the male killer not only alters the sex ratio, but also dispersal phenotype of its host. We make predictions on how host and parasite dispersal strategies and genotypes should coevolve depending on the ability of the parasite to influence host dispersal phenotype. Interestingly, evolution of separate host and parasite dispersal strategies facilitates coexistence.

Abstract ID: 1042

Antagonistic coevolution across scales: Does the now explain the past?

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Hosts evolve to minimize the fitness reduction caused by parasites, while parasites optimise the exploitation of their hosts. In coevolutionary models of this process high genetic specificity in host–parasite interactions is assumed. The widely cited Red Queen model suggests that the corresponding host resistance and parasite infectivity genes coevolve under balancing selection. Our work on the planktonic crustacean *Daphnia* and its bacterial pathogen *Pasteuria* confirmed that their coevolutionary dynamics are well described by the Red Queen model. Here I present a series of experimental and genomic studies with particular focus on the scale of coevolution, ranging from the short-term effects of selection observed across months to the long-term consequences for genome structure revealed by comparative genomics across species. The underlying genetic architecture of host resistance and parasite infectivity will serve as the guiding principle in this presentation across time scales. Our data are consistent with the predictions of the Red Queen model on the temporal and spatial levels of inference, giving a comprehensive picture of how balancing selection in form of Red Queen dynamics can shape long-term coevolution.

Abstract ID: 1138

Diverse coevolution paths towards coexistence of host-virus symbionts under antiviral stress

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Microbial communities are dominated by species interactions and coevolution, which respond to changes in the interplay of ecological and evolutionary processes. These eco-evolutionary processes can be altered when communities are exposed to chemicals. We studied how coevolutionary dynamics of a tripartite microbial system consisting of a heterotrophic flagellate, a giant virus and a virophage are affected when exposed to Predicted No Effect Concentrations (PNEC) of an antiviral. The giant virus parasitizes the host, while the virophage parasitizes the giant virus inhibiting its replication what favors host population survival. Virophage can also integrate into the host genome and being reactivated after host infection with the giant virus. Previous experiments without antiviral stress show coexistence and populations coevolution. Here, we compared ecological and evolutionary changes of communities for ~ 200 host generations when exposed to a single pulse, continues exposure and no exposure of the antiviral. We observed that population sizes and dynamics differ between communities, however, allowing coexistence in both the presence and absence of the antiviral. Host isolated from the end of the experiment survived virus infections and this was most pronounced for those isolated that were continuously exposed to the antiviral. Virus and virophage trait changes are still under study, preliminary results suggest virophage evolves towards higher replication and integration rate in the host genome. To conclude, even PNEC of an antiviral has the potential to interfere microbial interactions by altering population size and populations coevolution, which alter the form of symbiosis.

Abstract ID: 1162

Experimental coevolution and host dependency in a defensive symbiosis community

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Defensive microbial symbionts can protect hosts against pathogen infection. When attacked by coevolving pathogens, will hosts respond by depending on their symbionts or invest more in their own defences? We experimentally coevolved a tripartite community of genetically-diverse nematode host populations, virulent pathogens (*Staphylococcus aureus*), and defensive symbionts (*Enterococcus faecalis*). After 15 host generations, we detect signatures of both host and symbiont dependence during pathogen coevolution – as opposed to spill-over. We show evidence of greater host susceptibility to pathogen attack when coevolved symbionts are removed, in addition to symbionts trading-off free-living growth for within-host growth. We explore whether evolved host populations with high dependence on the symbiont are generally more susceptible to other pathogen species. Finally, we characterize host molecular evolution and reveal modes of selection as well as genomic signatures of dependence on the symbiosis for its defence. Together, these data provide new insight into how dependence may emerge in a defensive symbiosis within a coevolving community.

Abstract ID: 2401

The brain-gut axis of honey bees: Testing how microbiota affect individual and collective behavior

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The holobiont theory of evolution depicts the individual as deeply symbiotic with its gut microbes, which may influence host metabolism, immunity, and behaviour via signalling from the gut to the brain. This gut-brain axis takes on added complexity for social taxa, since individual behaviour can scale-up to affect the entire colony. Here, we use the Western honey bee (*Apis mellifera*) as a model to study how gut microbiota composition influence individual and social behaviour. Through a series of integrated field assays, we manipulate the bee brain-gut axis to measure how antibiotic depletion or probiotic enrichment of core worker gut fauna affect a bee's hygienic, defensive, foraging and recruitment behaviours. So far, we have observed a wide variety of changes consistent with a brain-gut axis that can alter individual as well as colony-level behaviours, potentially through immune modulatory pathways. We plan to further evaluate the functionality of this axis via 16S rRNA bacterial gene amplicon sequencing and histochemical staining of individual bee brains. Our findings should provide a test of the brain-gut axis in a highly social insect, and thus advance the brain-gut axis framework from its current focus on individuals into the realm of higher-order social interactions.

Abstract ID: 2172

Evolution of endosymbiotic *Wolbachia* bacteria across different hosts

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Wolbachia is an intracellular bacterium that is mainly transmitted vertically from mother to offspring, although evidence exists for occasional horizontal transfer even between unrelated host species. To explore these evolutionary dynamics in detail, we expanded the number of known *Wolbachia* genomes by screening over 30,000 publicly available shotgun sequencing data from more than 500 arthropod and nematode species. By assembling over 1000 of high quality genomes, we provide a large-scale collection of *Wolbachia* genomes that substantially increases host representation. Here we will present our main findings published in recent articles, as well as preliminary results of ongoing investigations to estimate the origin and divergence of *Wolbachia*. We generated phylogenies based on both core-genome and gene content that reveal recent horizontal transfers amongst distantly related hosts. We found various instances of gene function gains and losses in different *Wolbachia* super-groups and in sperm–egg incompatibility inducing strains which might indicate distinct selective pressure in different hosts. Overall, our results suggest that the diversity and the evolutionary history

of *Wolbachia* are driven by a combination of horizontal transmission and adaptation to the host.

Abstract ID: 2430

Microbial determinants of folivory in beetles

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My research group is interested in the evolutionary processes that shape mutually beneficial species interactions, with emphasis on why they form and how they facilitate adaptation in insects. Using tortoise beetles (Coleoptera: Chrysomelidae: Cassidinae) as a model, my talk will outline the mechanisms by which these insects house and transmit their obligate bacterial and fungal symbionts. I will discuss the physiological and evolutionary consequences of harbouring and co-evolving with a single clade of microbes for an upwards of 80 million years. Leveraging data from genomic and transcriptomic sequencing, microscopy and bioassays, I will address (i) the metabolic factors defining nutritional and defensive symbioses within the Cassidinae, (ii) how variation in these factors drastically shapes beetle physiology, host-plant use, and defensive chemistry, and, finally, (iii) the trade-offs governing symbiont localisation and transmission. Collectively, our findings highlight the key role of obligate symbioses in facilitating adaptation across a highly speciose clade of herbivorous insects, the leaf beetles.

Abstract ID: 1561

Dual nutritional symbionts in aphids: co-speciation and parallel evolution in symbiont genomes

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Nutritional obligate symbionts have co-evolved many times with insects that live on nutrient deficient diets. For instance, most aphids (Hemiptera: Aphididae) are engaged into an obligate symbiosis with *Buchnera aphidicola*, on which they rely for essential amino acids and vitamins provisioning. During the long-term co-evolution between *Buchnera* and aphids, *Buchnera* has undergone genome erosion and most of remaining genes code for metabolic functions that benefit their hosts. In several aphid lineages, multi-partner nutritional symbioses have evolved several times and an additional partner, often *Serratia symbiotica*, complements *Buchnera*. Though *Serratia* is found as a co-obligate partner in many aphids, it is unknown if it co-diversifies with its hosts. It is also unknown whether it evolves at the same pace as *Buchnera* and whether its presence, modifies the selective regime of the primary symbiont and promotes further genome erosion. Here we used whole-genome endosymbiont sequences of *Cinara* aphids that harbour both *Serratia* and *Buchnera*. Through phylogenomic reconstruction, we show that *Serratia* has been acquired several times in this lineage.

However, one of these acquisitions has led to 25 MY of co-speciation between the three partners. The shift, from facultative symbiont to obligate intracellular induced large genome reduction in Serratia, increased A+T content, and low rate of indels and nonsynonymous substitution. We further demonstrate that both symbionts undergo similar substitution rates and investigate whether their cohabitation induces relaxed selection on *Buchnera*'s metabolic functions. Our results show that independently acquired symbionts, at different stages of degeneration, can evolve at the same pace.

Abstract ID: 2016

Symbiont replacements are the rule rather than the exception in scale insects

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Obligate host-beneficial symbioses are often viewed as extremely stable over evolutionary time. In plant sap feeding insects, diverse microorganisms supplement essential nutrients lacking from the host diets. As a result, many of these insect lineages have maintained their ancient symbionts over long evolutionary time scales. Perhaps the most striking examples are *Sulcia muelleri* in Auchenorrhyncha or *Buchnera aphidicola* in aphids that have been co-diverging with their insect hosts for over 200 million years. However, there is growing evidence from insect lineages such as adelgids or scale insects suggesting that replacements of ancestral and well-established symbionts (as well as more recent co-obligate symbionts) occur more frequently than originally anticipated. Unfortunately, this pattern of symbiont replacements has been rarely investigated with rich taxon sampling and interpreted together with the host ecology and phylogeny. Scale insects (Hemiptera: Coccomorpha) are an ideal group to test this hypothesis since they have been shown to harbor a surprisingly diverse set of obligate microbial symbionts. Here, we used host-symbiont metagenomics and microscopy to investigate symbioses of these understudied scale insect lineages in detail. We confirm that the diverse microbial symbiotic systems of scale insects originate via constant replacements and partly link the replacements to ecological traits of the hosts and lineage-specific genome reduction of the symbionts.
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Abstract ID: 1920

Context-dependent resource allocation in the mutualism between figs and their pollinator fig wasps

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Stability of mutualisms has been explained by mechanisms like partner choice and host sanctions, which are context-dependent outcomes that highlight the dynamic nature of such interactions. Context-dependency in resource allocation within pollination

mutualisms is rarely explored, although most such mutualisms are mediated by resources. We investigated the dynamics of resource allocation in the fig–fig wasp brood site pollination mutualism, focusing on the closed fig inflorescence (syconium) within which seeds of the fig and the offspring of pollinator wasps develop. We introduced increasing numbers of experimentally manipulated pollinator wasps to produce syconia containing either seeds or galls alone or both. Significantly higher resources were allocated to syconia that contained both seeds and galls compared to those containing either of them alone. Although this increase did not translate to larger seeds or wasps in such syconia, a consistent pattern of slight increase was observed. This indicates the presence of interaction between plant and pollinator fitness components to maximize local resource allocation. Syconia containing only seeds produced higher number of seeds compared to those containing seeds and galls. Thus, galls can have a direct negative impact on fig fitness. Syconia walls were thicker when containing pollinator galls possibly to protect pollinators from externally-ovipositing parasitoids. Resource allocation to the syconium also increased in a density-dependent manner with increasing numbers of introduced pollinators. Therefore, resource allocation in pollinator mutualisms is dynamic, regulated by both interacting partners. Coevolution between partners and partner interdependence in resource allocation within pollination mutualisms need further exploration.

Abstract ID: 1577

Multiple keys to one lock: the role of molecular exaptation in novel intracellular endosymbiosis

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Paramecium bursaria is well recognized for its facultative symbiosis with the algae *Chlorella variabilis*, in which bidirectional transfer of benefits occurs in an evolutionarily stable association. This system is characterized by the phenomenon that symbiosis can occur between ciliates and algae that do not share an evolutionary history and which are therefore likely naïve to each other's biology. How these symbiotic leaps of faith occur despite the potential challenges presented to both parties remains an open question in the study of host-symbiont coevolution. To fill this gap in knowledge, we elucidated the molecular underpinnings of this symbiotic flexibility by coupling comparative transcriptomics with experimental cross-inoculations of *P. bursaria* with *C. variabilis*, the native symbiont of *P. bursaria*, and *Micractinium tetrahymenae*, the algal symbiont of the ciliate *Tetrahymena utriculariae*. We tested two hypotheses: 1) that similar genetic profiles are involved in endosymbiosis of *M. tetrahymenae* and *C. variabilis* with their respective native hosts and 2) that this shared suite of genes enables the infection of a novel host. We discovered that despite evolving in similar host environments, substantial non-overlap in pathways that are involved in inhabitation of ciliates exists between the two algae. Furthermore, we found a that significant number of genes that are not expressed under native symbiotic conditions in *M. tetrahymenae* are recruited for symbiosis with the novel host *P. bursaria*. Together, these results contribute to our understanding of how new intracellular endosymbioses can spontaneously establish and are facilitated by pre-existing molecular toolkits.

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Abstract ID: 1168

Endoparasitoidism promotes viral domestication

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During evolution, accidental integration of viral elements within eukaryotic genome may occur. These elements can sometimes provide major evolutionary advantages to recipient genomes: this is known as viral domestication. For instance, in some endo-parasitoid wasps (whose immature stages develop inside their hosts), the fusogenic property of viruses has been repeatedly domesticated following ancestral dsDNA viral integrations. Those endogenized viral genes are used by the female wasps as a delivery tool to inject virulence factors, essential to the developmental success of their offspring. Because all known cases of viral domestication involved endo-parasitic wasps, we hypothesized that this lifestyle (promoting close interaction between individuals) may have favored endogenization and domestication of viruses. By analyzing the genomic composition of 124 Hymenoptera genomes spread over the diversity of Hymenoptera and including free-living, ecto and endo-parasitoid species, we tested this hypothesis. Our analysis first revealed that double-stranded DNA viruses were more often endogenized and domesticated than expected based on their estimated relative abundance in viral communities infecting insects compared to other virus genomic structures (ssDNA, dsRNA, ssRNA). Secondly, our analysis revealed that endogenization and domestication of dsDNA viruses were more frequent in lineages with endo-parasitoid lifestyle compared to lineages with ecto-parasitoids or free-living lifestyles. Hence, these results suggest that endo-parasitoidism has favored the domestication of dsDNA viruses or conversely that dsDNA virus domestication has favored the evolution of endo-parasitoidism.

Abstract ID: 1169

Tumors alter life-history traits in the freshwater cnidarian *Hydra oligactis*

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While tumors can occur during the lifetime of most multicellular organisms across the tree of life and have the potential to influence health, how they alter life-history traits in tumor-bearing individuals remains poorly documented. Here, we explore this question using the freshwater cnidarian *Hydra oligactis*, a species whose individuals sometimes harbor tumors capable of vertical transmission when the host reproduces asexually by budding. We found that tumorous polyps under our experimental conditions have a reduced life expectancy compared to healthy ones. However, the formers also displayed higher asexual reproductive effort during their early life, by producing more often multiple buds and with a shorter time interval between reproductive episodes, than healthy ones. Because asexual reproduction in tumorous hydra always favors the transmission of tumor cells, it remains unknown if the altered reproductive strategy is adaptive for the host and/or for the tumor cells. Interestingly, a similar enhanced reproductive effort is also observed in the context of sexual reproduction (estimated through gamete production). Since tumoral cells are not transmitted through this reproductive way, this finding suggests that hosts may adaptively respond to tumors, compensating the expected fitness losses by increasing their immediate reproductive effort. This study supports the hypothesis that tumorigenesis has the potential to influence the biology, ecology and evolution of their multicellular hosts, and thus should be considered more by evolutionary ecologists.

Abstract ID: 1177

Endogenous viral elements in shrew genomes provide insights into Flaviviridae ancient history

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As viral genomic imprints in host genomes, endogenous viral elements (EVEs) shed light on the deep evolutionary history of viruses, ancestral host ranges, and ancient viral-host interactions. EVEs are thus genomic fossils to compensate for the absence of physical fossil traces of viruses. Flaviviridae are an important family of viruses, including well-known human pathogens, such as Zika, dengue, or hepatitis C viruses. Most EVEs derived from Flaviviridae have been identified in arthropods, but none, to date, in the genome of mammals, even though the family encompasses numerous mammal-infecting members. Through a comprehensive in silico screening of a large dataset of available mammalian genomes, our study (Li et al. https://doi.org/10.1101/2022.02.11.480044) identified two novel Flaviviridae-like EVEs in the reference genome of the Indochinese shrew (*Crocidura indochinensis*), a first in mammals. Homologs of these novel EVEs were subsequently detected in an additional 27 shrew species, including 26 species representing a wide distribution within the Crocidurinae subfamily and one in the Soricinae subfamily on different continents. Based on this wide distribution, we estimate that the integration event occurred before the last common ancestor of the subfamily, about 10.8 million years ago, attesting to an ancient origin of Flaviviridae.

Abstract ID: 1411

Protection of vulnerable colony members against nematode attack by social immunity in ants

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Ant colonies encounter a multitude of different pathogens, against which they are protected by individual, but also collective disease defence, where colony members cooperatively perform hygiene measures and engage in sanitary care of pathogen-exposed colony members. This allows the colony to efficiently control disease by “social immunity”. We here use a nematode-bacteria model to study the effects of worm-borne disease in ants and the colony-level anti-nematode defence. We find that the brood of the black garden ant Lasius niger is susceptible to the predatory nematode Heterorhabditis bacteriophora, whilst adults can protect themselves against nematode infection. Importantly, they provide sanitary care to the vulnerable brood, which effectively protects the colony offspring from nematode attacks and strongly increases its survival. We currently observe what factors form this protective effect, including sanitary behaviour, use of disinfectants, and morphological characteristics. We also study the costs of this social brood protection to the adults, particularly when the colony is facing multiple disease threats at the same time, including those that the adults themselves are also susceptible to. This allows us to understand the complex interplay of individual and social immunity to reach colony-level disease protection in social insects.

Abstract ID: 1459

Beyond the next variant: evolutionary interactions between host and hantavirus speciation

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Speciation of viruses is probably often driven by co-divergence with their hosts or by host-shifts. However, it remains generally unknown whether deep phylogenetic clades within named virus species in nature represent functionally or evolutionarily distinct units. Here we examined the evolutionary interactions between widespread phylogenetic clades within European Tula hantavirus (TULV) and multiple levels of evolutionary divergence in its natural host, the common vole (*Microtus arvalis*). Our fine-scale analyses revealed that the spatial transitions between TULV clades typically occur at the sub-kilometer scale in the open landscape - irrespective of the extent of gene flow or evolutionary divergence between host populations. Parapatric TULV clades differed genome-wide by 14 – 18% of which only 0.5 - 1% was non-synonymous sequence variation. Clade comparisons detected a single spike of positive selection located in the viral surface glycoprotein gene. Shifted geographic clines indicated that very few dominant alleles segregating between *M. arvalis* lineages constrain the distribution of TULV clades, and we identified single polymorphisms in the vole genomes explaining up to 38% of the variance in infection. However, recombination or reassortment between TULV clades was absent even within the same host lineage and the effective transmission of these RNA viruses between natural host populations is already impeded at surprisingly little ecological and evolutionary differentiation. In conclusion, evolutionary divergence within the host clearly promotes divergence in TULV overall but functional

speciation has happened also much below the level of recognized species. Adaptive processes can thus disconnect virus speciation from simple co-divergence with their hosts.

Abstract ID: 1949

Large-scale turnover of immune receptor gene copies in zebrafish

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Multicellular eukaryotes have evolved a plethora of diverse immune defences. In some cases, whole gene families have undergone vast expansions. A prominent example is the presence of more than 300 paralogous genes from the NACHT domain and Leucine-rich repeat containing (NLR) gene family of intracellular immune recptors in the model vertebrate zebrafish. Zebrafish NLRs are divided into four groups based on the sequences of their NACHT domain and most reside on the heterochromatic long arm of a single chromosome.
We used targeted PacBio sequencing to obtain sequence data for exons of NLRs from 93 zebrafish, representing two common laboratory strains (TU and KOELN) and four wild populations from the native range of the species. This allowed us to investigate the recent evolutionary trajectory of this gene family in far greater depth than was possible by analyzing a single reference genome.
We show that turnover of NLR genes is an ongoing and rapid process, and that laboratory domestication has led to a decline in copy numbers for both laboratory strains studied. Many NLRs appear to be under balancing selection, evidenced by high degrees of polymorphism in the exonic sequences. We propose that the high levels of sequence and copy number variation are possibly a signature of repeated adaptation to a wide array of pathogens.

Abstract ID: 1491

Intensity of sexual conflict affects longevity in *Drosophila melanogaster* subjected to FLX evolution

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Decrease in *Drosophila melanogaster* female longevity caused by mate harm is a classic example of interlocus sexual conflict. However intralocus sexual conflict may also have the potential to affect longevity, if males and females have different optimal lifespans. Here we used a previously established female-limited X chromosome (FLX) evolution experiment to investigate if longevity is primarily constrained by intra- or interlocus sexual conflict. We were able to disentangle these two effects, because although female-limited X chromosome evolution should induce release from intralocus conflict, the experimental protocol we used to enforce matrilineal inheritance of the X chromosome resulted in increased female control over mating rates occurred as a by-product. We did not find convincing evidence of intralocus sexual conflict over longevity in *D. melanogaster*. Instead, and in accordance with previous results, we found that longevity seems to mainly be subject to interlocus conflict. Specifically, we found that an increase in female control over mating rate resulted in longer female lifespan, but reduced male lifespan,

and that these effects were dependent on social context (isolated or in mixed-sex groups). Unlike previous studies, our experiment did not manipulate environmental conditions nor the adult sex ratio, which is likely to reduce both pre- and post-copulatory sexual selection. Our results therefore suggest that female choice is an important component in shaping longevity in this species.

Abstract ID: 1773

Heritability and age-related changes in genetic variation of telomere length in a wild passerine

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Telomeres play an important role in mediating cellular senescence, and telomere dynamics are linked with survival and lifespan, making it a popular candidate biomarker for senescence. To determine the evolutionary potential of telomere dynamics, and to characterize the selection pattern that gives rise to senescence, it is necessary to quantify genetic variation in telomere length (TL), and how such variation changes with age. In this study, we analysed a longitudinal dataset (2,156 samples from 1,267 individuals across 15 years) from a wild, insular house sparrow (*Passer domesticus*) population with complete life history and pedigree data. Using a series of 'animal' models, we investigated whether 1) TL changes with age; 2) TL is repeatable and heritable; and 3) there is genotype-by-age interaction in telomere length, resulting in changes in genetic variance with age. We confirmed that telomere length declines with age within, but not across, individuals, suggesting selective disappearance of old individuals with short telomeres. Repeatability and heritability were 15.2% (95% CrI: 10.2% – 21.0%) and 13.6% (95% CrI: 8.7% – 19.5%), respectively. For the first time in a wild population, we report a genotype-by-age interaction in telomere length, where genotypes differ in their rate of TL change, and additive genetic variance increases at older ages, confirming current evolutionary theory. Our findings supported the use of telomere dynamics as biomarkers of senescence, and encouraged further research in genetic correlations of telomere dynamics and fitness to better understand the evolution of senescence.

Abstract ID: 2084

Investigating molecular signatures of ageing across two origins of eusociality in bees

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Advanced eusocial insect species such as honeybees, leafcutter ants and termites seem to have overcome the fecundity/longevity life-history trade-off that is a basic tenet of solitary multicellular organisms; queens in some of these eusocial insect species have high reproductive output, yet live for one or two orders of magnitude longer than their lowly fecund, even sterile workers. Bees are an ideal group for investigating the apparent remoulding of the fecundity/longevity trade-off associated with advanced eusociality because they exhibit a wide range of social behaviours, both within and between species. Using a comparative approach, we analysed gene expression (GE) data of solitary, facultative, primitively, and advanced eusocial species from two taxonomic lineages that have independently evolved eusociality from their solitary ancestors: sweat bees (Halictinae) and corbiculate bees (Apinae). We quantified differences in GE between young and old individuals, including workers and queens of the eusocial species, to identify the genes underpinning fecundity and longevity. We used brain and fat body GE profiles across all species comparisons, which allows us to disentangle caste and age-specific signatures. Results of differential GE and co-expression network analyses suggest that changes in GE with age are associated with social status. Several genes and related gene networks are involved in the remoulding of the trade-off, including TOR and antioxidant pathways, while juvenile hormone titres appear not to be involved. Our results advance our mechanistic understanding of the molecular pathways underpinning this trade-off, and how and where they were reprogrammed along the sociality spectrum.

Abstract ID: 2183

Longitudinal characterization of maternal-age effect on germline mutation rate in the leafcutter ant

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Germline mutations (GMs) are the ultimate source of genetic diversity and the fuel for evolution, and the rate at which they arise, germline mutation rate (GMR), is thus central to many evolutionary questions. GMR increases substantially as individuals age (parental age effect), and a precise characterization of this variation requires within-pedigree longitudinal investigation of GMRs (i.e., comparing GMRs between offspring produced by the same parents at different ages). However, currently available GMR estimates are exclusively derived across pedigrees (i.e., across individuals produced by different parents at different ages), where inter-pedigree variation is inseparably confounded in the correlation between GMR and parental age. Moreover, GMR is predominantly studied in species with biparental inheritance, which greatly limits the fraction of analyzable genome because GMs can only be identified in regions where both parents contribute the same homozygous allele. By contrast, uniparental inheritance allows identification of GMs across the entire genome. In this study, we performed a longitudinal study to investigate maternal-age effect on GMR using four pedigrees of the leafcutter ant, *Acromyrmex echinatior.* In *A. echinatior*, inseminated mother queens produce unfertilized haploid eggs which develop into male (haplodiploidy); this implies that GMs in sons are always solely maternally inherited, which obviates the difficulties associated with parental heterozygosity. By deriving and comparing GMR estimates from four queens and their sons produced at young (1-4 years), middle (5-8 years) and old (> 9 years) maternal ages, we provide the first systematic characterization of age-dependency of GMR variation throughout life.

Abstract ID: 2378

Runs of homozygosity analyses on reduced genomic data allow correct ranking of inbreeding estimates

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Runs of homozygosity (ROHs) are proxy for genomic Identical-by-Descent segments and increasingly used as a measure for individual inbreeding. ROHs analyses are mostly applied to SNPs-arrays and whole-genome-sequencing data. Softwares used for their detection assume that non-genotyped genomic positions are non-variant. This assumption might be true for whole-genome-sequencing data, but not for reduced genomic representations and can lead to spurious ROHs detection. We simulated the outputs of whole-genome-sequencing, SNP-arrays and RAD-sequencing for populations of different sizes. We compared the results of ROHs calling with two softwares: *PLINK* and *RZooRoH*. We show that, when a sufficient fraction of genome is sequenced, ranks of ROHs-based inbreeding coefficients are conserved among individuals and most of the genome is correctly assigned within and outside ROHs. We show that SNP density can be used as a proxy for the suitability of the reduced-genomic data for ROHs analyses: *RZooRoH* required a minimum of 3,000 SNPs/Gb while *PLINK* required a minimum of 20,000 SNPs/Gb to conserve the ranks of inbreeding between WGS and RAD-sequencing. With reduced representation, we find ROHs distribution are consistently biased towards an underestimation of the total numbers of small ROHs and an overestimation of the total numbers of large ROHs. Finally, we discuss the relevance of using ROHs vs SNP-independent-based measures of inbreeding coefficients with reduced genomic representations.

Abstract ID: 2108

Monitoring within-species genetic diversity of amphibians with eDNA metabarcoding

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Ongoing habitat alterations and climate change can lead to a dramatic decline in local populations, and cost-efficient tools to rapidly estimate population genetic diversity in space and time are urgently needed. Here we used the common frog *Rana temporaria* (Linnaeus, 1758) from 10 wetland sites in the Italian Alps to: i) develop and test a standardized eDNA metabarcoding protocol for the monitoring of within-species genetic diversity (targeting a short fragment of the COI barcode region); and ii) critically compare the results of eDNA metabarcoding with those obtained from traditional genetic

sampling. Our results showed that a single temporal sampling replicate performed after spawning (and when egg clutches and/or larval stages are still present in the water) is sufficient to successfully characterize haplotype richness, but two temporal replicates are needed to obtain more accurate information on haplotype frequencies. We then demonstrated that standard genetic variability estimates (haplotype and nucleotide diversity) derived from eDNA metabarcoding are strongly correlated with those derived from traditional genetic data. Similarly, we also found a moderate but yet significant correlation between the population structures inferred from the two considered methods. Thus, our protocol proved to be a fast and effective tool that could be used for the establishment of a surveillance network, with the ultimate goal of monitoring temporal trends in the genetic diversity of pond-breeding amphibians.

Abstract ID: 997

The origin of meiosis from eukaryogenesis

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The origin of sexual reproduction in eukaryotes is an evolutionary mystery. Sexual recombination can promote purifying selection and reduce selective interference, but similar advantages are achieved in prokaryotes through lateral gene transfer (LGT). The selective pressures behind the evolution of a novel mechanism of genetic exchange in eukaryotes – sexual reproduction – are still obscure. In this talk, I discuss how the origin of meiotic sex is tightly linked to the process of eukaryogenesis. The transition from prokaryotes to eukaryotes involved an expansion in genome size, together with the proliferation of genomic repeats. Using computational models, I show that large genomes are vulnerable to the progressive accumulation of deleterious mutations through Muller's ratchet, whilst limiting LGT's ability to purge deleterious mutations. A high repeat density introduces an additional cost to LGT, because of the increased genomic instability arising from ectopic recombination. The way of avoiding catastrophic gene loss is to combine increased recombination length with the requirement for sequence homology – a first step towards meiotic homolog pairing. Homology along extended sequences of DNA allows recombination to take place across a considerable fraction of each chromosome, which is sufficient to halt the decay of eukaryotic-sized genomes through Muller's ratchet. The transition to linear chromosomes and homolog pairing minimises the risk of ectopic recombination and the associated loss of genetic information, allowing the evolution of larger and more complex eukaryotic genomes.

Abstract ID: 1086

Adaptive evolution under rewired genetic codes

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The standard genetic code is extremely robust to the effects of point mutations: the missense mutations it allows are conservative with respect to key physicochemical properties of amino acids. Recent advances in synthetic biology enable the engineering of organisms with rewired genetic codes, making the rational design of non-standard

genetic codes an important challenge. As a means to enhance evolvability, previous work has proposed rewired genetic codes that maximize the mutagenic potential of point mutations. Here we study the effects of such rewired codes on adaptive evolution. We characterize the topographies of empirical genotype-phenotype landscapes for three different proteins under the standard genetic code, as well as under a variety of rewired codes, and perform population-genetic simulations on these landscapes. We show that more robust genetic codes in general cause smoother genotype-phenotype landscapes, suggesting that such codes, perhaps counterintuitively, promote evolvability, because in a smooth landscape the evolving population is more likely to reach the global adaptive peak than in a rugged landscape. Indeed, our population-genetic simulations show this to be the case under high mutation supply. In particular, we show that populations using the genetic codes specifically designed for increased evolvability do not in general reach higher fitness values than populations using more robust codes. Based on our results, we suggest several alternative genetic codes, requiring only few changes compared to the standard genetic code and compatible with a previously engineered 57-codons *E. coli* strain, that we expect to provide increased evolvability compared to the standard genetic code.

Abstract ID: 1681

Population genetics of small isolated populations

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Small isolated populations are a raw material for speciation. Populations that get isolated from the main population are often small and soon begin evolving independently. However, small populations are prone to impacts of drifts and inbreeding which makes them vulnerable to extinction. With whole genome sequences of several endangered populations of tigers and rhinocerous we show that small isolated populations often purge some of their deleterious allele loads. However, whatever deleterious alleles remain in the population, are in high frequency and homozygosity. This might lead the population to extinction. We further observe with simulations and emperical observations that migrations from a different population although increases the deleterious allele load, also leads to decrease in frequency of deleterious alleles and their homozygosity. Does this indicate that allopatric species also needs mild gene flow from other populations?

Abstract ID: 1716

Through the lens of experimental evolution: a genome-wide view of the mutation process in *C. elegans*

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Experimental investigations into the rate, spectrum and fitness effects of spontaneous mutations are central to the study of evolution. In order to reveal the genome-wide consequences of mutations under drift versus selection, we experimentally evolved 35 mutation accumulation lines of *Caenorhabditis elegans* in parallel for 409 generations at three population sizes (N = 1, 10, 100 individuals) followed by massively parallel Illumina paired-ends sequencing to assess the interaction between mutation and selection at a

genome-wide scale. In this talk, I synthesize key conclusions from multiple studies investigating all major classes of variants (SNPs, small indels and CNVs) in both the mtDNA and nuclear genomes with a focus on their (i) rates of origin, (ii) genomic features and sequence context, and (iii) the relative roles of selection versus drift in shaping their evolutionary dynamics. Our results provide support for as well as refute some preceding conclusions about the mutation process in *C. elegans* that were based on partial genomes and older sequencing technologies. We demonstrate a significant negative correlation between population size and (i) the accumulation of mtDNA mutations, (ii) gene deletion rates and (iii) transcript abundance of duplicated genes. Notably, there was no correlation between the frequency of nuclear SNPs, nonsynonymous substitutions or small indels with population size. The differences between the results for mtDNA mutations and gene copy-number changes on the one hand, and nuclear SNPs and small indels, on the other, are consistent with the view that the former have, on average, more detrimental effects on fitness.

Abstract ID: 2317

Pervasive selection biases inferences of the species tree

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Despite the importance of natural selection in species' evolutionary history, phylogenetic methods that take into account population-level processes typically ignore selection. The assumption of neutrality is often based on the idea that selection occurs at a minority of loci in the genome and is unlikely to compromise phylogenetic inferences significantly. However, genome-wide processes like GC-bias and some variation segregating at the coding regions are known to evolve in the nearly neutral range. As we are now using genome-wide data to estimate species trees, it is natural to ask whether weak but pervasive selection is likely to blur species tree inferences. We developed a polymorphism-aware phylogenetic model tailored for measuring signatures of nucleotide usage biases to test the impact of selection in the species tree. Our analyses indicate that although the inferred relationships among species are not significantly compromised, the genetic distances are systematically underestimated in a node-height-dependent manner: that is, the deeper nodes tend to be more underestimated than the shallow ones. Such biases have implications for molecular dating. We dated the evolutionary history of 30 worldwide fruit fly populations, and we found signatures of GC-bias considerably affecting the estimated divergence times (up to 23%) in the neutral model. Our findings call for the need to account for selection when quantifying divergence or dating species evolution.

Abstract ID: 1066

Integrating phylogenetic estimation with complex evolutionary models in phylogenetic inference

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In empirical studies, phylogenetic inference is frequently split from the inference of the diversification history and parameters. First, a phylogeny is reconstructed under a simple

model of evolution such as the Yule process (in Bayesian inference) or no model at all (in Maximum Likelihood inference). In both cases, all the phylogenetic uncertainty is then discarded and a single phylogeny is used to fit more complex models such as the SSE family of models, with evolutionary regimes tied to a lineage-specific character. This procedure is widely used, however the impact of using two different models to first estimate the tree and then fit evolutionary parameters has not been evaluated. Here, we compare the results of this two-step process to full phylogenetic inference, which combines substitution and clock models with a more complex tree model in a Bayesian inference and thus co-estimates the phylogeny and the evolutionary model from molecular data. We evaluate the impact of both methods on the accuracy of the phylogeny estimate as well as the reconstruction of complex evolutionary histories.

Abstract ID: 1788

The evolutionary impacts of synonymous mutations

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During the 50 years since the genetic code was cracked, our understanding of the evolutionary consequences of synonymous mutations has undergone a dramatic shift. Synonymous codon changes were initially considered selectively neutral, and as such, exemplars of evolution via genetic drift. However, the pervasive and non-negligible fitness impacts of synonymous mutations are now clear across organisms. Despite the accumulated evidence, it remains challenging to incorporate the effects of synonymous changes in studies of selection, because the existing analytical framework was built with a focus on the fitness effects of nonsynonymous mutations. I will trace the development of this topic and discuss the evidence that gradually transformed our thinking about the role of synonymous mutations in evolution. I suggest that our evolutionary framework should encompass the impacts of all mutations on various forms of information transmission. Folding synonymous mutations into a common distribution – rather than setting them apart as a distinct category – will allow a more complete and cohesive picture of the evolutionary consequences of new mutations.

Abstract ID: 1811

Testing Wright's intermediate population size hypothesis – when genetic drift is a good thing

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In his 1931 monograph, Wright predicted that genetic drift would overwhelm selection in small populations, and selection would dominate in large ones, but he also concluded that drift could facilitate selection in populations of intermediate size. He predicted that drift and selection would act together to prevent accumulation of genetic load ("degeneration") and promote allele frequency changes that are "relatively rapid, continuing, irreversible, and largely fortuitous." In spite of these assertions, the idea that drift and selection would act together in populations of intermediate size has been almost completely ignored. In collaboration with Michael Wade, I used forward-time simulations with random mating and discrete generations to test the hypothesis that drift facilitates

selection in populations of intermediate size. We find that selection generates asymmetrical distributions of Δq, and this asymmetry is greatest for population sizes between ~20 and ~200, resulting in drift facilitation of selection. Drift facilitation reduces the accumulation of drift load and inbreeding load for populations of intermediate size compared to small and large populations under deleterious mutation pressure (s and h ranging from 0 to 0.2). Fixation of beneficial mutations is facilitated in intermediate populations when dominance is low and selection is weak. Compared to predictions of fixation time for codominant beneficial mutations from diffusion equations, drift facilitation accelerates fixation in populations of intermediate size, but fixation time is retarded in large populations. Our results suggest that intermediate population sizes promote purging and fixation of beneficial mutations, and may result in relatively rapid adaptation.

Abstract ID: 1840

Reproductive barriers and genomic hotspots of adaptation during allopatric species divergence

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Theory predicts that in allopatric populations, genomic divergence and reproductive barriers will be driven largely by random genetic drift, and thereby evolve slowly in large populations. However, local adaptation and divergence under selection may also play important roles, which remain poorly characterised. Here we address three key questions in young allopatric species: (a) How widespread are genomic signatures of adaptive divergence?, (b) What is the functional space along which young sister species show divergence at the genomic level?, and (c) How quickly might prezygotic and postzygotic reproductive barriers evolve? Analysis of 82 re-sequenced genomes of the Oriental *Papilio polytes* species group revealed surprisingly widespread hotspots of intense selection and selective sweeps at hundreds of genes unique to each species, and spanning all chromosomes, rather than divergence only in a few genomic islands. These genes perform diverse ecologically important adaptive functions such as wing development, colour patterning, courtship behaviour, mimicry, pheromone synthesis and olfaction, and host plant use and digestion of secondary metabolites, that could contribute to local adaptation and subsequent reproductive isolation. Divergence at such functional genes appeared to have reproductive consequences: behavioural and hybridisation experiments revealed strong assortative mate preference (prezygotic barriers) as well as postzygotic barriers to hybridisation in timespans as short as 1.27 my, indicating that speciation was already complete, rather than incipient. Our study thus demonstrates an underappreciated role of intense selection and potential local adaptation in creating genome-wide hotspots of rapid molecular evolution and divergence, during differentiation and speciation in young allopatric species.

Abstract ID: 1923

Topological comparison of coalescent tree inference tools.

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Several methods for inferring gene genealogies from genetic variation data have been developed in recent years. They can handle much larger sample sizes than the previous ones. We focused on **tsinfer** and **Relate**, two programs that allow inferring coalescent trees from genetic data for thousands of individuals, at low computational cost. However, there was still no topological comparaison for the generated trees. We propose a comparison based on multiple topological indices showing differences in behavior between the two programs.
To generate genetic datasets corresponding to coalescent trees with different levels of imbalance, we implemented a simulation-based approach modeling Cultural Transmission of Reproductive Success (CTRS). CTRS is a positive correlation between the sibling size of an individual and his/her number of children. It has been shown in multiple human populations. It directly impacts the coalescent tree shape, whose level of imbalance increases with CTRS, which favors access to reproduction for individuals with large sibling size.

Abstract ID: 1921

Jumping over the genomic cliff: demographic history and adaptations in the Norwegian lemming

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The Norwegian lemming (*Lemmus lemmus*) is a small rodent distributed across the Fennoscandian mountain tundra and the Kola Peninsula. Endemic to this area, it has been suggested to evolve during the Pleistocene and inhabit this region since before the Last Glacial Maximum. However, the exact origins of the species, its phylogenetic position relative to the Siberian lemming (*Lemmus sibiricus*), a closely related species, and the presence of contemporary or ancestral gene flow between both species are still largely unknown. Moreover, *L. lemmus* displays characteristic phenotypic adaptations to their environment (i.e., coat color, thermoregulation, circadian rhythms) that are not present in other cold-adapted lemmings. To investigate these questions, we sequenced the complete genomes from five modern and two ancient *L. lemmus*, along with modern genomes from *L. sibericus* western lineage, *L. sibericus* eastern lineage, and *L. trimucronatus*. We reconstruct the population genomic history of *Lemmus* to investigate the origins of *L. lemmus*, determine whether the western and the eastern lineages of *L. sibericus* are the same or distinct species, estimate the divergence times for all of these species, and examine the presence of gene flow among *Lemmus* species. Finally, we investigate the genomic basis of the adaptations that make *L. lemmus* unique in the context of the other *Lemmus* species.

Abstract ID: 1433

Testing hypotheses of coevolutionary key innovations with CRISPR, caterpillars, and cabbages

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Coevolution is responsible for much of the Earth's biodiversity, with key innovations driving speciation bursts on both sides of a coevolutionary interaction. A classic coevolutionary system is that of mustards and the Pierid caterpillars that eat them, where mustards have evolved increasingly complex glucosinolate-myrosinase defenses and Pierid caterpillars have adapted to detoxify them. These chemical defenses and detoxification mechanisms are considered key innovations, as they have been linked with increased speciation rates in their respective clades. However, few studies have investigated the function and fitness consequences of the genes underlying these adaptations, or those underlying key innovations in general. To address this gap, we used CRISPR/Cas9 gene editing in the butterfly species *Pieris brassicae* to manipulate two closely-related gut enzyme genes responsible for glucosinolate detoxification (*NSP* and *MA*). We found that *NSP* and *MA* are required for survival on plants containing glucosinolates and that differences in *MA* and *NSP* expression arise in response to variable glucosinolate profiles, concordant with their detoxification performance. Importantly, this concordance was only observed when using natural host plants, likely reflecting the complexity of the interaction between these gut enzymes and natural plant variation in glucosinolates and myrosinases. We also discovered that signatures of positive selection for *NSP* and *MA* can be detected across *Pieris* species. In sum, our findings reveal that the coevolutionary dynamics between Pieridae butterflies and their host plants are both ongoing and more complex than previously thought, with gene regulation and activation representing key components of this plant-insect interaction.

Abstract ID: 2093

Predicting the phenotype from the genotype?-The case of the vomeronasal organ of semiaquatic mammals

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The vomeronasal system or accessory olfactory system is a sensory system involved in the detection of pheromones. It comprises the accessory olfactory bulb in the anterior brain and the vomeronasal organ located in the anterior nose. Although it is present and functional in most mammalian species, it was found to be non-functional and anatomically reduced or absent in aquatic mammals. An important marker gene is *Trpc2*, which was found to be inactivated in a previous study, using a comparative genomic approach, not only in the species for which a reduction of the vomeronasal structures was documented, but also for the semiaquatic Phocidae and Lutrinae. Here we used diceCT to determine the anatomical condition of the vomeronasal organ in two members of these taxa, respectively the semiaquatic Eurasian otter (*Lutra lutra*) and the harbour

seal (*Phoca vitulina)* to test if the genotype is reflected in the phenotype. We added two more semiaquatic mammalian species, the rodents *Myocastor coypus* and *Ondatra zibethicus* for comparison. All specimens were stained with Lugol's iodine, µCt scans were acquired and visualized as 3D models. The vomeronasal organ of the otter is present, but comparatively small and it is absent in the harbor seal. The VNO of the two rodent species is present and appears to be well developed. We conclude that the inactivation of *Trpc2* is reflected in a reduction of the vomeronasal organ, however it is not possible to determine the extent of this reduction.

Abstract ID: 2236

DNA methylation patterns in the placenta of viviparous fish

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When the interests of males and females over investment in reproduction diverge, this can lead to sexual conflict. The evolution of viviparity and its adaptations may increase the potential for conflict between males and females - and possibly between mother and offspring -, and also sets the stage for a genetic conflict between both paternal and maternal alleles in embryonic tissues and between maternal and embryonic genes in embryonic tissues. Such conflict has the potential to affect gene regulation in multiple ways, including via changes in epigenetic marks such as DNA methylation, which can modulate and silence gene expression in key tissues. We investigated the incidence of DNA methylation in the embryonic component of the placenta (trophotaenia) of several species of a family of viviparous fish (*Goodeidae*) that differ in the degree of sexual dimorphism of colours, courtship and morphology suggestive of sexual conflict. We conducted Whole Genome Bisulphite Sequencing on trophotaeniae and on muscle tissue as a control. Here, we describe the DNA methylation patterns of the trophotaenia across 4 different species which contrast in the levels of dimorphism, courtship complexity and trophotaenia type, and explore the gene functions associated with Differentially Methylated Regions.

Abstract ID: 1014

Sex differences in parental responses to offspring begging

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Mothers, fathers and offspring regularly clash over how much care offspring should receive. Because optimal levels of parental investment differ for these individuals, parent-offspring and sexual conflicts emerge. Offspring can beg to demand more resources from their parents, but do mothers and fathers respond to offspring begging in the same way? What factors generate sexual dimorphism in communication? We lack an empirical synthesis to answer these questions. We do not even have formal predictions,

as our theoretical framework for parent-offspring communication has only modeled mothers. We therefore combined a comparative meta-analysis on 30 bird species and a quantitative genetics model to determine how and why the sexes differ in their response to offspring signals. Our comparative analyses showed that males respond more to offspring begging than females in species with stronger pair bonds (i.e., with lower sexual and parent-offspring conflict); while females respond more in species with weaker, more promiscuous pair bonds (i.e., with greater conflict). We formalize and extend these findings in our model, examining how mating systems and sex differences in the cost of care affect the evolution of offspring begging and male and female responsiveness. Our results demonstrate that sex differences in parent-offspring communication are driven by variation in evolutionary conflicts. Furthermore, they indicate the necessity of communication theory modelling multiple, distinct responder classes.

Abstract ID: 1696

Sex-dependent effects of parental age on offspring fitness in a cooperatively breeding bird

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Parental age can have considerable effects on offspring phenotypes and health. However, intergenerational effects may also have longer-term effects on offspring fitness. Few studies have investigated parental age effects on offspring fitness in natural populations while also testing for sex- and environment-specific effects. Further, longitudinal parental age effects may be masked by population-level processes such as selective disappearance of poor-quality individuals. Here, we used multi-generational data of Seychelles warblers (*Acrocephalus sechellensis*) to investigate the impact of parental age on offspring lifespan and lifetime reproductive success. We found negative effects of maternal age on female offspring lifespan and lifetime reproductive success, likely driven by within-mother effects. There was no difference in annual reproductive output of females born to older versus younger mothers, suggesting that offspring lifetime reproductive success differences are driven by offspring lifespan. In contrast, there was no association between parental age and male offspring lifespan. However, lifetime reproductive success, but not annual reproductive success, of male offspring increased with maternal age, via between-mother effects. No within- or between-individual paternal age effects were found for female offspring, but fathers that reached old age produced male offspring with higher lifetime reproductive success. We did not find strong evidence for environment-dependent parental age effects. Our study provides evidence for sex-dependent parental age effects on offspring lifetime fitness. These results add to the growing literature indicating the importance of intergenerational effects on long-term offspring performance, highlighting that these effects can be an important driver of variation in longevity and fitness in the wild.

Abstract ID: 1945

Cultural evolution in the wild: tracking the landscape of diversity in bird song

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The population processes that play a role in organismal evolution—like dispersal, immigration and turnover of individuals—also have the potential to shape traits that are transmitted culturally, such as bird song. These processes are assumed to be important determinants of change, diversification, and loss of animal culture. However, teasing their relative contribution apart in the wild requires dense trait sampling and detailed individual life-history data—both notoriously hard to acquire. To this end, we have built a multi-generational dataset containing the full song repertoires of hundreds of individuals from a population of great tits (*Parus major*, Wytham Woods, UK) that is the subject of an exhaustive long-term survey. While always remaining within the bounds of the relatively small species-typical acoustic space, great tit songs are surprisingly diverse; individual birds differ in the size and novelty of their repertoires, and the 'cultural landscape' within populations shifts every year. We are taking advantage of this and our long-term dataset and, using new computational tools to study bird song, are describing how song cultural diversity responds to population processes and changes at different scales across space and time. Here we will present results from the first part of the project, where we show how both an individual's natal environment and immigration status contribute to song cultural diversity and turnover at the population level.

Abstract ID: 2400

Using machine learning to understand optimal camouflage in Cepaea snails

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Concealment from predators is often critical for survival, and selection for crypsis can be an important evolutionary driver of animal phenotypes. Traditional experimental approaches that isolate specific mechanisms of concealment have transformed our understanding of how camouflage can function with respect to different habitats and perceivers. However, these approaches fail to explain holistic animal phenotypes and whether an animal's appearance is optimal under given conditions, or subjected to as-yet unidentified constraints. Here, we predict optimal camouflage in natural environments using a machine learning approach that simulates an evolutionary arms-race between predators and prey. Prey phenotypes evolve across simulated evolutionary time to improve crypsis against natural backgrounds, with detectability to predators modelled using neural networks. We apply this approach to *Cepaea* land snails to evaluate the degree to which their polymorphic shell patterns represent optimal habitat-specific camouflage. We document *Cepaea* morph frequencies across varying habitat types and

compare these to predicted optimal forms, identifying the patterns that best conceal 3D snails in different habitats. Our machine learning approach to understanding the evolution of optimal camouflage is broadly applicable across species and circumstances, providing a powerful tool for understanding the selection imposed on animal colour patterns by different predators in diverse environments.

Abstract ID: 1095

Context-dependence of pre- and postcopulatory sexual selection in Drosophila prolongata

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The strength of sexual selection is thought to be driven by population density and the operational sex ratio due to their influence on the absolute and relative encounter rates between sexual competitors and potential mates. Both population parameters may themselves be influenced by the abundance and distribution of important resources and the degree to which they can be monopolized by certain individuals of the population. However, empirical studies on the relative contributions of these factors to the strength of, and covariation between, pre- and postcopulatory sexual selection are currently lacking. Here, we experimentally manipulated the density and composition of populations of individually marked *Drosophila prolongata* that were allowed to interact freely in artificial arenas with uneven distributions of dietary and oviposition substrate. Across five days, we monitored the context-dependent distributions of flies (e.g. monopolization of resources), social interactions, and individual mating frequencies and combinations. We then assigned parentage to the offspring to disentangle the effects of these social dynamics on both pre- and postcopulatory fitness outcomes. *Drosophila prolongata* is unusual among drosophilid flies, in that males are larger than females and exhibit exaggerated forelegs that they use in male-male competition and elaborate courtship displays, and they can employ alternative reproductive strategies to gain matings. Further, females vary substantially in their mating frequency, thereby causing considerable variation in the level of postcopulatory sexual selection.

Abstract ID: 1297

Sexually-selected weaponry and the risk of extinction under increasing temperature

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Exaggerated sexually-selected traits, occurring more commonly in males, help individuals to increase reproductive success, but are costly to produce and maintain. These costs on the one hand may improve population fitness by intensifying selection

against maladapted males, but on the other hand may increase the risk of extinction under environmental challenge. However, the impact of sexually selected traits on extinction risk have not been investigated experimentally. We used replicate populations of a male-dimorphic mite, *Rhizoglyphus robini,* to test if prevalence of an elaborate, sexually-selected weapon affected the risk of extinction under gradual temperature increase (2^0C per generation). As temperature increased, individual survival decreased, but this effect was much more dramatic in populations with high weapon prevalence, compared to populations in which weapon expression was low. Consequently, the former was significantly more prone to extinction than the latter, with 75% vs 8% populations going extinct, respectively. Extinctions occurred despite partial suppression of the weapon expression at increased temperature and were not explained by increased male mortality. Our results provide the first, to our knowledge, experimental evidence demonstrating dramatic effect of elaborated sexual traits on the risk of extinction under environmental challenge.

Abstract ID: 1328

The role of associative learning in the evolution of sexual preferences.

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How do female sexual preferences for male ornamental traits arise? The developmental origins of female preferences are still an understudied area, with most explanations pointing to genetic mechanisms. One intriguing, little-explored, alternative focuses on the role of associative learning in driving this process. According to this hypothesis, a preference learned in an ecological context can be transferred into a sexual context, resulting in changes in mating preferences as a by-product. I tested this hypothesis by first training female guppies to associate either orange or black colour with food delivery; I then presented videos of males with computer-manipulated coloured spots and measured female preference towards them. I also allowed females from both treatments to mate with males differing in their ratio of orange-to-black spots and measured the males' reproductive success. After training, female sexual preferences significantly diverged among treatments in the expected direction. In addition, orange males sired a greater proportion of offspring with females food-conditioned on orange compared to those conditioned on black. These results show that mating preferences can arise as a by-product of associative learning, which, via translation into variation in male fitness, can become associated with indirect genetic benefits, potentially leading to further evolution.

Abstract ID: 2032

Sexual selection in females and the evolution of polyandry

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The pioneers of sexual selection theory proposed that males are generally *eager* whereas females are rather *coy* with respect to mating. However, the *polyandry revolution* shifted this male-centred view towards a more nuanced perspective acknowledging that females often benefit from multiple mating, which may ultimately promote female-female competition for access to males. Despite this paradigm shift, sexual selection in females is still often considered a rare peculiarity. We present meta-analytic evidence from 77 species across a broad range of animal taxa to show that females typically benefit from multiple mating and that these fitness gains promote the evolution of more polyandrous mating systems. Our results imply that the potential for sexual selection to operate in females is widespread across the animal tree of life, which may contribute to a more balanced perspective of sexual selection in both sexes.

Abstract ID: 2163

Is sexual selection widespread across angiosperm species?

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Sexual selection is a potent force for driving the evolution of plentiful animal phenotypes and for increasing genetic quality. Sexual selection thinking solely hinges on the anisogamous nature of sexual reproduction by which females produce less numerous and larger gametes than males, thus fostering competition among males. Therefore, sexual selection theory should be universally valid for all sexually reproducing organisms displaying anisogamy, which includes plants. Yet, direct tests of fundamental concepts from the theory of sexual selection in the plant kingdom are lacking. This can be attributed to the rarity by which the central parameter in sexual selection, the number of sexual partners (*i.e.* mating success), is quantified in plant studies. Promisingly, the only two studies that have quantified mating success in plants have confirmed key predictions of sexual selection thinking, known as Bateman's principles, with male reproduction relying more on mate acquisition than female reproduction. Here we systematically re-analyse published parentage analyses in plant populations to provide a systematic quantification of the strength of sexual selection through classical Bateman metrics. Specifically, we estimate a genetic proxy of mating and reproductive success by performing parentage analysis and quantify their linear relationship in each sex. Our first analyses of a dozen of such datasets confirms the validity of Bateman's principles across these plant species. By overcoming a major conceptual barrier in the study of sexual selection in plants, our results point to the pressing need to comprehensively test predictions of the sexual selection theory in plants.

Abstract ID: 2325

Attractive males have more male offspring, but why are results so heterogeneous?

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The fascinating idea that female birds may be able to adjust the sex ratio of their broods to the quality of their mating partner generated considerable research. It was argued that the reproductive success of male offspring is influenced more by the inherited paternal attractiveness/quality than that of female offspring, thus females should produce male-biased broods when mated to an attractive partner. However, the case studies differ in terms of whether they support this prediction, and even earlier meta-analyses came to different conclusions. There has been little attempt to investigate the biological factors that may be behind the observed heterogeneity of the results. Extra-pair paternity may be such a factor, if male quality dependent sex ratio adjustment has evolved because of indirect genetic benefits. Using meta-analytic approach we found that the effect size of male traits on brood sex ratio was small, but significantly different from the null expectation. However, the variation in the effect sizes was unrelated to extra-pair paternity. This suggest that male quality dependent sex ratio adjustment exist and may be driven by direct benefits rather than indirect genetic benefits. We also tested if the effect sizes are influenced by whether the focal male trait is indeed under sexual selection, as it is assumed by the sex allocation theory. We found that the effect sizes were smaller if this assumption was not met, indicating that studies that neglect the assumptions of the tested hypotheses may lead to the underestimation of the mean effect size.

Abstract ID: 1099

Nutrigonometry: bringing geometry into nutritional ecology

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Nutrition is a fundamental factor that links the expression of all life-histories traits across the tree of life. Yet, nutrition is complex and rely on the interaction of multiple nutrients for physiological and behavioural effects. A recent framework was proposed to guide experimental investigations in nutrition known as the Geometric Framework (GF). GF is powerful as it allows for experiments where the interaction between multiple nutrients to be studied simultaneously. However, GF's power has been limited by the lack of mathematical and statistical frameworks to extract meaningful information from the output multidimensional data obtained using the framework. In this talk, I will first present the (short) history of GF and the analytical developments that have advanced the field of nutritional ecology and enabled statistical insights from GF studies. Next, I will present the cutting-edge models and frameworks being developed in the field which truly brings geometry into the Geometric framework. In particular, I will present our recent work showing how different (Machine Learning) models estimate properties in GF data, and how better experimental designs can improve the accuracy of our biological insights using GF. I will also talk about the other properties that can be obtained from GF data, namely, curvature, surface-area, and holes, and discuss their putative biological

meaning. Together, the talk will provide a historical view of the analytical developments in the field of nutritional ecology using GF. Note to Math-averse: this is meant to be an enjoyable talk, with only few formulas but still fun. Come along!

Abstract ID: 1217

Fungal cultivars altruistically recycle their own contents in nutritional rewards for farming ants

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Leafcutter ants evolved a fungus-farming system for food ca. 15 mya, strategically inoculating, provisioning, protecting, and consuming a single domesticated cultivar, *Leucoagaricus gongylophorus*. The ants provision their fungal cultivar with fresh plant material, and the cultivar produces nutritional reward structures unique among all fungi—swollen hyphal cells called gongylidia. The molecular and cellular mechanisms of gongylidium formation are currently poorly understood, which limits our understanding of whether and how ant farmers can regulate crop productivity. We used microscopic imaging and *in vitro* experiment to describe gongylidia ultrastructure and cellular growth. Our results indicated that gongylidia form by a process of autophagy whereby growing gongylidia cells recycle their own cellular contents (organelles, proteins, glycogen) into food for the ants. We hypothesize that autophagic recycling provides important benefits since the cultivar's organelles would yield reliably available and chemically predictable metabolic precursors during periods of plant shortage. We next sequenced the transcriptome of gongylidia and mycelium in order to identify differentially expressed genes related to autophagy and the pathways derived from this process. Since autophagy inhibitors decreased gongylidia production under *in vitro* conditions, we expect to find upregulated genes related to autophagy or post-autophagy in gongylidia compared to mycelium. More generally, we propose that this autophagic recycling pathway represents an ultimate domestication step—that is only possible in a lifetime committed symbiosis—where symbiont traits can freely evolve without the need for typical screening/sanctioning/policing mechanisms that characterize all other symbioses involving openness and/or partner promiscuity.

Abstract ID: 1954

Human, dietary and microbiome DNA from a 7,200 year masticated plant material from North America

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Over the last decade, several hundred ancient genomes have been generated from skeletal remains. This approach, however, is based on destructive intervention on irreplaceable and finite human remains, and thus is often in conflict with descendant Indigenous community values. We can address these concerns by turning from skeletal material to recovering DNA from ancient quids – wads of masticated plant fibres, discarded by persons during their lifetime, and which are often found in archaeological sites from dry regions of North America. We have successfully generated authentic ancient human, faunal, floral, and microbial DNA from three quids ranging from 7,400 to 9,200 years ago. We obtained a low-coverage human genome from the youngest of those quids, allowing us to demonstrate that the chewer was more closely related to Indigenous Americans than any other worldwide population. Furthermore, using least common ancestor metagenomic pipelines, we retrieved non-human eukaryotic DNA present - such as deer and cattail - which represent recent meals of that individual. Finally, we can reconstruct the chewer's oral microbiome, including the presence of pathogenic human Gammaherpesvirus 8 in one of the quids. We show here that ancient DNA from masticated material can provide insights in both human population history, diet and microbiome shifts, as well as pathogen prevalence through time.

Abstract ID: 2028

Genetically-mediated diet acquisition helps to maintain phenotypic diversity among Atlantic salmon

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Where and when individuals acquire resources frequently displays a genomic basis, with genetic diversity leading to differential resource use and the expression of diverse phenotypes. While such genomic diversity appears to be maintained by fitness trade-offs in resource use, it is often unclear as to what ecological mechanisms mediate the expression of different phenotypes. To explore this topic, we combined individual-level marine diet data of Atlantic salmon with genotypes at two life history genomic regions, *vgll3* and *six6*, that are known to affect age at maturity in salmon. For both regions, individuals with the early '*E'* allele tend to mature earlier and at a smaller size (within an age group) than those with the late '*L'* allele. Our analyses revealed that across age classes, older fish ate proportionally fewer crustaceans than younger fish with a clear ontogenetic switch towards piscivory. Within one sea winter fish, individuals that were homozygous for the *E* allele at *vgll3* ate fewer crustaceans than *L* homozygotes, however, this pattern was reversed among multi-sea winter fish. Furthermore, *six6* displayed a mass-dependent relationship where heavier *E* homozygotes had a greater likelihood of having fish in their diet than lighter *L* homozygotes. These results provide evidence for variation in diet as a functional ecological link between genomic and phenotypic diversity in age at maturity in Atlantic salmon. Anthropogenically-mediated changes in prey availability are likely to impact the

phenotypic variation displayed by Atlantic salmon, reducing population stability through portfolio effects and the erosion of ecologically important phenotypic diversity.

Abstract ID: 1623

Population-bottleneck selects some but not all social traits in social bacterium *M. xanthus*

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Explaining evolution and maintenance of cooperation is one of the cornerstones of evolutionary biology. Theory and previous studies have demonstrated that increased kinship between individuals as a result of population-bottleneck promotes the evolution of social traits. However, for organisms that express multiple social traits, it is not clear if population bottlenecks will have similar effects on all social traits.
Gram-negative bacterium *Myxococcus xanthus* has a complex lifecycle with several social behaviours such as predation, sporulation in multicellular fruiting bodies, and spore germination. We performed an evolution experiment in which all social behaviours of *M. xanthus* were under selection. This experiment was conducted in two regimens, one that introduces a stringent population-bottleneck (1%) between transfers and second one with a relaxed population-bottleneck (15%) between transfers.
Analysis of the evolved and ancestral *M. xanthus* populations suggests possible trade-offs between life-history traits. We observed an increased efficiency for predation and spore germination in relaxed bottleneck lines, but their sporulation/fruiting body development efficiency decreased. Interestingly, we saw an opposite trend in stringent regimens where sporulation/fruiting body development was efficient, but predation and germination efficiencies decreased.
Further, analysis of natural isolates of *M. xanthus* also revealed trade-offs between sporulation, predation, and germination.
Thus, using lab evolution experiments and analysis of natural populations of social bacteria we demonstrate trade-offs between distinct social traits. Importantly, we demonstrate that, among the negatively correlated traits, population bottlenecks can determine which traits are favoured and which are selected against.

Abstract ID: 2061

Nutrition on imbalanced diets: Evolutionary strategies across different ant species

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Macronutrients, such as proteins and carbohydrates, are critical components in the longevity and fecundity trade-off across different animals. Whereas high protein diets maximize reproduction but shorten lifespan, high carbohydrate diets increase longevity at the cost of reproduction. Nevertheless, no evidence for such a trade-off exists in social insects. In ants, long-lived and highly fecund queens feed on proteins while short-lived workers consume carbohydrates. However, ant species differ tremendously in their colony structure, having a handful of totipotent individuals to several million workers that

usually are sterile or in some cases can develop ovaries (queenless colonies) and produce males from unfertilized eggs. Ant workers are, therefore, an ideal model to disentangle the trade-off between reproduction and longevity. Here, we studied 16 ant species differing in the reproductive potential of workers, colony size, and geographical origin. We used the geometric framework for nutrition to test the link between the nutritional needs of workers and these specific traits. Workers were isolated into sub-groups and confined to different protein to carbohydrate P:C ratios for 270 days. We recorded daily the mortality and monthly the fecundity rates. In addition, we measured the head size and protein and fat content of workers. Our results showed that each species has its optimal diet, but the resistance to unbalanced P:C ratios was better for fatter than leaner species. We will discuss the effect of the different diets on the longevity and fecundity of workers and their link with colony size and the geographical origin of each species.

Abstract ID: 1094

Evolution of the avian forelimb and implications for flight

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The evolution of flight across many organisms has captured the imagination of researchers for decades. However, birds are the most speciose and diverse group that has ever taken to the sky. Recent evidence supports the notion that the evolution of modern avian flight was a gradual accumulation of features over time rather than an abrupt event. Several studies have used the scaling relationships of the avian forelimb and associated characteristics to demonstrate the size reduction associated with flight and the influence on avian forelimb evolution. However, despite intense efforts, no temporal trend in relative forelimb length has been found in early birds. Here, using Bayesian phylogenetic comparative methods that account for heterogeneous signals in the data, we simultaneously investigate the allometric relationships of the avian forelimb whilst testing for a temporal trend in relative wing length. Our results reveal a sustained increase in relative wing length in birds over 80 million years. In addition, we highlight the phylogenetic position of the allometric shift associated with flight in dinosaurs. We provide the first evidence that a long-term trend of increasing relative wingspan in Mesozoic birds ultimately led them to dominate the volant niche space resulting in their spectacular subsequent radiation.

Abstract ID: 1202

Milk, seminal fluid, eggs, feces… Evolution and impact of socially transferred materials

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Since the dawn of life, transfers of metabolized material between individuals have created some of the greatest innovations of evolution. When biological material is transferred from one individual's body to another (via sperm, eggs, milk, etc.), manipulative molecules that induce a physiological response in the receiver are often transferred along with the primary cargo. These socially transferred materials offer excellent study systems for indirect genetic effects, where the genome of one individual can affect the development, behavior and fitness of other individuals. Indirect genetic effects are known to strongly drive evolution, but in theoretical literature the exact behavioral and molecular mechanisms behind them are treated as black boxes. Through socially transferred materials, the influence of one individual on others can be analyzed quantitatively and from a molecular perspective. The bioactive and transfer-supporting components in these materials show signs of convergent evolution, to the point where they can be used in applications across taxa and type of transfer. As the composition of these materials is typically highly dynamic, understanding what exactly is transferred in which environmental contexts will help assessing their fundamental evolutionary and physiological role. We outline the main research steps and methods for studying these materials, and discuss the most important future directions for this field of research. Our synthesis, drawing from interacting phenotype models, the inclusive fitness framework, game theory and signal theory, provides the necessary conceptual framework for understanding the transformative role of social transfers in evolutionary biology.

Abstract ID: 1493

Opsin gene expression changes with development in ray-finned fishes (Actinopterygii)

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Fish often change their habitat and trophic preferences during development. Dramatic functional differences between embryos, larvae, juveniles and adults also concern sensory systems, including vision. Here we focus on the photoreceptors (rod and cone cells) in the retina and their gene expression profiles during development. Using comparative transcriptomics on 63 species, belonging to 23 actinopterygian orders, we report general developmental patterns of opsin expression, mostly suggesting an increased importance of the rod opsin (*RH1*) gene and the long-wavelength sensitive (*LWS*) cone opsin, and a decreasing importance of the shorter wavelength sensitive cone opsin throughout development. Furthermore, we investigate in detail ontogenetic changes in 14 selected species (from Polypteriformes, Acipenseriformes, Cypriniformes, Aulopiformes and Cichliformes), and we report examples of expanded cone opsin repertoires, cone opsin switches (mostly within *RH2*) and increasing rod:cone ratio as evidenced by the opsin and phototransduction cascade genes. Our findings provide molecular support for developmental stage-specific visual palettes of ray-finned fishes and shifts between, which most likely arose in response to ecological, behavioural and physiological factors.

Abstract ID: 1610

Evolution of territoriality in hylid frogs: ecology, morphology and lineage diversification

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Intrasexual selection has been less studied than intersexual selection in a phylogenetic framework, despite in theory both are directly linked to many evolutionary processes and traits. Here, we use treefrogs of the family Hylidae — the second most speciose anuran family — to analyze the evolutionary dynamics of territoriality, an intrasexual-selected behavior. We considered two behavioral proxies with different levels of aggression, territorial call and physical combat, as well as one morphological trait, the prepollical spine. We estimated phylogenetic signal of these traits, and tested their relationship with type of water body used for reproduction, habitat complexity in vegetation layers, male body size, sexual size dimorphism, and diversification rates. We used literature and unpublished data to build two datasets with distinct levels of certainty and ran phylogenetic analyses. Behavioral proxies associated with territoriality (territorial call and physical combat) exhibited intermediate levels of phylogenetic signal in the family, whereas phylogenetic signal for the presence of prepollical spine was strong. We did not find support for the hypothesis of reproduction in lotic water favoring occurrence territorial behavior, and we found that this behavior is not correlated with habitat complexity. Male

body size and sexual size dimorphism were not correlated with the presence of territorial call and physical combat. Finally, diversification rates were positively correlated with territorial call only considering the full dataset, but negatively correlated with physical combat across hylid clades. Our results indicate that distinct territorial behaviors can have opposite effects on evolutionary processes

Abstract ID: 1784

Evolutionary dynamics of pigmentary grey and non-iridescent structural colour blue in Tanagers

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Birds are one of the most colourful animal taxa in the world and they achieve this diversity in several ways. Avian colour production mechanisms range from pigmentary (pigment deposition) to structural (nanostructural arrangements), or the combination of both, and basic components of feathers (keratin, air, and appropriate pigment) are involved in all of them. It has been shown that in some instances, evolution between pigmentary and structural colours can proceed by rearrangement of the nano-structural elements of feathers. For example, iridescent colouration has been shown to evolve from black colouration in grackles and allies. Recently, a similar evolutionary pathway between grey and blue colouration has been proposed that involves melanosomes rearrangement and organization of keratin and air into colour producing nanostructure. Evidence for this evolutionary link is currently lacking. Here, we test the evolutionary relationship between grey and blue colouration across species in a colourful clade of South American birds (Tanagers) and identify a potential transition state between grey and blue colouration – slate. Using digitally calibrated images of museum specimens to measure colouration, our analyses determine the distinctiveness of colour categories (grey, slate, blue) in colourspace. Following, we identify the most likely pathway in colour evolution across species: from grey to slate to blue. While slate colour has the highest rates of gain and loss indicating an evolutionarily unstable and transitionary state, blue colour showed low rates of gain and loss but only from slate colouration. Together, our work reveals a new pathway in the evolution of blue colouration.

Abstract ID: 1815

Species-level timeline of mammal evolution integrating phylogenomic data

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High-throughput sequencing projects generate genome-scale sequence data for species-level phylogenies. However, state-of-the-art Bayesian methods for inferring timetrees are

computationally limited to small datasets and cannot exploit the growing number of available genomes.
In the case of mammals, molecular-clock analyses of limited datasets have produced conflicting estimates of clade ages with large uncertainties, and thus the timescale of placental mammal evolution remains contentious. Here we develop a Bayesian molecular-clock dating approach to estimate a timetree of 4,705 mammal species integrating information from 72 mammal genomes. We show that increasingly larger phylogenomic datasets produce diversification time estimates with progressively smaller uncertainties, facilitating precise tests of macroevolutionary hypotheses. For example, we confidently reject an explosive model of placental mammal origination in the Palaeogene and show that crown Placentalia originated in the Late Cretaceous with unambiguous ordinal diversification in the Palaeocene/Eocene.
Our Bayesian methodology facilitates analysis of complete genomes and thousands of species within an integrated framework, making it possible to address hitherto intractable research questions on species diversifications. This approach can be used to address other contentious cases of animal and plant diversifications that require analysis of species-level phylogenomic datasets.

Abstract ID: 1757

Selection on males increases population viability

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Selection on males has been proposed to both help and harm population viability. Sexual selection is generally thought to be more intense in males than females, leading theoreticians to propose that selection on males more effectively purges the genome of deleterious mutations. However, selection on males can also produce sub-optimal female phenotypes because females and males share a genome, but have fundamentally different ecologies. As the (generally) more important sex to population demography, this sexual conflict is expected to reduce population viability. It is therefore unclear what net effect selection on males has on population fitness and extinction risk. Here, I will present the results from an experiment I used to test how selection on males affects resistance against extinction. I took *Drosophila melanogaster* populations and allowed them to evolve in response to selection acting on one sex, while eliminating a response to selection on the other. Then, I split these populations into families and recorded the rate at which they went extinct. I found that a male-limited response to selection decreases extinction rate relative to populations that experienced an unconstrained selection response. This result provides evidence that selection on males has an overall positive effect on population viability, and has implications for the evolution and ongoing maintenance of sexual reproduction.

Abstract ID: 2476

Phenotypic plasticity drives phenological changes in a Mediterranean blue tit population

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Many natural populations are showing earlier phenology induced by climate change, such as the passerines' breeding time. While understanding the nature of such changes is key to predict the responses of wild populations to ongoing climate change, genetic changes have been rarely investigated. Our study investigated potential genetic changes for laying date, a trait expected to evolve, as it has been reported to be heritable and under directional selection. We brought these questions in a Corsican blue tit population, whose average laying date has significantly advanced over 40 years, and we here determined whether this response is of plastic or evolutionary origin, using quantitative genetics. As estimating fitness in wild population is difficult, we integrated this challenge by comparing two fitness proxies and using models accounting for their zero inflation. We showed that this population showed no genetic changes related to their laying date, and only a plastic response to environmental fluctuating selection. We further discuss the modeling of such trait evolution and the conservation consequences of our results.

Abstract ID: 1630

The impacts of publication bias on ecology and evolutionary biology

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Large replication efforts in medical and social sciences have estimated alarmingly low rates of replicability, now widely known as the “replication crisis”. We are yet to have an equivalent replication effort in our own fields of ecology and evolution. Therefore, no clear proof exists that ecology and evolution are amid a replication crisis (although they are likely). By reanalysing 102 ecological & evolutionary meta-analyses, we have quantified two statistical indicators: publication bias and statistical power, both of which can be used retrospectively to assess study replicability. We have found that two types of publication biases, the small-study effect and the decline effect, are both common among the meta-analyses. Further, by using a meta-meta-analysis (2nd order meta-analysis), we show that, currently, evolutionary and ecological meta-analyses are overestimating their overall effects by ~20%. Moreover, many studies in ecology and evolution are severely underpowered (~20%) and provide inflated effects, which do not reflect ‘true’ effects (overestimated by 2-3 times). Therefore, our findings strongly suggest that a replication crisis is real in ecology and evolution. We discuss the implications of this crisis for the field and what we can do as an individual and as a community to resolve these important problems.

Abstract ID: 1700

Hamilton´s force of selection during ontogenesis

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The life history and patterns of ageing and mortality that organisms experience are shaped by evolution. Hamilton´s force of selection measures the intensity of natural selection on different genes and during different life stages. It is widely assumed that the force of selection is constant during prematurity, as any mortality in these cohorts is

balanced out by an increase of expected reproduction. In contrast, many taxa show high and declining mortality rates during early development, a phenomenon for which the term ´ontogenescence´ has been coined. A constant force of selection during prematurity is predicated on the absence of parent-offspring dependencies such as parental care or sibling replacement, as Hamilton himself already pointed out. At the same time, offspring of many taxa are fully dependent on their parents during embryonal development and early childhood, and this can be elegantly incorporated in a simple class-structured model. Under these conditions, instead of being constant, the force of selection generally increases up until offspring become independent, thus providing a candidate explanation for heightened mortality rates during ontogenesis. These findings are discussed in the context of functional and age-specific gene activation patterns.

Abstract ID: 2373

Ecological and evolutionary interactions of divergent lineages of an amphipod species complex

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Recent discoveries of vast cryptic diversity in various aquatic invertebrate groups pose a challenge for understanding of their ecology, biodiversity patterns, and evolutionary interactions. In order to get insight into processes that may influence coexistence of cryptic species, we study deeply divergent lineages of the hyper-diverse *Gammarus fossarum* complex (Crustacea: Amphipoda) in the Western Carpathians, focusing on their distribution at various spatial scales, mating preferences and reproduction isolation, and host-parasite interactions. The studied lineages seem to be of Miocene age and apparently survived Pleistocene glaciations throughout the whole Carpathian Arc. We confirmed frequent and temporally stable syntopic occurrence of two or three lineages within submontane streams in eastern Czechia, which provides ample opportunity for their direct interactions. Mixed precopulatory pairs in syntopy were extremely rare, even under very imbalanced lineage ratios, confirming a strong prezygotic reproductive barrier between studied lineages; this is congruent with the species delimitation analyses on both nuclear and mitochondrial markers. A detailed study on diversity and infection patterns of microsporidian parasites suggested that apart from taxa commonly detected in gammarid amphipods (genera *Nosema*, *Cucumispora* and *Dictyocoela*), studied lineages of the complex host numerous additional microsporidian clades, some never previously characterized molecularly. Common microsporidians do not seem selective for particular host lineages but more detailed data from syntopic sites will provide insight into potential differences in their prevalence between distinct hosts. The project further aims to evaluate microhabitat preferences, trophic ecology, and functional morphology of these coexisting *Gammarus* lineages.

Abstract ID: 1281

Genomic evidence of a sexually selected trait capturing and purging genetic load

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The evolution of costly traits like deer antlers and peacock trains, which drove the formation of Darwinian sexual selection theory, has been hypothesised to both reflect and affect patterns of genetic variance across the genome, but direct tests are missing. Here, we used an evolve and re-sequence approach to reveal patterns of genome-wide diversity associated with the expression of a sexually-selected weapon that is dimorphic among males of the bulb mite, Rhizoglyphus robini. Populations selected for the weapon showed reduced genome-wide diversity compared to populations selected against the weapon, particularly in terms of the number of segregating non-synonymous SNPs, indicating enhanced purifying selection. This increased purifying selection reduced inbreeding depression, but outbred female fitness did not improve, possibly because any benefits were offset by increased sexual antagonism. The majority of SNPs that consistently diverged in response to selection were initially rare and overrepresented in exons, and enriched in regions under balancing or relaxed selection, suggesting they are likely moderately deleterious variants. These diverged SNPs were scattered across the genome, further demonstrating that selection for or against the weapon and the associated changes to the mating system can both capture and influence genome-wide variation.

POSTERS

Abstract ID: 2480
Poster board number:
P001

Variation in wild-derived and classical laboratory strains of the house mouse model organism

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The classical laboratory strains (CLS) of the house mouse are the most frequently used animal model in biomedicine. However, despite its indispensable usage in science, leading to more than 30 Nobel Prize awards, its utilization in evolutionary studies is limited. This is due to the CLS being a mixture of three mouse genomes and displaying limited genetic variability. A suitable substitution for evolutionary-based studies can be wild-derived strains. However, there is no systematic overview of these resources. Similarly, data on their genetic or phenotypic variation is scarce. Here we present genetic and morphological data of ~ 90 WDS representing 5 species, 3 subspecies, 8 natural Y consomic and several classical laboratory strains. We compare genetic variability using sequences of 163 whole mtDNA and 111 samples of the *Prdm9* gene (associated with sterility in mice) plus copy number variation at two sex chromosome-linked genes *Slx*/*Sly* in 53 mice. Additionally, we assess morphological and reproductive performance in all strains. We document that the WDS capture huge natural variation – for example, mitogenome data show there are 1315% SNP in WDS relative to CLS; similarly, while 17 CLS share 2 alleles in the *Prdm9* gene, the 111 WDS display 46 haplotypes. The results suggest that the variation, which has accumulated during 5–6 MYR and is preserved in WDS, is a perfect tool for genetic, behavioural and ecological evolutionary studies. The WDS are available to the scientific community (contact the first author – jpialek@ivb.cz). Further details are provided at https://housemice.cz/en/strains.

Symposium: S01. Tug of war between the sexes: The transcriptomic architecture of sex-linked traits (id: 6)

Abstract ID: 1219
Poster board number:
P002

Evolutionary consequences of sex loss on male fitness and sex-biased gene expression in pea aphids

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Shifting from sexual reproduction to parthenogenesis constitutes a major life history change with deep evolutionary consequences, including changes in selective pressures on sex-related traits. In asexual populations, traits that evolved under sexual reproduction might become useless or maladaptive and decay via selective or non-selective processes. The pea aphid *Acyrthosiphon pisum* shows intraspecific variation in reproductive mode, with cyclically parthenogenetic (CP) lineages displaying the ancestral reproductive mode (alternance of sexual and asexual generations) and obligately parthenogenetic (OP) lineages, producing no sexual females but still males. As OP and CP populations are geographically separated, OP males have limited reproductive opportunity (and thus are dead ends regarding gene transmission). We thus hypothesized that male-related traits would decay in OP lineages. This was tested by measuring male production and reproductive success in 12 OP and 12 CP lineages. Male production in OP lineages was strongly reduced as expected under active selection against this costly trait, while OP male fertility was only slightly diminished, supposedly because of slow drift-driven decay. Then, to investigate the consequences of sex loss at the genomic level, gene expression was quantified by RNAseq in males, asexual and sexual females (where applicable) from 4 OP and 4 CP lineages. Statistical analyses are underway to investigate how the expression and sequences of genes showing sex-specific or sex-biased expression in CP lineages changed under asexuality, as a consequence of the relaxation of selection on sexual morphs and the cessation of intra-locus conflict between morphs in OP lineages.

Abstract ID: 1277
Poster board number:
P003

Mechanisms driving development of male-larger sexual size dimorphism in a lizard

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Squamate reptiles were considered indeterminate growers for a long time. However, recent studies demonstrate that bone prolongation stops in many lizards through the closure of bone growth plates. This has important consequences for questions concerning the proximate causes of sexual size dimorphism. The traditional model of highly plastic and indeterminate growth would correspond more to a long-term action of a sex-specific growth regulator. Oppositely, determinate growth would be more consistent with a regulator acting in a sex-specific manner on the activity of bone growth plates

operating during the phase when a dimorphism in size develops. We followed the growth of males and females of the male-larger gecko *Paroedura picta* and monitored the activity of bone growth plates, gonad size, and levels of steroids. We also studied the expression of steroid hormone receptors (*AR, ESR1, ESR2*) and genes from the insulin-like growth factor network (*IGF1*, *IGF2*, *IGF1R* and *IGF2R*) in livers. Specifically, we measured gene expression before the onset of dimorphic growth, at the time when males have more active bone growth plates and clear sexual dimorphism, and after a period of pronounced growth in both sexes. We found a significant spike in the expression of *IGF1* in males around the time when dimorphism develops. This suggests that sexual size dimorphism in male-larger lizards can be caused by a positive effect of high levels of *IGF1* on bone growth. The peak in *IGF1* resembles the situation during pubertal growth spurt in humans, but in lizards, it seems disconnected from sexual maturation.

Abstract ID: 1484
Poster board number:
P004

Sexual selection in the red seaweed *Gracilaria gracilis*

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Sexual selection, i.e. selection arising from competition for mating partners and/or for gametes encounter, is expected to be stronger in males of anisogamous species. Bateman's principles state that sexual selection is stronger in males than in females, only if the variance in (i) reproductive and (ii) mating success is larger for males and (iii) relationship between reproductive success and mating success (Bateman's gradient) is also stronger for males. It has been widely demonstrated in animals, but much less well known in others anisogamous species, such as plants. Here, we focus on the haploid-diploid red algae *Gracilaria gracilis* in which sex is determined in the haploid phase. Even, if there is no evidence of sex-linked traits in male and female gametophytes, this alga displays all necessary elements for the operation of sexual selection: sexual dimorphism in gamete size and number, the zygote develops on and is nourished by the females. Previous studies have shown some evidences for non-random mating in natural populations suggesting the existence of male/male competition or female choice. However, Bateman's principles were not tested. In this study, we performed an exhaustive sampling of males and females present in a natural population. Life history traits were measured in each individual and we used paternity analyses to determine male and female reproductive and mating success. Testing the effect of sexual selection on algae is opening up the possibility of studying sexually antagonistic selection and differential gene expression in a species where there is very limited sexual differentiation.

Abstract ID: 1795
Poster board number:
P005

Brain transcriptome architecture in a species with sex reversal: a three sex chromosome orchestra

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It is commonly assumed that sex differences in phenotypic traits underlie differences in gene expression. This state of art has challenged biologists attempting to understand the molecular basis of sexual dimorphism and sexual conflicts. In species with genetic sex determination systems, sex chromosomes are expected to play a substantial role in sexual dimorphism. However, their effect is not as straightforward to determine, especially since we usually have two genotypic sexes that we cannot distinguish from phenotypic sexes. The African pygmy mouse, *Mus minutoides*, is a wild mouse species with three sex chromosomes: the classic X, Y and a feminizing X* chromosome. The latter originates from a mutation on the X and induces a sex reversal in X*Y individuals. There are therefore three female genotypes in natural populations: XX, XX* and X*Y females, while all males are XY. X*Y females considerably differ from XX and XX* females on many traits (e.g. life history traits, behaviours, physiology) and recently, it has been pointed out that the combination of a feminizing X* and a Y chromosome gave birth to a third sexual phenotype. In this study, we evaluate the consequences of this unusual sex determination system on the brain transcriptomic architecture. We aim to understand whether gene expression reflects phenotypic or genotypic sex and investigate the molecular basis of phenotypical divergences between individuals. Furthermore, we discuss the relative part of each sex chromosome in shaping the three sexual phenotypes in *M. minutoides*.

Abstract ID: 1836
Poster board number:
P006

The evolutionary potential of brown trout in the context of interacting anthropogenic stressors

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Proliferative kidney disease (PKD) caused by *Tetracapsuloides bryosalmonae* (Phylum Cnidaria, Subphylum Myxozoa) has been associated with the significant declines in many brown trout (*Salmo trutta*) populations in the Swiss Plateau. The PKD parasite's virulence increases at warmer summer temperatures, however, the effect of multiple stressors on virulence is currently unknown. We study the possible role of a further stressor, the common micropollutant diclofenac. This anti-inflammatory drug is believed to have caused the Indian Vulture Crisis and has a toxic effect in the kidney of freshwater fish, the primary target of PKD. 840 experimentally bred juvenile brown trout were randomly assigned to one of three environmentally relevant diclofenac concentrations (0, 50, 250 ng/L) and either to *T. bryosalmonae* spores or a no-spores treatment (6 treatments in total, 140 fish in each). Growth, nephrosomatic index, and other stress indicators were measured fortnightly for 3 months. Tissue samples were taken to determine genetic sex, multi-locus heterozygosity, and family identity. We are currently finishing the statistical analyses and will answer the following questions: (i) does exposure to diclofenac increase the virulence of PKD, (ii) do the sexes differ in their tolerance to the pollutant, the pathogen, and the combination of both, and (iii) what are the roles of family identity and individual heterozygosity in tolerance to the various

stressors. We will discuss our findings in the context of the management of the evolutionary potential of wild populations.

Abstract ID: 2081
Poster board number:
P007

Sex-biased genes and their role in speciation in the Scarce Swallowtails

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Genes are termed sex-biased if their expression is unique to one sex or if it is significantly differentially expressed between the sexes. In several systems sex-biased genes have been shown to evolve quickly, to be often sex-linked, and are potentially influenced by sexual selection, yet we still don't know to what extent their evolution plays a role in divergence during speciation. Specifically, by virtue of their faster evolution, sex-biased genes may contribute to incipient reproductive isolation, and as a result the early barriers to gene flow we see between diverging species. To investigate this I have generated RNAseq data to identify sex-biased genes in males and females of the Scarce Swallowtail butterflies (*Iphiclides podalirius* and *I. feisthamelii*). These sister species diverged at least 1.2 MYA in southern Europe, and a hybrid zone persists to this day north of the Pyrenees. I fit explicit models of the speciation process across the whole genome to identify barriers to gene flow and to investigate whether sex-biased genes contribute disproportionately to species divergence.

Abstract ID: 2086
Poster board number:
P008

How many alleles and transcripts have sex-specific fitness effects in Drosophila?

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Sex differences in selection are thought to help purge the genome of deleterious mutations, though this benefit may be offset by unresolved sexual conflict. The proportion of loci and expressed transcripts that are under sex-specific (as opposed to sex-concordant) selection is an important but largely unknown parameter determining the net effect on adaptation. Here, we used the Drosophila genetic reference panel - a set of inbred populations with sequenced genomes and transcriptomes - to conduct genome-wide and transcriptome-wide association studies, with a holistic measures of male and female fitness as the target phenotype. By applying multivariate mixture modelling, we estimate how many alleles and transcripts show same- or opposite-sign associations with fitness in each sex. Our results suggest that sexually antagonistic loci are rare, yet there are many sexually antagonistic transcripts (i.e. RNAs whose abundance correlates postively with male fitness and negatively with female fitness, or vice versa). Thus, selection on males likely has a net beneficial effect on females in our study population, but nevertheless there is extensive unresolved sexual conflict in the composition of the transcriptome.

Abstract ID: 2090
Poster board number:
P009

Modelling Wolbachia-induced cytoplasmic incompatibility in oak gallwasps with cyclic parthenogenesis

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We are generally interested in understanding the interplay of genetic and epigenetic mechanisms and how biotic and abiotic factors contribute to sex-biased gene expression. As Hymenoptera lack sex chromosomes and males and females only differ in ploidy, Hymenoptera are an ideal system for studying how sex-specific traits are built from a common genome. Here, we present a mathematical model that determines the likelihood of cytoplasmic incompatibility (CI), a reproductive manipulation that can be induced by the endosymbiont Wolbachia. CI leads to embryonic mortality in offspring of males and females with differential infection status. We addressed the hypothesis that Wolbachia can induce CI and derived a mathematical model to investigate the spread of a bacterial infection in naive populations and to determine the likelihood of CI occurrence. Model validation was performed with published data from Wolbachia-infected populations of oak gallwasps that typically exhibit a life cycle with alternating sexual and asexual generations. We started with measurements of infection frequencies and maternal transmission in the sexual generation and then extended the model by estimates of mtDNA-haplotypes, which, like Wolbachia, are maternally inherited, and can therefore be associated with infection. With both approaches we predict a high likelihood for the presence of CI in these populations. Our model is not restricted to gallwasps, but can easily be generalized to investigate the occurrence of CI in other species. Future work will address which genes are differentially affected by infection of male and female individuals. Functional studies are planned in the well-established Nasonia system.

Abstract ID: 2205
Poster board number:
P010

A gene copy number arms across a species barrier

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Copy number variant genes may start CN arms races over transmission. One such arms race between genes on the X and Y chromosomes was demonstrated in lab mice: *Slx* and *Sly* compete over transmission by altering the fertilization success of X and Y bearing sperm. Here we ask whether this effect can be seen in nature, where, unlike in inbred lines, the fixed CN and regulatory genes have standing variation, allowing natural selection to counter CN/gene product escalation. As models, we use two house mouse subspecies that hybridise in Europe. Y chromosomes of the eastern subspecies (*Mus musculus musculus*) have introgressed onto western (*M. m. domesticus*) genomic

backgrounds. This introgression was accompanied by sex ratio distortion, consistent with the *Slx*|*Sly* arms race mechanism described for inbred strains. We measure *Slx*|*Sly* CN and expression levels across an Invasion transect where Y chromosomes introgress and a Control transect with little introgression. Mean *Sly* CN was ~1.3 fold higher on both sides of the Control relative to the Invasion transect. However, there is a relative deficit in the CN of *Slx* where Y chromosomes invade, suggesting the role of *Slx* in combatting *Sly* effects identified in lab strains also plays out in nature. Nevertheless, we find males from the Invasion transect with similar *Sly* vs *Slx* expression levels despite very different relative CN. We suggest standing variation for upstream regulation of *Slx*|*Sly* is being co-opted in nature where their arms race is reducing population fitness.

Symposium: S02. Sex chromosome evolution: the canonical model and so much beyond (id: 963)

Abstract ID: 986
Poster board number:
P011

Young X chromosome evolution

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Sex chromosomes arise from a pair of autosomes when one of them acquires a sex-determination gene. Recombination is often suppressed between X and Y chromosomes. In the absence of recombination, the efficiency of selection is greatly reduced, leading to the degeneration of the Y chromosome. Consequently, many X-linked loci become hemizygous in males. Differences in evolutionary rates and selective pressures between autosomal and hemizygous X-linked loci have been explored theoretically and empirically. In the early stages of X chromosome evolution, many X-linked loci have a functional gametolog on the Y despite not recombining in males, and how this shapes their evolution is not well explored. I have modelled evolutionary rates of diploid X-linked loci and found reduced efficiency of selection on the young X chromosome compared to autosomes. This provides a theoretical explanation for degeneration of young X chromosomes observed in some species. To confirm empirically "neo-X degeneration" hypothesis, and further quantify how selective pressures change following the transition of an autosome into an X chromosome, I am comparing genomic and population genomic data from pairs of closely related species, where one lineage acquired new sex chromosomes.

Abstract ID: 1070
Poster board number:
P012

Neo-sex chromosome evolution in morabine grasshoppers

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In Orthoptera, sex determination lies in chromosomal differences: males are heterogametic (X0) and females homogametic (XX) for the sex chromosomes. In the

morabine grasshoppers Vandiemenella viatica species complex, multiple chromosomal fusions between the ancestral X chromosome and autosomes (neo-X) resulted in the formation of new Y chromosomes (neo-Y) in different races/species. How the orthopteran sex chromosomes first evolved from autosomes and what kind of sex-specific changes occur in newly evolved sex chromosomes remains largely obscure. We believe that sexually antagonistic selection may drive X-autosome fusion by suppressing recombination and strengthening the linkage between sex-determining and sexually antagonistic loci. By using chromosome-level assemblies and resequencing data of viatica species representing pairs of karyotypes with and without neo-sex chromosomes (X0/neo-XY), we show that the non-recombining region of the P24XY neo-Y chromosome race is a ~50Mb fragment exhibiting male-specific alleles. The fragment contains hundreds of genes and stretches of DNA that are duplicated and inverted from regions found at the same and different chromosomes. Essentially, the neo-Y non-recombining region contains functional sex-determining genes, genes involved in spermatogenesis, fertility, and reproduction, illustrating its integrated role as masculinizing supergene. Contrary to popular expectations following recombination suppression, the neo-Y chromosomes show no sign of degeneration and gene loss and are less prone to repeat accumulation compared to other regions of the genome. We provide new insights on how large X-A fusions, inversions, and duplications involving regulatory genes may drive the evolution of co-adapted genes clusters, sex-limited chromosomes, and orthopterans' neo-sex chromosomes in particular.

Abstract ID: 1286
Poster board number:
P013

No evidence for faster evolution on Z chromosome in chameleons of the genus *Furcifer*

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The faster X/Z-effect hypothesis expects that the genes linked to X/Z chromosomes should accumulate mutations faster than the autosomal genes, mainly due to different selection pressure in males versus females, enhanced fixation of recessive beneficial mutations, mutational and recombination differences between sexes, mutations associated with dosage compensation mechanisms, or the smaller effective population size of X/Z chromosomes. Even though faster adaptive evolution of Z/X-linked genes has been reported in various insect and vertebrate species, contradictory results were reported in fruit flies and primates. Furthermore, the absence of a faster-X/Z effect has been shown in beetles and butterflies. The aim of our research was to examine the existence of a faster-Z effect in chameleons of the genus *Furcifer,* a lineage with differentiated ZZ/ZW sex chromosomes. We sequenced the genomes of four species of *Furcifer* chameleons in Illumina platform and we compared the substitution rates of nonsynonymous mutations normalized for the rate of synonymous mutations between autosomal, Z-specific and pseudoautosomal genes relative to outgroups with different sex determination systems. Our results show that there is no significant difference between these three categories of genes, which indicates the absence of a faster adaptive X/Z-effect in the chameleons of the genus *Furcifer*. We conclude that X/Z-specific genes might not always accumulate nonsynonymous mutations faster. Additional studies are needed to explore the difference in evolutionary rates between genomic

regions, type of heterogamety and mechanisms of dosage compensation across independently evolved sex chromosomes.

Abstract ID: 1420
Poster board number:
P014

Neo-faster-Z: chromosome fusion facilitiates adaptation on a butterfly sex chromosome

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The rate of divergence for Z or X chromosomes is usually observed to be greater than autosomes, but the proposed evolutionary causes for this pattern vary, as do empirical results across taxa. Even among moths and butterflies (Lepidoptera), which generally share a single-origin Z chromosome, the handful of available studies give mixed support for faster or more adaptive evolution of the Z chromosome, depending on the species surveyed. Here, we examine the molecular evolution of Z chromosomes in two previously-unstudied lepidopteran species: the Carolina sphinx moth and the monarch butterfly, the latter of which possesses a recent chromosomal fusion yielding a segment of newly Z-linked DNA. We find evidence for both faster and more adaptive Z chromosome evolution in both species, although this effect is strongest in the neo-Z portion of the monarch sex chromosome. The neo-Z is less male-biased than expected of a Z chromosome, and unbiased and female-biased genes drive the signal for adaptive evolution here. Together these results suggest that male-biased gene accumulation and haploid selection have opposing effects on long-term rates of adaptation and help explain the discrepancies in previous findings as well as the repeated evolution of neo-sex chromosomes in Lepidoptera.

Abstract ID: 1471
Poster board number:
P015

Dynamics of transposable element accumulation in non-recombining regions

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Transposable element (TE) activity is generally deleterious to the host fitness, so that genomes often evolve TE control mechanisms and TE copies are purged by recombination and selection. In the absence of recombination, the number of TE insertions usually accumulates, but the dynamics of such accumulation are little known. In this study, we investigated the tempo of TE accumulation in the non-recombining genomic regions of 15 *Microbotryum* species, leveraging on a unique dataset of 21 independent evolutionary strata of recombination cessation of different ages in closely related species. We show that TEs have rapidly accumulated in young non-recombining regions and that their accumulation has slowed down when reaching ca. 40% of occupied base pairs, ca. 1 MY following recombination suppression, to then accumulate

more linearly up to 60% in the oldest evolutionary strata (4 MY). Specific superfamilies repeatedly expanded in independent non-recombining regions, and in particular *Helitrons,* despite not being abundant before recombination suppression. In addition, we found that *Copia* and *Gypsy* retrotransposons, the most abundant TEs in *Microbotryum* genomes, were over-represented in non-recombining regions and have accumulated through bursts, both in the non-recombining regions of the mating-type chromosomes and in the autosomes of *Microbotryum* species at the same time. This finding supports the TE reservoir hypothesis, i.e., that the TEs accumulated in non-recombining regions have a genome-wide impact by transposing to recombining regions. This study thus sheds light on important processes and improves our knowledge on genome evolution, in particular the degeneration in non-recombining regions and its genome-wide consequences.

Abstract ID: 1473
Poster board number:
P016

Divergent evolution of genetic sex determination mechanisms along environmental gradients

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Sex determination (SD) is a crucial developmental process, but its molecular underpinnings are very diverse, both between and within species. SD mechanisms have traditionally been categorized as either genetic or environmental SD, depending on the type of cue that triggers sexual differentiation. Mixed systems, in which SD is affected by genetic as well as environmental factors, are however more prevalent than previously thought. Such systems nonetheless remain understudied in the context of evolutionary stability and dynamics. We have developed a theoretical model to explore how environmental influences on SD genes can affect evolution of SD mechanisms. We found that environmental effects on expression levels of genes within SD regulatory mechanisms can easily trigger evolutionary divergence of SD mechanisms. This may lead to the stable coexistence of multiple SD mechanisms and to spatial variation in the occurrence of different SD mechanisms along environmental gradients. We applied the model to the SD system of the housefly, a global species with worldwide latitudinal clines in the frequencies of various SD systems, involving multiple different genes. We found that it correctly predicted these clines if specific genes in the housefly SD system were assumed to have temperature-dependent expression levels. We conclude that environmental sensitivity of gene regulatory networks may play an important role in diversification of SD mechanisms.

Abstract ID: 1474
Poster board number:
P017

Mechanism and drivers of sex chromosome turnover in Atlantic salmon

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While many taxa have stable old sex chromosomes that follow a canonical path of isolation, differentiation and degeneration. In some groups turnover of sex chromosomes have happen frequently. In salmonid fishes, the male determining gene, *SdY*, is located on different chromosomes in different species. Moreover, in some species such as Atlantic salmon, *SdY* has more than one chromosomal location that is maintained as a polymorphism. The polymorphic nature of salmon sex chromosome suggests that Atlantic salmon are in the process of sex chromosome turnover, providing an excellent opportunity to test the mechanism driving turnover. We used de novo long-read nanopore sequencing of several Atlantic salmon and its sister species brown trout along with the more distantly related Arctic char and European grayling to assemble sex chromosomes. Using these assemblies and short-read sequencing we characterise the size of the male-specific region, establish its mechanism of movement and identify the drivers of sex chromosome turnover.

Abstract ID: 1516
Poster board number:
P018

Sex chromosome evolution in the plant genus Mercurialis

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Dioecy has a scattered distribution across the phylogeny of flowering plants, but clades that are almost fully dioecious present opportunities for studying the evolution of potentially the same sex chromosomes in diverging lineages. The genus *Mercurialis* (Euphorbiaceae) is one such clade. Previous work suggested the presence of a region of suppressed recombination on the homomorphic sex chromosomes of dioecious diploid *M. annua* and has confirned a shared ancestral Y chromosome across the genus that has also introgressed across species boundaries. Here, we present the results of new long-read genome assemblies of a female (XX) and a male (YY) of diploid *M. annua* to provide more detail on the size, gene content and genomic environment of its sex chromosomes. We then combine these assemblies with population genomic datasets from other *Mercurialis* species to infer changes in the size of the non-recombining region among lineages. Our results imply that the sex determining region of diploid *M. annua* is located in, or close to, a pericentromeric region, where low recombination rates and high repeat content likely predated the evolution of sex chromosomes. Our results also provide evidence for multiple independent extensions of the non-recombining region on the ancestrally conserved sex chromosomes across the genus *Mercurialis*, including other diploid and polyploid species. *Mercurialis* continues to provide exceptional material for studying the evolution of sexual systems and sex chromosomes in plants.

Abstract ID: 1569
Poster board number:
P019

Effect of inversions on suppression of recombination and sex chromosome evolution in fission yeast

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The canonical theory for sex chromosome evolution says that sex chromosomes evolved from a pair of homologous chromosomes with a sex-determining locus, followed by the incorporation of sexually antagonistic alleles through recombination arrest. Inversions are assumed to be the main mechanism of recombination suppression. Successive incorporation of loci with sexual antagonistic alleles will lead to divergence of the sex chromosomes over time, however little experimental evidence for this process exists. We used the fission yeast *Schizosaccharomyces pombe* as a model species to study the evolution of the first steps of sex chromosome evolution. Artificially introduced inversions of different sizes around the mating-type locus are used to study how such inversions affect the suppression of recombination, within and outside of the inversion. Suppression of recombination will be measured by tetrad dissections and bulk segregant re-sequencing. Using as antagonistic alleles selectable markers located at different distances from the inversion, with competition assays and experimental evolution, we test how the inversion size affects the dynamics of linkage disequilibrium buildup. Under antagonistic selection, invasion of the inversion is expected. These experiments will show how existing inversions affect **the rise of new strata in sex chromosomes and empirically test the existing model for sex chromosome evolution in a highly tractable system.**

Abstract ID: 1641
Poster board number:
P020

Convergence and divergence in the evolution of stickleback sex chromosomes

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How and why sex chromosomes evolve has fascinated biologists for over a century. But despite the considerable attention they have received, two important questions still remain unanswered: 1) why are sex chromosomes so strongly conserved in some taxa, and so labile in others? and 2) why do sex chromosomes lose recombination? In sticklebacks, some species share conserved sex linked regions, while others have evolved entirely new sex chromosomes, making them an ideal lineage in which to address the above questions. To that end, we have recently assembled, phased, and curated the Y chromosomes of two *Gasterosteus* species (*G. aculeatus*, *G. wheatlandi*). With these resources, we are able to perform high resolution comparisons of sequence evolution, gene traffic and regulatory divergence on the sex chromosomes. The similarities and differences observed in these comparisons shed light on the most important drivers of sex chromosome evolution in these species. In addition, we have now identified the sex chromosomes in several species of stickleback, and notably, we find that the same gene has been recruited twice among different species. This convergence allows us to speculate on the importance of the architecture of the sexual development pathway in influencing sex chromosome evolution.

Abstract ID: 1645
Poster board number:
P021

Scarlet tide – the first report of sex chromosomes in red algae

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Red algae belong to the oldest evolutionary lineages of photosynthetic eukaryotes and comprise one of the largest phyla of algae on the planet. Most of the red algal species are multicellular and macroscopic, live in marine environment and have a complex life history with alternation of three, rather than two, generations. Particularly interesting are the aspects of the evolution of sex determination during the haploid life stage (UV sex chromosomes). However, the sex chromosomes in red algae have never been described to date. Here, we use high-quality genomic and transcriptomic datasets and comparative genomics from three species of red algae to provide the first analysis of the red algal UV sex chromosomes. We characterized the genomic architecture and gene content of both the female (U) and the male (V) sex chromosomes and their nonrecombining regions, and we investigated sex biased gene expression in order to understand sexual differentiation in this group of organisms. The UV system in these red algae shows distinct evolutionary history not only from the well-studied XY and ZW systems but also from the other algal UV systems described so far. Nevertheless, some striking similarities exist, indicating the universality of the underlying processes shaping sex chromosome evolution across major eukaryotic supergroups.

Abstract ID: 1693
Poster board number:
P022

ZW sex-chromosome evolution and contagious parthenogenesis in Artemia brine shrimp

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Eurasian brine shrimp (genus *Artemia*) have closely related sexual and asexual lineages of parthenogenetic females, which produce rare males at low frequencies. Although they

are known to have ZW chromosomes, these are not well characterized, and it is unclear whether they are shared across the clade. Furthermore, the underlying genetic architecture of the transmission of asexuality, which can occur when rare males mate with closely related sexual females, is not well understood. We produced a chromosome-level assembly for the Eurasian species *A. sinica* and characterized in detail the pair of sex chromosomes of this species. We combined this with short-read genomic data for the sexual species *A. sp. Kazakhstan* and several lineages of *A. parthenogenetica,* allowing us to perform a first in-depth characterization of sex-chromosome evolution across the genus. We identified a small differentiated region of the ZW pair that is shared by all sexual and asexual lineages, supporting the shared ancestry of the sex chromosomes. We also inferred that recombination suppression has spread to larger sections of the chromosome independently in the American and Eurasian lineages. Finally, we took advantage of a rare male, which we backcrossed to sexual females, to explore the genetic basis of asexuality. Our results suggest that parthenogenesis is likely partly controlled by a locus on the Z chromosome, highlighting the interplay between sex determination and asexuality.

Abstract ID: 1731
Poster board number:
P023

Convergence Evolution of a Dosage Compensation System

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Long noncoding RNAs (lncRNAs) are important regulatory elements of gene expression. For example, the lncRNA *XIST* acts as a major effector of the X-inactivation process in females in placental mammals, while the lncRNA *roX2* mediates increased transcription on the male X chromosome in *Drosophila melanogaster*. Recently, it was found that *Anolis carolinensis* - the green anole lizard - has XY chromosomes, with a degenerate Y chromosome and perfect dosage compensation of the X chromosome between the two sexes. This compensation is achieved through over acetylation of the X chromosome in males. However, the genetic factors (such as lncRNAs and proteins) that control this process in *A. carolinensis* remain unknown. Using a new approach using RNA-seq data, we found an unannotated lncRNA on the X chromosome, which we named *MAYEX* (Macromolecule Amplify Expression on the X). *MAYEX* is the sole lncRNA in *A. carolinensis* that is expressed specifically in males; it has 3,700 bases and consists of two exons and is strongly associated with the histone acetylation machinery. This lncRNA is conserved in other lizard species and originated at least 55 million years ago. Data on chromatin structure shows that the X chromosome chromatin is structured around the *MAYEX* locus, and chromatin-RNA association data shows that *MAYEX* is in close contact with multiple regions of the X chromosome. Overall, our results indicate that the X-chromosome dose compensation in *A. carolinensis*, as in placentals, marsupials, and *Drosophila*, is closely linked to the evolution of cis-active lncRNAs that serve as hotspots for transcriptional regulation.

Abstract ID: 1760
Poster board number:
P024

Sex-linked genomic variation among populations of an intertidal snail, *Littorina saxatilis*

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Identifying the sex-determination system in species with young homomorphic sex chromosomes has been challenging due to incomplete chromosomal differentiation. Assessing the role of ecology in sex chromosome evolution is needed in order to understand the selective forces involved. The sex-determination system of *Littorina saxatilis* provides an excellent study system with two ecotypes (Crab and Wave) and many contact zones in the presence of gene flow. Although a female-heterogametic sex-determination system has been found recently in the Crab ecotype, the sex-determination system in the Wave ecotype of the same localities remained unclear. In this study, samples were collected from multiple intertidal habitats on small islands in southwest Sweden. We utilised a recently-published workflow (SexFindR) to conduct coverage-based and variant-based analyses as well as kmer-based GWAS analysis on whole genome sequencing data of 99 individuals to identify sex-specific genomic regions or sex-determining loci in both *L. saxatilis* ecotypes. A combination of sexually antagonistic selection and divergent natural selection between the two ecotypes may explain variation in the sex-determination system and sex-specific differentiation patterns.

Abstract ID: 1820
Poster board number:
P025

Chromosome marker suggests rearrangements in Sex Chromosomes in Brazilian complex species of frogs

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Physalaemus cuvieri-Physalaemus ephippifer is an interesting species complex of frogs, which is composed of at least five distinct genetic lineages based on mitochondrial DNA sequences, 3RAD markers and cytogenetic data. Heteromorphic Z and W sex chromosomes are found in *P. ephippifer*, which are likely homeologous to chromosome pair 9 of specimens of lineage 1B of "*P. cuvieri"* (L1B), the sister clade of *P. ephippifer*. In a previous study, a probe derived from microdissection, which detected the pericentromeric region of Zq and Wq of *P. ephippifer*, was mapped to the pericentromeric region of 9p of L1B specimens from Urbano Santos. Additionally, in some *P. ephippifer* individuals, this probe also detected an interstitial site in Zq. Here, we used the same probe (Zqper probe) to investigate specimens from Araruna, which clustered within L1B in phylogenetic analyses based on mitochondrial DNA sequences. The probe detected a pericentromeric region in 8q, which was adjacent to a nucleolus organizer region (NOR). This chromosome 8 differs from chromosome 9 of L1B, which bears a

distal NOR in the long arm and the Zqper site proximally in the short arm. In contrast, 8q of specimens from Araruna is similar to the long arm of the sex chromosomes of *P. ephippifer*, which also bear a distal NOR. However, chromosome pair 8 of females from Araruna are not heteromorphic, differing from sex chromosomes of *P. ephippifer*. These data suggest that complex chromosome rearrangements have been involved in sex chromosome evolution in this group of frogs.

Abstract ID: 1821
Poster board number:
P026

Polymorphism of a satDNA in a zone of secondary contact of lineages with distinct sex chromosomes

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The species complex *Physalaemus cuvieri–Physalaemus ephippifer* consists of five major lineages and presents a wide karyotype diversity. Curiously, only *P. ephippifer* has heteromorphic Z and W chromosomes. Incongruences between mitochondrial DNA and 3RAD datasets suggested the existence of a secondary contact zone (CZ) between *P. ephippifer* and Lineage 1 of "*P. cuvieri"* (L1). However, previous cytogenetic analyses of this CZ failed to identify F1 hybrids and showed heteromorphic Z and W resembling *P. ephippifer*, although they were not identical, suggesting no current hybridization. To better characterize this CZ, we analyzed the distribution of clusters of PcP190 satDNA, which is known to vary considerably between the parental lineages, being mapped to 3p, Zq and Wq of *P. ephippifer* and to centromere/pericentromere of all chromosomes of L1. We mapped PcP190 satDNA to karyotypes of specimens from three Brazilian localities in a transect, including a CZ between *P. ephippifer* and L1. We found a clinal variation in the number of PcP190 clusters and several PcP190 sites were present in a heterozygous condition. The lowest number of chromosomes carrying PcP190 clusters (4 to 9) were found in a site near *P. ephippifer* occurrence areas, whereas the highest numbers (13 to 17) were found in specimens from a locality close to L1 areas. Additionally, PcP190 mapping differed the sex chromosomes found in CZ from those of *P. ephippifer*. Our findings reinforce the hypothesis of ancient hybridization between *P. ephippifer* and L1, which may have driven a fast sex chromosome evolution in this group.

Abstract ID: 1871
Poster board number:
P027

Sex chromosome discovery and dosage compensation mechanism in the Cuban wood snake

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Recent studies have revealed an extensive variability in sex determination systems in snakes. ZZ/ZW sex determination systems have been identified in all studied caenophidian snakes and in the Madagascar boa *Acrantophis* sp. cf. *dumerilii*, while

XX/XY sex determination systems have evolved likely independently in two species of boas (*Boa imperator, B. constrictor*) and a python (*Python bivittatus*). In order to expand our knowledge on the evolution of sex determination in snakes, we explored the presence of sex chromosomes in the Cuban wood snake *Tropidophis melanurus*, a representative of an outgroup lineage to the above-mentioned snakes. We applied both cytogenetic (karyogram reconstruction, C-banding, comparative genome hybridization) and genomic methods (comparative gene coverage analysis between sexes, analysis of expression of sex-linked genes). Our results revealed the species possesses a unique XX/XY sex determination system with highly differentiated sex chromosomes. The X-specific gene content of the Cuban wood snake is not shared with the sex chromosomes of any other reptilian lineage, which suggests that it is a apomorphy of the lineage. We discuss the contribution of the results for furthering our understanding of the the evolution of sex chromosomes and dosage compensation mechanisms in snakes and other reptiles.

Abstract ID: 1937
Poster board number:
P028

The ant-cricket, a new model of sex chromosome evolution?

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Sex chromosome evolution has puzzled scientists for decades. The classical model implies that sex chromosomes derive from a pair of autosomes. After apparition of a sex-determining locus, recombination is locally suppressed and the proto-X(/Z) and proto-Y(/W) chromosomes start diverging. Progressively, the non-recombining Y(/W) chromosome accumulates deleterious mutations and decays. In the last steps, the Y(/W) is considerably shorter, and shares almost no homology with the X(/Z). This model however is mostly based on the observation of few model organisms with old sex chromosomes. The development of new models, especially with young sex chromosomes, is thus necessary. Here we describe the X and Y sex chromosomes of the ant-cricket *Myrmecophilus myrmecophilus*. We built a long-read based female assembly and conducted a population genomic survey using RADseq data. We found the X chromosome to correspond to more than a quarter of the genome. Interestingly, our results indicate that the X and Y chromosomes feature little sequence divergence, but the Y represents only one third of the X in length. This raises the possibility of an important loss of Y chromosome sections before extensive X-Y divergence, or the emergence of a neo-XY system following the fusion of the X with an autosome. Finally, our RADseq data suggest the co-existence in some populations of two different Y haplotypes. Altogether, these results pinpoint the ant-cricket as a promising new model of sex chromosome evolution.

Abstract ID: 1955
Poster board number:
P029

Variations on a background of conservation of sex chromosomes in lacertids

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Substantial evidence has been accumulating in support of the strong conservation of sex chromosomes in lacertids. The combination of different analytical approaches has been very helpful in resolving conflicting results and in keeping the research in this field on track. One still unsolved question is what happens with those few species with multiple sex chromosome systems. Viviparous populations of *Zootoca vivipara* from western Europe present a Z1Z2W system, presumably due to a fusion of an ancestral W chromosome with an autosome. Through genome-wide synteny analyses and mapping WGS reads on the *Z. vivipara* genome, we show that either the rearrangements that gave rise to that system were rather more bizarre than initially proposed, or the genome has been mis-assembled. Similar multiple sex chromosome systems characterize two *Iberolacerta* species from the Pyrenees, *I. bonnali* and *I. aurelioi*. Using cross-species chromosome painting, we show that the biarmed neo-W chromosome of *I. bonnali* does indeed appear to have been produced by a W-autosome fusion. Through chromosome painting and reciprocal genomic cross-species hybridization, we also show that female-specific sequences (W chromosome) are not conserved among *Iberolacerta*, *Timon lepidus* and *Lacerta schreiberi*, notwithstanding a generally good conservation of the other chromosome elements. Finally, after identifying several thousand sex-linked (Z) and autosomal factors in *I. monticola*, we carried out an extensive mapping of those factors on the genomes of both *Lacerta agilis* and *Podarcis muralis*, to show that transpositions involving the Z and the autosomes have taken place several times during the evolution of these species.

Abstract ID: 2033
Poster board number:
P030

Investigating the sex locus in the haplodiploid Argentine ant

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Haplodiploidy, whereby females are diploid and males are haploid is ubiquitous in Hymenoptera (bees, wasps and ants). The prevailing model of sex determination in Hymenoptera is complementary sex determination (CSD), where heterozygous genotypes at the CSD locus determine femaleness, while hemi/homozygous genotypes determine maleness. To date, the molecular mechanism of CSD has only been deciphered in the honey bee. Most ant species are assumed to have a similar system because diploid males, a hallmark of CSD under haplodiploidy, have been observed in various species across the ant phylogeny. We developed the Argentine ant *Linepithema humile* as a model for studying sex determination and its regulatory pathways in ants. We obtained over 200 diploid males and females from inbred lab families. Leveraging a new chromosome-scale reference genome, we pinpointed a 14 kb region that is heterozygous in all females and homozygous in all male. This region shows no homology to the honey bee CSD locus. Furthermore, we identified seven major haplotypes segregating at this new locus with an additional 182 field-collected males and females from multiple populations. We found that heterozygosity at this locus determines the

expression of an uncharacterized gene, which likely directs sexual development via the regulation of sex-specific splicing of key regulators of insect sex determination. Manipulation of the expression level of this gene led to sex reversal, providing a functional demonstration of its role as the primary trigger in *L. humile* sex determination.

Abstract ID: 2176
Poster board number:
P031

Cytogenetic analysis of the members of the snake genera *Cylindrophis*, *Eryx* and *Python*

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Female heterogamety (ZZ/ZW system) was for a long time assumed in all snakes, stemming from the differentiated and often heteromorphic sex chromosomes in the species-rich group of caenophidian snakes. However, the recent discovery of two independently evolved XX/XY sex determination systems in the non-caenophidian genera *Python* and *Boa* sparked a new drive for sex chromosome research in other, less studied, snake lineages. In this study, we examined seven species from the non-caenophidian genera *Eryx*, *Cylindrophis* and *Python* by conventional and molecular cytogenetic methods. All species from the genus *Eryx* have karyotypes with 2n = 34 chromosomes, while *Cylindrophis ruffus* and *Python regius* have 2n = 36 chromosomes. Although all studied species have similar karyotypes in terms of chromosome morphology, we detected variability in the distribution of heterochromatin, telomeric repeats and rDNA loci. Heterochromatic blocks were detected mainly in the centromeric regions in all species, but accumulations were detected in pericentromeric and telomeric regions in few macrochromosomes in the species of the genus *Eryx*. All species show the expected topology for telomeric repeats at the edge of all chromosomes, with the exception of *E. muelleri*, where additional accumulations were detected in the centromeres of three pairs of macrochromosomes. The rDNA loci accumulate in one pair of microchromosomes in all species except *Python regius*, where they are located in two pairs of microchromosomes. Sex-specific differences were not detected, suggesting that these species have either homomorphic, poorly differentiated sex chromosomes, or lack sex chromosomes.

Abstract ID: 2210
Poster board number:
P032

A supergene underlies social polymorphism in the desert ant

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Cataglyphis niger displays polymorphism in colony structure. While most colonies are monogyne (having a single queen), others are polygyne (having multiple egg-laying

queens) and form large supercolonies that may consist of hundreds of nests. We investigated the genomic and evolutionary basis of this polymorphism. We sampled 30 nests from a single population where both the social forms are represented. We used dyadic aggression assays to distinguish the social forms. We then used reduced-representation genomic sequencing (RAD-seq) to genotype 20– 24 individuals per nest. Kinship analyses was carried out to confirm social structures. When Fst values were compared between monogyne and polygyne samples, hundreds of high Fst loci were detected, all of which were located in an ~8Mbp region on one chromosome, suggesting the presence of a supergene— a group of tightly linked genes in a region of suppressed recombination. We also observe high linkage disequilibrium in this region of the chromosome, further supporting this hypothesis. This chromosome is analogous to so-called “social chromosomes” described in other ant species. We identified similarities and highlight differences in the distributions of genotypes among social structures that indicate possible underlying mechanisms. I will present our work so far and discuss ecological and evolutionary hypotheses on how this genomic architecture is maintained in this species.

Abstract ID: 2215
Poster board number:
P033

Identification of ZZ/ZW sex chromosomes in the Madagascan leaf-tail geckos

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Geckos are a highly diversified reptilian lineage with a remarkable variability in sex determination (environmental or genotypic), the type of heterogamety (ZZ/ZW or XX/XY) and the degree of sex chromosome differentiation. Therefore, geckos represent a magnificent group to explore the evolution of sex chromosomes. We explored for the first time three species of the Madagascan leaf-tail geckos of the genus *Uroplatus* with cytogenetic and genomic methods. The cytogenetic analysis revealed ZZ/ZW sex chromosomes with highly differentiated and heterochromatic W chromosome in all three species. The comparative gene coverage analysis between sexes in *Uroplatus henkeli* revealed an extensive Z-specific chromosomal region, with gene content partially homologous to chicken chromosome 28. This genomic region has been co-opted for the role of sex chromosomes in several vertebrate lineages, including monitors and beaded lizards (Helodermatidae) and monotremes, and includes the gene *amh* as a prominent candidate sex-determing locus. A comparative qPCR method revealed homology of the ZZ/ZW sex chromosomes in all three tested leaf-tail geckos. These sex chromosomes seem not to be present in other gekkotan lizards, including the closely related genera *Ebenavia* and *Paroedura*. These results indicate that the sex chromosomes of *Uroplatus* geckos can be at least 50 MY old. We discuss and revise current knowledge on the evolution of sex determination in geckos in the light of our novel findings.

Abstract ID: 2260
Poster board number:
P034

Evolution of sex chromosomes in chameleons

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Chameleons are fascinating creatures, well known for their unique features, such as extremely long projectable tongue, prehensile claws, independent eye movements, and the ability of certain species to communicate through colour changes. Although much information is available on chameleon biology, very little is still known about their sex determination. Genotypic sex determination has been suggested in several species based on equal sex ratios across several incubation temperatures, but out of 222 species of the family Chamaeleonidae, sex chromosomes have been described so far only in two genera, namely female heterogamety in six species of the genus *Furcifer* and male heterogamety in two species of the genus *Chamaeleo*. In the current project we applied comparative genome coverage of Illumina DNAseq reads to uncover sex chromosome gene content in *Furcifer pardalis* and *F. lateralis* and we tested homology of sex chromosomes across six genera of chameleons by quantitative PCR. Our results indicate that members of the genus *Furcifer* share homologous ZZ/ZW sex chromosomes, which are not present in other tested chameleons. We can conclude that ZZ/ZW sex chromosomes evolved in the genus *Furcifer* at least 41 Mya. Interestingly, as in therian mammals, lacertid lizards and *Paroedura* geckos, the region syntenic to the chicken block 4p was co-opted for the role of sex chromosome in the chameleons of the genus *Furcifer*, making these groups an excellent model for the study of convergent evolution of sex chromosomes from the same genomic region.

Abstract ID: 2276
Poster board number:
P035

Discovery and ecological impact of minute sex chromosomes in Sphagnum (peat moss)

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Sex in haploid dioicous bryophytes is often determined by non-recombining U/V sex chromosomes that segregate among spores during meiosis. While a 1:1 segregation pattern is expected, bryophyte sex ratio biases are often observed in the wild (particularly under stressful conditions), where one sex (usually female) is favoured. Sphagnum, a bryophyte and a keystone member of peatland communities for its role in global carbon cycling, outcompetes other organisms through ecosystem engineering and the generation of hyper-acidic conditions. Sphagnum also displays sex-ratio bias, but tends to be skewed toward males. To uncover the environmental conditions and genetic mechanisms that contribute to sex-ratio biases, we generated two high-quality genome assemblies for two species of *Sphagnum* (*S. divinum* and *S. angustifolium*) and sequenced an F1 pedigree for QTL mapping. The genome assemblies reveal small (~5Mb) non-recombining sex chromosomes, derived from ancient whole genome

duplications and rearrangements that occurred during Sphagnum's long evolutionary history. Furthermore, QTL mapping within the Sphagnum pedigree population showed these newly discovered sex chromosomes directly impact Sphagnum's ability to grow under harsh pH conditions via trans-regulatory interaction with autosomal QTLs. These sex-specific interactions are dependent on environment and are indicitive of antagonistic pleiotropy, where allelic combinations in males that are beneficial in one condition were detrimental in another. This suggests separate adaptive strategies are employed by males and females in Sphagnum under abiotic stress conditions and provide a possible explanation for sex-ratio biases in bryophytes.

Abstract ID: 2283
Poster board number:
P036

Neo-sex chromosome evolution in butterflies of the tribe Danaini

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Moths and butterflies (Lepidoptera) are the most speciose taxon with female heterogamety, i.e. sex chromosome constitution WZ/Z0 in females and ZZ in males. The classical theoretical model postulates that sex chromosomes derived from an autosome pair that acquired a sex determining factor. The sex-limited chromosome Y or W subsequently differentiated due to suppressed recombination resulting in gene decay and accumulation of repetitive sequences. However, it was recently proposed that the lepidopteran W chromosome evolved from a supernumerary B chromosome. The canonical differentiation could be studied in lepidopteran neo-sex chromosomes formed by fusion of the ancestral sex chromosomes with an autosome. Although the neo-sex chromosomes were considered rare in groups with female heterogamety, they are common in Lepidoptera. Indeed, repeated sex chromosome-autosome fusions have been reported in a monarch butterfly, *Danaus plexippus*, and its congeners. In the present study, we investigated the evolutionary origin of the *Danaus* neo-sex chromosomes within the tribe Danaini. We sequenced and *de novo* assembled genomes of *Tirumala*
septentrionis (Danaina), *Ideopsis similis* (Amaurina), *Idea leuconoe* (Euploeina)
and *Lycorea cleobaea* (Itunina) and identified Z-linked scaffolds by comparison of read-depth between sexes. Our results revealed that the *Danaus* neo-sex chromosomes occurred in a common ancestor of Danaina, Amaurina, and Euploina, some 20-30 Mya. Remarkably, independent neo-sex chromosomes evolved in *L. cleobaea* and multiple ancestral autosomes became sex-linked in *I. similis*.

Abstract ID: 2303
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P037

Evolution of sex chromosomes in pholcid spiders (Araneae: Pholcidae)

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Most spiders are placed into the infraorder Araneomorphae, which consists of two clades, Haplogynae and Entelegynae. Spiders are remarkable for their unusual sex chromosomes. Many haplogynes exhibit the X_1X_2Y system, which is presumably ancestral for araneomorphs. This system comprises usually metacentric chromosomes, which pair achiasmatically by ends of arms during male meiosis. The spider X_1X_2Y system had been mistaken for the X_1X_20 system for a long time, due to the tiny size of the Y chromosome. Therefore, knowledge on evolution of the X_1X_2Y system is still scarce. To trace transformations of this system, we have focused on pholcids, which are among the most species-rich spider families. Chromosomes of the X_1X_2Y system differ in the pattern of their evolution in pholcids. Evolution of some lineages was accompanied by an enormous increase in size of the Y chromosome. The X_1X_2Y system has often converted into multiple X or XY systems, which retained the original achiasmatic pairing, and subsequently into the X0 system. Complex systems $X_1X_2X_3Y$ and $X_1X_2X_3X_4Y$ of ninetine pholcids are also derived from the X_1X_2Y system. Their formation has included fissions or nondisjunctions of X chromosomes. Nucleolus organizer regions (NORs) have spreaded frequently (at least five events) to sex chromosomes. Sex chromosome-linked NORs of the subfamily Pholcinae are located at chromosome ends involved in pairing. This pattern suggests involvement of NORs in achiasmatic pairing of sex chromosomes. In some species these NORs degenerated. Supported by Ministry of Education, Youth, and Sports of the Czech Republic (project LTAUSA 19142).

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P038

Sex chromosomes expression evolution in Drosophila spp. spermatogenesis

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Meiotic Sex Chromosome Inactivation (MSCI) is a transcriptional silencing of sex chromosomes in the early stages of male meiosis. A recent publication showed the presence of downregulation on the D. melanogaster X chromosome and also it was observed a similar pattern for the ancient X chromosome, commonly called dot. However, the impact of MSCI on the Drosophila genus is unknown. To investigate the evolutionary panorama of MSCI, we used RNA-seq data of the three main phases of spermatogenesis (mitosis, meiosis, and post meiosis) which was obtained according to the Vibranovski et al. (2009) technique of dissection. The isolation was performed in four species of Drosophila genus: D. melanogaster, which the mechanism was broadly studied and we use to compare with D. simulans, a close specie of D. melanogaster; D. willistoni, which has a neo-X chromosome and it belongs to a sister group and D. mojavensis, a specie from an external group. Although the differences in morphology and RNA quantity for each species, we found similar expression profiles of spermatogenesis for all transcriptomic data using k-means clustering. Moreover, an underrepresentation of overexpressed genes on the X and dot chromosomes in meiosis compared to mitosis was found in three of these four analyzed species. Interestingly, D. willistoni Neo X shows a similar under expression in meiosis, suggesting a presence of MSCI, as observed in muller A of D.melanogaster. Overall, we found that MSCI is generally preserved in the genus Drosophila, including when it comes to X chromosomes of different ages.

Abstract ID: 2342
Poster board number:
P039

Sex determination in the oribatid mite *Hermannia gibba*

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Sex chromosomes have evolved independently in many different taxa, the most common being the XY male heteromorphic system. However, this is not the only system and even independent of specified sex chromosomes there is a large variability and factors that have an influence on the development of males and females. Only little is known about the genomic sex determination large soil-living animal groups such as mites. Oribatid mites are one of the oldest terrestrial arthropod group and used as non-model organisms for the evolution of sex. We aim to identify the sex determination system in the sexual oribatid mite *Hermannia gibba.* We combined morphological and genetic approaches to gain a deeper understanding of how sex is determined in such basal species. We generated sex-specific pooled data (Pool-seq) and a *de novo* genome assembly. Accurate and reliable (putative) sex related SNPs were estimated from genome-wide allele frequencies. Furthermore we identify sex-linked regions using a coverage estimation - and kmer approach. Whith this study light is shed on sex determination in oribatid mites for the first time

Abstract ID: 2352
Poster board number:
P040

The S-locus supergene controlling heterostyly in primroses originated via stepwise duplications

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Supergenes are defined as nonrecombining genomic regions ensuring the coinheritance of multiple, coadapted genes. Similar to sex chromosomes, supergenes controls complex trait polymorphisms and are predicted to undergo analogous evolutionary trajectories. Despite the importance of supergenes in adaptation, little is known on how they originate. A classic example of supergene is the S locus controlling heterostyly, a floral heteromorphism which in Primula - the main model for studying heterostyly - is characterized by the cooccurrence of two complementary, self-incompatible floral morphs, named ‘pin’ and ‘thrum’. The Primula S locus comprises five genes clustered in a ca. 300-kb region absent in ‘pin’ plants and hemizygous in ‘thrums’ – a pattern analogous to the Y chromosome in dioecious species. Here, by leveraging the chromosome-scale genome assembly of the heterostylous Primula veris (cowslip) that we generated together with comparative genomic analyses, we demonstrate that the S-locus evolved via multiple, asynchronous gene duplications and independent gene translocations. Furthermore, we propose a mechanism for the origin of S-locus hemizygosity via nonhomologous recombination involving the newly discovered two pairs of CFB genes flanking the S locus. Finally, we detected only weak signatures of degeneration in the S locus, as predicted for hemizygous supergenes.

Abstract ID: 2375
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P041

Linking gametologue evolution to human sex differences in gene expression and disease

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Humans exhibit sex differences in susceptibility to many disorders, including female-biased autoimmune disease and male-biased early-onset neurodevelopmental conditions. These differences are likely to (in part) reflect evolved sex differences in brain gene expression. Of particular interest are the gametologues: genes that have retained functional copies on the X and Y chromosomes despite having ceased recombination over evolutionary time. Recent work suggests that gametologues vary in X-Y functional equivalence and tissue-specific co-expression patterns. However, we currently lack an understanding of: 1) how co-expression patterns between X-Y members compare to their co-expression patterns with all other genes (‘coupled co-expression’); 2) the mechanisms that drive co-expression; or 3) the functional impacts of differential co-expression with X versus Y gametologues. To address these gaps, we used a large, published human gene expression dataset (GTEx V8) to characterize gametologue co-expression and coupled co-expression across >40 tissues. These measures were correlated across tissues and pairs (asymptotic regression: $p<0.001$, pseudo $R^2=0.84$), with larger deviations among the most sexually differentiated tissues (testes, prostate, mammary). X-Y pairs that ceased recombination more recently exhibited more similar promoter, DNA, and protein sequences (ANOVA: $p<0.001$). Promoter sequence similarity predicted average co-expression across gametologue pairs (rho=0.681; p=0.021), suggesting that higher co-expression reflects shared regulatory mechanisms. Finally, genes showing higher co-expression with X or Y gametologues were associated with sex-biased

conditions (Y>X: autism, ADHD in brain tissues; X>Y: autoimmune disease in many tissues; p_{adj}<0.001). This work improves our understanding of how sex chromosome evolution has influenced the human transcriptome and sex differences in disease.

Abstract ID: 2448
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P042

De-novo genome assembly of the dwarf willow *Salix herbacea* reveals the sex-linked region

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Evidence from sex chromosome systems at early stages is key to understanding the evolution of sex. A high turnover of recently emerged sex chromosomes was proposed in the willow family (Salicaceae). *Salix herbacea* is a dwarf alpine willow with primary sex differentiation and female bias in natural populations. However, the genetic basis of the sex-determination system and sex ratio bias remains unknown. Here, we report the first draft genome assembly of a female *Salix herbacea* using PacBio HiFi long reads, which was ~330.04Mb in size with a scaffold N50 of 10.75Mb. 98% of genome sequences were anchored to 19 pseudochromosomes. 97.9% of conserved single-copy orthologs were identified showing high contiguity and completeness of this genome assembly. Based on genetic variation, coverage differences and K-mer analysis of short reads from pool-seq and individual re-sequencing of females and males, we detected a female-specific region of 1.5Mb on chromosome 15, suggesting a female heterogametic (ZW) system, as in closely related species (*S. viminalis*, *S. purpurea*). The region contained a high proportion of transposable elements possibly associated with low recombination. Using female-specific K-mers, sex markers were designed and will be used to identify the sex of plants in controlled crosses of *Salix herbacea*. Sex-specific markers as well as the high-quality genome assembly of *Salix herbacea* provide valuable genomic resources that will allow us to further elucidate the mechanism of sex ratio bias and sex determination in *Salix herbacea* and across the Salicaceae family.

Symposium: S03. Diversity and evolution in sperm, ova, and other primary reproductive traits (id: 937)

Abstract ID: 993
Poster board number:
P043

Macroclimatic and maternal effects on the evolution of reproductive traits in lizards

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Much of life-history theory rests on fundamental assumptions about constraints on the acquisition and allocation of energy to growth and reproduction. In general, the allocation

of energy to reproduction depends on maternal size, which in turn depends on environmental factors experienced throughout the life of the mother. Here, we used phylogenetic path analyses to evaluate competing hypotheses about the environmental and maternal drivers of reproductive traits in lizards. In doing so, we discovered that precipitation, rather than temperature, has shaped the evolution of the life history. Specifically, environments with greater rainfall have enabled the evolution of larger maternal size. In turn, these larger mothers produce larger clutches of larger offspring. However, annual precipitation has a negative direct effect on offspring size, despite the positive indirect effect mediated by maternal size. Possibly, the evolution of offspring size was driven by the need to conserve water in dry environments, because small organisms are particularly sensitive to water loss. Since we found that body size variation among lizards is related to a combination of climatic factors, mainly precipitation and perhaps primary production, our study challenges previous generalizations (e.g., temperature-size rule and Bergmann's rule) and suggests alternative mechanisms underlying the evolution of body size.

Abstract ID: 1016
Poster board number:
P044

Sperm morphology and reproductive success in the hermaphroditic flatworm, *Macrostomum lignano*

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In reciprocally-mating simultaneous hermaphrodites, where individuals mate frequently in order to donate sperm, they unavoidably also receive sperm from their partners. As a result, post-copulatory sexual selection—through sperm competition and cryptic female choice—is expected to be very important in simultaneous hermaphrodites. Research on the reciprocally-mating free-living flatworm *Macrostomum lignano has shown that most of the variance in male reproductive success is indeed explained by post-copulatory fitness components, such as the sperm donor's ability to store sperm in a sperm recipient and to convert stored sperm into successful fertilizations.* Sperm morphology in *M. lignano* is complex, and includes the anterior feeler and the two stiff lateral bristles. In this ongoing project, we aim to understand the significance of these structures in attaining sperm storage, and ultimately fertilization success, in a mating partner. A range of GFP(+) inbred *LM* isolines of *M. lignano*, exhibiting between-line genetic variation in sperm morphology, provide a suitable platform to investigate the role of sperm morphology in reproductive success. The GFP(+) LM lines express a green fluorescent protein ubiquitously in all cell types, including the sperm cells, thus enabling us to differentiate GFP(+) sperm from GFP(-) sperm within a recipient's female sperm storage organ. By competing LM line donors against a common GFP(-) competitor, we study the relative competitiveness of contrasting sperm morphologies in the post-copulatory fitness components. The results from this study will improve our understanding of post-copulatory sexual selection in the generally less studied simultaneously hermaphroditic systems.

Abstract ID: 1043
Poster board number:
P045

Impact of thermal stress from hot exposure events during heatwaves on reproduction in a model insect

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Reproductive form and function are sensitive to thermal stress. More frequent, intense hot exposure events during heatwaves (HEE, few hours of very high temperatures during summers), poses a risk to biodiversity when the tolerance threshold for thermal safety margins is exceeded. It is also predicted that under continued global warming, several recurrent sub-lethal HEE episodes are likely to increase. Exposures lasting just a few hours can have compounding negative effects on life functions. We currently know very little on the extent of damage to reproduction or other functions across taxa. In the model insect system, *Tribolium castaneum* (the red flour beetle), we measured how HEEs might disrupt phenotypic expression of reproductive traits (e.g., sperm and testes) and its consequences on fertility. In a fully factorial design, we exposed males to varying degrees of experimental HEEs (recently occurred globally). Sexually mature adult males that developed under standard lab conditions were exposed to either 30°C (controls) or thermal stress due to a HEE (42–50°C in 2°C intervals for 2, 5 or 10 hrs followed by a 24-hr "rest"). Sperm length, coefficient of variation (CV) in sperm length, testes volume, CV in testes follicles and fertility thermal limits (FTLs) were quantified after male HEEs. This allowed us to systematically measure the extent of damage and the impacts of sub-lethal HEEs on reproduction. These findings and future work will help us study the extent to which HEEs disrupt reproductive function and its consequences on population viability.

Abstract ID: 1102
Poster board number:
P046

Selection on sperm size in response to promiscuity and variation in female sperm storage organs

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Sperm cells are exceptionally morphologically diverse across taxa. However, morphology can be quite uniform within species, particularly for species where females copulate with many males per reproductive bout. Strong sexual selection in these promiscuous species is widely hypothesized to reduce intraspecific sperm variation. Conversely, we hypothesize that intraspecific sperm size variation may be maintained by high among-female variation in the size of sperm storage organs, assuming that paternity success improves when sperm are compatible in size with the sperm storage organ. We use individual-based simulations and an analytical model to evaluate how selection on sperm size depends on promiscuity level and variation in sperm storage organ size (hereafter, female preference variation). Simulated species with high promiscuity showed stabilizing selection on sperm when female preference variation was low, and disruptive selection when female preference variation was high, consistent with the analytical model results. With low promiscuity (2-3 mates per female), selection on sperm was stabilizing for all

levels of female preference variation in the simulations, contrasting with the analytical model. Promiscuity level, or mate sampling, thus has a strong impact on the selection resulting from female preferences. Further, for species with low promiscuity, disruptive selection on male traits will occur under more limited circumstances than many previous models suggest. Variation in female sperm storage organs likely has strong implications for intraspecific sperm variation in highly promiscuous species, but likely does not explain differences in intraspecific sperm variation for less promiscuous taxa.

Abstract ID: 1249
Poster board number:
P047

Comparative proteomics of the perivitelline layer – the site of avian sperm-egg interaction

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Fertilisation requires interaction between the egg and sperm. Miscommunication between the two gametes can lead to incompatibilities, loss of fertility, and failure to produce a viable zygote. Sperm and egg proteins underlying this interaction are a potential post-mating pre-zygotic mechanism of female choice and species recognition. To understand sperm-egg interactions, and how they may contribute to reproductive barriers, we need to identify and explore these proteins across species. Thus far, research in model systems has identified some interacting sperm and egg proteins, including lysin and VERL in abalone, and Izumo1 and Juno in mice. In birds, sperm interact with the membrane surrounding the yolk, the inner perivitelline layer (IPVL). We used a proteomics approach to characterise the IPVL across eight passerine species to identify candidate proteins involved in sperm-egg interactions. Immediately before fertilisation, the sperm membrane weakens, and the contents of the acrosome (a vesicle in the sperm head) are released. Proteins released in this acrosome reaction are in a position to interact with the egg. Two phenomena distinguish avian fertilisation. Firstly, the IPVL is required to induce the acrosome reaction. Secondly, polyspermy is essential for fertilisation. In addition, in passerine birds, sperm length (40-300µm) and acrosome volume (0.48-7.18µm3) varies considerably across species. We take advantage of this natural variation to explore how IPVL protein composition and structure differ across species and how variation in sperm morphology may influence the IPVL and sperm-egg interactions. Our results give insights into avian sperm-egg interaction and proteins that may underlie barriers to hybridisation.

Abstract ID: 1347
Poster board number:
P048

How does social environment affect oviposition decisions?

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Individuals plastically adjust their investment in reproduction based on the prevailing social environment to increase their potential fitness. Response to varying social contact in males has been widely studied, yet less is known about responses in females. This is

surprising, given that in many species females have a greater control over progeny success through oviposition decisions – e.g., they can often choose the size and sex ratio of their brood, its paternity, and its location. Social environment might drive trade-offs between competition and cooperation at multiple life stages. In many metamorphosing species larvae benefit from communal feeding, however in certain conditions they can also be cannibalistic. Plus some, in their egg stage, secrete antimicrobial and anti-cannibalistic pheromones ('public goods' that not only benefit the individual, but also the local population), but ovipositing eggs in an existing cluster comes at an increased risk of competition. With all these complex social interactions, females must consider the benefits of public goods and the costs of competition and larval travel when choosing potential oviposition sites. Here we alter the pre- and post-copulation social environment in *Drosophila melanogaster*, by varying female housing density and the presence of conspecific eggs, to understand the impact of this variation on oviposition site selection decisions and subsequent fitness.

Abstract ID: 1359
Poster board number:
P049

Mitochondrial DNA copy number variation in birds and its relationship to sperm midpiece length

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Tremendous variation in sperm morphology is observed across the animal kingdom. In birds, the length of the midpiece, which is formed when several mitochondria fuse during spermatogenesis, explains a considerable amount of this variation. The midpiece is one of the main structural components of the sperm cell and is an important source of energy used for the propulsion of the sperm, mainly generated by oxidative phosphorylation reactions in the fused mitochondria. However, there is still little known about the total number of mitochondria that form the midpiece. In this project, we aim to identify the relationship between the length of the midpiece and the copy number of mitochondrial DNA (mtDNA). To test the hypothesis that sperm with longer midpiece have a higher number of mtDNA, we analyse a range of wild passerine species representing extreme ends of sperm phenotypic variation and major phylogenetic clades within Passerides. We use universal primers to amplify a region of the mitochondrial cytochrome c oxidase subunit I (COI) gene and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) as a single reference gene for nuclear DNA, and employ quantitative real-time PCR on rinsed sperm samples to measure the relative number of mtDNA copies across species. Our findings will be important for better understanding sperm motility and uncovering the association between sperm midpiece length and mitochondrial loading in wild passerines.

Abstract ID: 1783
Poster board number:
P050

How reproductive modes influence the egg size/clutch size trade-offs in salamanders?

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Mothers apply two basic strategies to maximise their reproductive success: i) increasing offspring numbers or ii) allocating more nutrients into larger offspring. However, the mother's optimal investment into more or larger offspring is traded off. Moreover, offspring size and number are under the selection of the environment. Salamanders (Caudata) with their variable reproductive output and strategies constitute an attractive model system for investigating relationships among parental investment and its predictors. Using 208 species of newts and salamanders representing all major urodelan lineages, we compare egg size, clutch size, their trade-off and total reproductive output measured as clutch volume applying phylogenetically informed models. We classified reproductive strategies as (i) aquatic or terrestrial egg-laying or (ii) the use of standing or still waters, or terrestrial environment as juvenile habitats. We also examined the effects of macroclimatic factors on each reproductive output metrics. We find that terrestrial egg-laying only reduce clutch size, whereas various larval/juvenile environments also influence egg size. Our results confirm the negative association between egg size and clutch size in aquatic breeders; however, this trade-off disappears in terrestrial breeders. Moreover, reproductive strategies influence the association between the reproductive output and its environmental predictors, especially clutch size and precipitation. Our study highlights that reproductive strategies do not only impact on egg and clutch size per se, but also influence the trade-off between them. We also demonstrate that increasing degrees of terrestriality may lead to greater independence from abiotic environmental conditions during reproduction.

Abstract ID: 2056
Poster board number:
P051

Effects of egg size and carotenoid content on juvenile growth and survival in brown trout

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Maternal environmental effects can play important roles in early life, but their effects on population dynamics remains unclear. Laboratory-based studies on salmonid fish, such as the brown trout (*Salmo trutta*), have established that egg size and egg carotenoid content significantly influence growth and/or tolerance to infection at embryo and larval stages. However, little is known about the relevance of such egg characteristics on juvenile performance in the wild. We used wild-caught brown trout to perform two full-factorial *in vitro* breeding experiments, used some of the resulting offspring for controlled laboratory experiments (Wilkins et al. 2017, Oecologia 185, 351-363), and released the remaining offspring into a natural streamlet. We recaptured 0+ juveniles after their first summer and used microsatellite and sex-linked markers to determine sex-specific growth and survival per experimental family. We are currently finishing the analyses and will present answers to the following questions: (i) to what degree does the laboratory study predict juvenile performance in the wild, and (ii) what is the relative importance of egg size and egg carotenoids on juvenile growth and survival in the wild. We will discuss our findings in the light of female life-history strategies and their effects on population dynamics.

Abstract ID: 2157
Poster board number:
P052

Sperm competition in lampreys

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Sexual selection can be a powerful driver of speciation. The role of precopulatory sexual selection (e.g. male contest) in speciation has been widely studied but few studies investigated the influence of sperm competition in this context. Here we studied the role of sperm competition in speciation between two lamprey ecotypes whose taxonomic status is still debated. First, we assessed the sperm velocity and sperm concentration in *Lampetra fluviatilis* and *L. planeri*. Second, we performed sperm competition experiments between ecotypes, either at equal sperm volume or equal sperm number with ova of both ecotypes. We observed an opposite pattern in sperm traits of both ecotypes with a higher sperm concentration and a lower sperm velocity for *L. planeri* compared to *L. fluviatilis*. The outcomes of sperm competition experiments resulted from these differences in sperm traits and no cryptic female choice was observed. At equal sperm volume, *L. planeri* males had a higher fertilization success than *L. fluviatilis* males, and vice versa at equal sperm number. Our results demonstrate the role of sperm number and sperm velocity in sperm competition success and show the absence of postcopulatory prezygotic barrier between these lamprey ecotypes.

Abstract ID: 2194
Poster board number:
P053

Influence of storage time on the DNA integrity and viability of spermatozoa of the spider crab

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The spider crab *Maja brachydactyla* is a decapod crustacean very common in the European Atlantic coast. Fertilization in this species is internal and takes place simultaneously with the extrusion of the eggs into the abdominal cavity of the females. The females are capable of fertilizing successive broods without new matings, because they have seminal receptacles where they store the sperm from copulations with one or

more males. In Galicia, the estimated number of broods per each annual reproductive cycle is three. For this reason, the time that the sperm remains stored can be a determining factor in the viability of the broods and larvae.
In this study, 12 virgin females were crossed in captivity and dissected in batches of 3 females at 0, 1, 2 and 3 months. In addition, 15 females that had last copulated between 5 and 15 months before being sacrificed were dissected. The masses extracted from the seminal receptacles of these 27 females were used for viability (esterase activity) and DNA integrity (comet assay) tests.
The results obtained show that the DNA integrity of the spermatozoa drops sharply during the first three months of storage. Thereafter, the percentage of cells with damaged DNA remains stable. In the case of viability, 60% of spermatozoa are no longer viable after the 4th month.
Therefore, what is the evolutionary advantage of having seminal receptacles to accumulate sperm if the sperm is damaged at times longer than 4 months? This paper discusses this reproductive strategy.

Abstract ID: 2204
Poster board number:
P054

Comparative analysis of heteromorphic sperm in the gastropod genus *Littorina*

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In some species, males exhibit sperm heteromorphism: they produce both fertilizing sperm (eusperm) and anucleate, non-fertilizing parasperm. In some species, parasperm form a physical barrier to prevent insemination from other males; however, in many other species, the role of parasperm is not so obvious, but paternity-assurance is a likely function. In gastropods, the morphology of parasperm is highly variable between genera, such as lancet-shaped in *Fusitriton*, conical in *Conus*, and round in *Littorina*. Within the seminal vesicle, filiform eusperm are attached to parasperm by the tip of their acrosomes, and it is hypothesized that parasperm provide nutrients during this storage period. However, as eusperm become detached upon mating, this attachment is not an advantage for eusperm within the female reproductive tract. Additionally, parasperm in *Littorina* species do not form a physical barrier to prevent subsequent matings. Sperm competition exists in *Littorina,* and is extremely high in some species, thus parasperm could facilitate optimal fertilization conditions for their related eusperm - as has been shown in *Lepidoptera*. To better understanding the evolution and function of parasperm in *Littorina* snails, we examined variation of both eusperm and parasperm within and among several species of *Littorina* including two different ecotypes of *L. saxatilis and L. fabalis*. We compared eusperm length and parasperm size among different *Littorina* species and ecotypes. Furthermore, we compared proteins from eusperm and parasperm from a subset of these taxa to identify parasperm-specific proteins that may be involved in paternity-assurance.

Abstract ID: 2390
Poster board number:
P055

The gene regulation response to insemination in the reproductive system of the ant

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The queen-worker caste system is the defining characteristic of the eusocial insect and is a typical example of environmentally-induced phenotypic polymorphism. In this system, the diploid individuals develop as reproductive females and workers which lose their reproductive opportunity for a lifetime and become assistants to their mother queen. In the ant, the gyne identity, the primary reproductive female caste, was hatched from their pupae case. However, only the inseminated gynes will become the true queens that undertake the reproduction for their whole life. The differentiation between virgin gynes and inseminated queens refers to the transition of reproductive roles where these females' organs and behaviours diverged considerably. The comparative molecular basis of queens and virgin gynes differentiation after insemination in the ant remains to be revealed. How the genetic regulatory networks (GRN) differ in the process of insemination directly related to the reproduction of a whole colony thus is a fundamental but necessary topic for understanding the caste differentiation mechanism. Here, we focus on the reproductive of *Monomorium pharaonis*, intending to clarify: i) How the ovary anatomy and gene regulating network altered in response to insemination. ii) Whether and how insemination-induced GRN for reproductive role differentiation interacted with the GRN mediating gyne-queen caste differentiation in the spermatheca and brain. iii) The common sociality feature between ants and bees promoted us to investigate further whether the insemination-induced role differentiation GRN within the gyne-queen caste shared homologous modules with a regulatory mechanism in these social species.

Symposium: S04. The evolutionary ecology of mating systems (id: 29)

Abstract ID: 1054
Poster board number:
P056

Unusually long parental care in Malagasy shorebirds

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Parental care is costly to the parents but beneficial to offspring, thus natural selection is expected to produce optimal care strategies that balance these costs and benefits. Since parents typically produce several broods of offspring throughout their life, parental care in most organisms tends to be short and limited only to those periods of offspring life when the parents can make a substantial contribution to offspring survival, e.g. where young need intense care, nursing or protection. In our recent work, however, we discovered that Malagasy shorebirds have unusually long parenting. In temperate zones parenting in precocial shorebirds rarely extends beyond 4 weeks post-hatching, however, in Madagascar we noticed parents attending their young for up to 8 weeks. As sub-tropical species generally live longer than temperate species, this could create different trade-

offs. By investigating three Malagasy shorebirds (Kittlitz's plover, white-fronted plover and Madagascan plover) that breed sympatrically in our study area in SW Madagascar, we are quantifying the costs and benefits of their care. Our working hypothesis is that uneven adult sex ratios could potentially influence the different parenting strategies in these three species. While most studies investigating the costs and benefits of avian care focus on the period from hatching to fledging, our work on this unusually long post-fledging care will shed further light on the evolutionary forces that influence the diversity of parental strategies. Importantly, since one of the plover species (Madagascar plover) is endangered, our work will contribute to the protection of this species and its breeding habitat.

Abstract ID: 1160
Poster board number:
P057

Androgenesis to induce polyploidy and hybridization in the invasive Corbicula clam genus

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One peculiar way to depart from canonical outcrossing is to reproduce through maternal genome loss, namely androgenesis. This reproductive mode consists in a father clonality, where only the male nuclear DNA is transmitted to the offspring. The maternal chromosomes do not participate to the embryo formation, via absence of fertilization, production of anucleate oocyte, or genome expulsion. The progeny can be haploid, from a reduced male gamete only, or diploid, through gamete fusion, diploidization, or even unreduced gamete production. Moreover, androgenesis is often associated with other peculiarities, such as polyploidy and hybridization. While this reproductive strategy was reported only in a few unrelated taxa, it appears as a system that promotes invasiveness in some of them, where androgenetic lineages display wide distributions compared to their sexual relatives. This is notably the case of the animal clam genus *Corbicula*. The native range of this freshwater bivalve encompasses Asia, Oceania, Africa and Middle-East, where both androgenetic and sexual lineages are found, sometimes in sympatry. During the last century, the genus was found in America and Europe, and is now widespread in main freshwater systems where they reach high densities. However, only androgenetic lineages were found in the invasive range. Androgenesis allows distinct *Corbicula* lineages to exchange mitochondrial and even nuclear genes, and the relationships between them are blurred by this mating system, with the occurrence of lineages showing both sexual and androgenetic features. Using genetics, histology and cytology, our study aims at understanding the origin and consequences of androgenesis in *Corbicula* clams.

Abstract ID: 1188
Poster board number:
P058

A model of stable trioecy and its transition toward and from dioecy in metapopulations

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Evolutionary transitions from hermaphroditism to dioecy are thought often to pass via gynodioecy through the spread of male-sterility mutations. While a mutation for male sterility eventually needs to segregate at a nuclear locus for dioecy to evolve from gynodioecy, theory has shown that the first step in the transition can be the spread of a male-sterility mutation with cytoplasmic inheritance. Another crucial step in the transition from gynodioecy to dioecy is the spread of males caused by one or more female-sterility mutations. Here, we analyse a model that considers the evolution of populations with both cytoplasmic male sterility and nuclear female sterility. We find both conditions for the evolution of dioecy as well as for the stable maintenance of 'trioecy' (the co-occurrence of males, females and hermaphrodites), with phenotype frequencies that correspond to those observed in at least one widespread case of trioecy. We also present results of simulations of our model in a metapopulation in which the maintenance of bisexual and unisexual phenotypes depends on an interplay between frequency-dependent selection on the sex allocation within populations and selection for reproductive assurance via self-fertilizations at the metapopulation level. We briefly discuss the implications or our model for understanding the role of cytoplasmic male sterility in transitions between combined and separate sexes.

Abstract ID: 1320
Poster board number:
P059

Selection for male stamina can help explain costly displays with cost-minimizing female choice

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In many species, male lifespan is shorter than that of females, often attributed to sexual selection favouring costly expression of traits preferred by females. Coevolutionary models of female preferences and male traits predict that males can be selected to have such life histories, however, this typically requires that females also pay some costs to express their preferences. Here we show that this problem diminishes when we link coevolutionary models of costly mate choice with the idea of stamina. In our model, the most successful males are those who can combine high attendance time on a lek — or, more generally, tenacious effort in their display time budgets — with high viability such that they are not too strongly compromised in terms of lifespan. We find that an opportunistic female strategy, that minimizes its costs by mating with highly visible (displaying) males, often beats other alternatives. It typically resists invasion attempts of genotypes that mate randomly in the population genetic sense, as well as invasion of stricter ways of being choosy (which are potentially costly if choice requires e.g. active rejection of all males who do not presently display or risky travel to lekking sites). Our model can produce a wide range of male time budgets (display vs. self-maintenance). This includes cases of alternative mating tactics where males in good condition spend much time displaying, while those in poor condition never display yet, importantly, gain some mating success due to females not engaging in rejection behaviours should these be very costly to express.

Abstract ID: 1336
Poster board number:
P060

Genetic basis and genomic consequences of loss of distyly in *Linum*

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Distyly is a floral polymorphism where individuals have one of two types of flowers with reproductive organs in reciprocal positions. Distyly promotes pollen exchange and prevents self-pollination, but it can break down due to changes in the pollination environment, and if the benefits of reproductive assurance compensate for the costs of inbreeding. Despite the long-lasting interest of evolutionary biologists in distyly and its breakdown, the genetic basis and genomic consequences of loss of distyly remain relatively unknown. Here, we investigate the genetic basis and the genome-wide consequences of loss of distyly in *Linum trigynum*. We first leveraged genome assemblies of *L. trigynum* and the closely related distylous *L. tenue* to identify candidate mutations for loss of distyly. We identified a frameshift mutation in an *S*-locus gene as a candidate causal mutation for the breakdown of distyly. Haplotype-based analyses suggest that this mutation arose only once and further spread leading to the formation of a well-differentiated lineage. Next, we leveraged population genomic data from ~400 individuals representing 16 populations to assess the genome-wide selective consequences of the loss of distyly in *L. trigynum*. This study contributes to our understanding of the genetic basis of mating system shifts in distylous lineages and highlights the broader implications of such evolutionary transitions.

Abstract ID: 1356
Poster board number:
P061

The genetic basis of asexuality in *Artemia parthenogenetica*

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Evolutionary transitions from sexual to asexual reproduction have been recorded in numerous invertebrates although the causes and mechanisms responsible for the loss of sexual reproduction remain largely unknown. One of the mechanisms proposed to give rise to new asexual lineages within sexual species is 'cryptic sex' between asexually produced rare males and sexual females of closely related species. The offspring produced from such crosses tend to acquire asexuality genes from their asexually produced fathers in a phenomenon known as 'contagious asexuality'. Identifying the genes responsible for asexuality and their transmission is crucial to understanding the evolutionary causes and consequences of transitions to asexual reproduction. In this study, we use *Artemia parthenogenetica*, an obligately parthenogenetic species of brine shrimp reported to occasionally produce rare males to identify and characterise genomic regions potentially involved in determining the asexuality phenotype. We use RAD-sequencing data obtained from asexual lines produced by crossing and backcrossing rare *A. parthenogenetica* males with females of a closely related sexual species. By genotyping individuals from different, independently generated asexual lineages, we try to identify loci consistently associated with asexuality, and therefore potentially linked to the asexuality-determining genomic regions. Identification of such regions can help determine how old and widespread contagious asexuality is in *Artemia* and its consequences for genome-evolution.

Abstract ID: 1444
Poster board number:
P062

Theoretical predictions on the effects of self-fertilisation on speciation

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Many hermaphroditic plants and animals self-fertilise. Selfing has well-known consequences on population genetics, which may influence speciation rates. On the one hand, because it increases genetic drift and reduces migration rate among populations, selfing may be expected to promote speciation. On the other hand, because it reduces the efficacy of selection, selfing may instead be expected to hamper ecological speciation. Here, we combine analytical and simulation analyses to better understand if and how selfing affect the build-up of reproductive isolation in allopatry and parapatry. We test how fast populations with various rates of selfing accumulate mutations leading to genetic incompatibilities. In allopatry, we found that when speciation requires the population to pass through a fitness valley caused by underdominant and compensatory mutations, selfing reduces the depth and/or breadth of the valley, and thus overall facilitates the fixation of incompatibilities. When speciation does not require the population to pass through a fitness valley, as in the Bateson-Dobzhanzky-Muller model, the lower effective population size and higher level of genetic structure in selfing populations facilitate the fixation of incompatibilities. Interestingly, local adaptation does not always speed up speciation in outcrossing relative to selfing populations. In parapatry, preliminary results allow us to investigate how reduced gene flow in selfing populations promote reproductive isolation. Our work helps to clarify how selfing lineages

may speciate and diversify over time, and emphasises the need to account for within-population polymorphism to better understand macroevolutionary dynamics.

Abstract ID: 1469
Poster board number:
P063

The complex pathway of sympatric speciation by floral mimicry

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Sympatric speciation in angiosperms may be favored by pollination niche shifts where reproductive characters of a mimic species evolve towards a plant model, generating assortative mating during the process. Here, we report the sympatric speciation of a mimic plant facilitated by ecological adaptation and genetic introgression. The narrow endemic cactus, *Eriosyce chilensis* (and its variety -*albidiflora*) recently diverged from a bird-pollinated progenitor (*E. litoralis*) to mimic the pollination niche of a bee-pollinated model (*E. mutabilis*). Pollen limitation in the progenitor species, coupled with adaptive benefits of the shift in the bee-pollination niche fostered reproductive isolation and rapid sympatric speciation in the mimic species. Subtle genomic admixture between the model *E. mutabilis* and the mimic *E. chilensis* suggests that introgression may facilitate phenotypic convergence towards a new adaptive optimum consisting of ubiquitous bee pollination. Our findings suggest that protecting regions that harbor endemic species is crucial for preserving the unique processes that promote the generation of new diversity.

Abstract ID: 1723
Poster board number:
P064

Reducing genetic load via sexual selection:the role of environmental variance in male mating success

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The accumulation and fixation of mildly deleterious mutations (genetic load) is a major genetic factor that determines the persistence of small populations. Sexual selection is predicted to reduce the genetic load, and thereby increase population persistence, when mating success negatively covaries with genome-wide mutation load. However, increasing strength of phenotypic sexual selection can simultaneously reduce effective population size N_e, which may counteract the removal of deleterious mutations by reducing the efficacy of selection. Further, while theory has so far assumed that variance in male reproductive success stems entirely from genetic effects, empirical work has demonstrated a large environmental component. When phenotypic sexual selection

similarly amplifies genetic and environmental effects, both will contribute to the variance in reproductive success and thereby reduce N_e. The net consequences for the accumulation of genetic load and resulting population persistence are then unclear. We use a genetically explicit individual-based model to examine how environmental variance underlying male mating success shapes the ability of sexual selection to slow down the accumulation and fixation of genetic load and population extinction. With larger environmental variance, sexual selection increased the rate of fixation and the mean selection coefficient of fixed mutations, resulting in increased genome-wide mutation load and declining population persistence times. Our results highlight that considering environmental variance underlying phenotypic sexual selection in males tilts the balance between positive and negative effects of sexual selection towards the negatives, thereby questioning the effective contribution of sexual selection in reducing genome-wide mutation load in natural populations.

Abstract ID: 1787
Poster board number:
P065

Demographic history and selection in association with mating system variation in Arabis alpina

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Flowering plants show remarkable reproductive diversity. From obligate outcrossers, to mixed-mating systems and finally to predominantly self-fertilisers, different strategies have evolved to guarantee reproduction without compromising their capacity to adapt to new environments. Commonly, a transition to self-compatibility is accompanied by changes in morphological and genomic traits which directly affect the species' survival. The alpine rock-cress (*Arabis alpina*) of the family Brassicaceae demonstrates a full range of different outcrossing rates. Here, we are using a whole genome resequencing dataset of 128 individuals representing 13 populations across Europe, to unfold the demographic history of the species and describe the genomic signatures that evolved alongside it. Divergence population genetic analyses point to a range expansion that coincided with the retreat of the ice sheet at the end of the Last Glacial Maximum, in agreement with the expectation that self-compatible individuals have higher chances to colonise uncovered areas than their outcrossing relatives. Our findings suggest that this process resulted in a continental-wide, continuous gradient of outcrossing rates, gradually decreasing from the outcrossing populations of southern Europe to predominantly selfing in Scandinavia. We describe a possible source for the present-day Scandinavian population and investigate the signatures for positive selection along the genome to discover candidate regions that facilitated the transition to selfing.

Abstract ID: 1817
Poster board number:
P066

Multiple mating rescues offspring sex ratio but not number in a haplodiploid exposed to heat stress

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Reproduction is generally more sensitive to high temperatures than survival and arguably a better predictor than the latter for the response of populations to climate change. Still, how temperature simultaneously impacts male and female reproductive success, mating system and operational sex ratio remains an open question. Here, we addressed how a sublethal high temperature affects the reproductive system of the spider mite Tetranychus urticae. Males and females maintained at 25°C or 36°C during development were paired and the fertility of both sexes, their mating and remating eagerness, and the paternity of the offspring of females with different mating histories were measured. Female and male fertility decreased at 36°C compared to 25°C, resulting in lower offspring production and a male-biased sex ratio, respectively. However, when females remated, the pattern of first-male sperm precedence typical of this species was disrupted, with more than one male contributing to the offspring. This was accompanied by reduced mating eagerness in pairs with partially sterile males and increased remating eagerness in pairs in which at least one sex was partially sterile in the first mating. The observed temperature-induced changes in pre- and post-copulatory traits allowed restoring the offspring sex ratio but did not recover the offspring number. Our results show that temperature induces changes in the spider mite mating behaviour and mating system, potentially affecting sexual selection and sexual conflict. However, such changes may not be sufficient to buffer the impact of extreme temperatures on their populations.

Abstract ID: 1960
Poster board number:
P067

Network Theory to elucidate the interplay between sexual selection and metapopulation structure

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In recent times there has been a surge of interest in the application of social network analyses to the study of animal social behaviour. Network approaches can also be used to understand the extent and the drivers of interactions between the two sexes; the study of sexual networks is emerging as a key tool to understand the evolution of reproductive interactions. In this communication we present preliminary but relevant data on the role of sexual selection and sexual conflict evolutionary history, and their interplay with population subdivision, on the architecture of socio-sexual networks. Along several years we implemented an experimental evolution approach using an insect model system characterized by strong sexual selection and sexual conflict, the seed beetle Callosobruchus maculatus. In our selection experiment we manipulated both the strength

of sexual selection and the presence of metapopulation structure in a total of 16 selection lines for over 90 generations. Then, using a system of data acquisition based on computerized tracking of individuals we obtained data on the frequency and duration of socio-sexual contacts, which enabled us to build networks. We compared network architectures, in terms of global and individual levels measures widely used in network analysis (betweenness, clustering, strength and density), across selection regimes. Using a combination of mixed modelling and approaches using randomizations we present results showing that the evolution of sexual networks may be modulated by sexual selection intensity and the spatial structure of populations.

Abstract ID: 2164
Poster board number:
P068

Unilateral adaptation - how trichomes change pollinators' behavior in sexually deceptive flowers

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The close adaptation between the sexually deceptive orchid *Ophrys* and its pollinators offers great potential to study evolutionary processes. *Ophrys* flowers resemble female bees and attract males for pollination in a species-specific manner. Therefore, to understand speciation processes within *Ophrys*, it is important to study pollination-relevant traits of the flower lip (labellum), with which the bees interact during 'pseudocopulations'. So far, knowledge is limited on the intraspecific significance of the labellum's surface structure. In this study, we address the importance of trichome patterns on the labellum, aiming to link genetics, phenotype, and reproductive fitness. Therefore, we studied the expression of genes likely important for trichome development, comparing trichome-rich and trichome-less tissues of the labellum. Additionally, to get detailed insights into trichome-dependent behavior of pollinators during 'pseudocopulations', field experiments were performed in which untreated flowers (control) and flowers after removal of trichomes in different regions (basal, median, and apical) were offered to male pollinators. This revealed that behavioral changes on the basal and apical treated flowers were present. The removal of basal trichomes resulted in a significant decrease of 'pollinia removal' frequency and therefore had a direct impact on plant reproductive fitness. Manipulation of trichome density in different parts of the lip allowed us to shed light on the ecological function of trichomes, and to assess the importance of the spatial patterning. In conclusion, this study contributes to understanding the role of trichomes in pollinator interaction and the genetic basis of trichome development by identifying candidate genes active in this process.

Abstract ID: 2189
Poster board number:
P069

The development of a decoy: spatial and temporal map of *Ophrys sphegodes* labellum

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Sexual deception in pollination is a strategy employed by plants to secure pollination, where flowers resemble female insects to attract the males. This pollination strategy acts as a powerful reproductive barrier that is responsible for species diversification, so speciation. The Mediterranean orchids of the genus *Ophrys* are a suitable model to study this mechanism because their relationship with their pollinators is highly species-specific, so a change in olfactory or tactile cues causes a pollinator shift. Mainly, these cues are emitted by a specialized petal called labellum, that is of key importance for pollinator attraction. Currently, we lack a deep understanding of its development and cell type distribution. In this study, we focus on the species *Ophrys sphegodes* to create a temporal and spatial map of the labellum, using a combination of microscopy and Micro Computer Tomography. We that the adaxial epidermis, the part of the labellum that mostly interacts with the insect, is composed by three main cell types: long trichomes, conical cells and speculum's cells, each type clearly compartmentalised. We described eight developmental stages of the labellum based on . This spatial and temporal map will serve as a first step for future studies on floral tissues development in *Ophrys*, from a morphological, genetic and ecological perspective. Furthermore, this study will contribute to better understand the mechanism of sexual deception and its implication in ecological speciation.

Abstract ID: 2256
Poster board number:
P070

Male mate choice evolves as a by-product of adaptation to larval crowding in Drosophila melanogaster

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Typically, as a result of substantial costs of reproduction, females are expected to exercise strong mate choice. However, there is emerging evidence for male mate choice in organisms such as *Drosophila melanogaster* with appreciable courtship and ejaculate related costs for males. Studies have shown that *D. melanogaster* males tend to bias their mate choice towards larger, younger, and well fed females, which results in direct benefits to male fitness. We investigated male mate choice in populations of *D. melanogaster* adapted to larval crowding. Previous work has shown that flies from the selected populations have evolved smaller body size and increased courtship frequencies compared to control populations. We offered males from selected and controlled populations a two-way choice between large or small females from their own populations. We found that when grown at low larval densities both selected and control males exhibited a bias towards courting and mating with large females, consistent with earlier work. However, when grown at high densities, selected males showed a significantly reduced preference for larger females, while control males continued to strongly prefer larger females. Our results clearly show that male mate choice can evolve

as a by-product of adaptation to larval crowding. This could be a consequence of selected males evolving efficient courtship towards small sized females they encounter in their population every generation.

Abstract ID: 2293
Poster board number:
P071

Genetic underpinnings of species-specific sexual signaling mechanisms in parasitoid wasps

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The evolution and maintanence of intraspecific sexual signaling is essential for successful reproduction. In insects, sexual signals are often based on semiochemicals, which commonly exibit high species specificity. However, our understanding of how exactly sexual signals are chemically encoded, as well as the genetic basis that generate and maintain species-specific chemical patterns is comparatively limited. In the parasitoid wasp genus *Nasonia*, female cuticular hydrocarbons (CHCs) can function as species-specific sexual cues, eliciting preference and attraction in conspecific males. Particularly, males of *N. longicornis* exibit a strong preference towards conspecific female CHC profiles, over females of the sister species *N.giraulti*. We exploited the haplo-diploid sex determination of *Nasonia* to generate males with recombinant genotypes between *N. giraulti* and *N. longicornis*, which further yielded recombinant clonal female sibships by backcrossing the males to both parental strains. In a comprehensive quantitative trait loci (QTL) analysis, we correlate genotypes of the haploid recombinant fathers with variant CHC profiles and species-specific sexual attractiveness in the resulting diploid clonal female sibships. With this approach, we shed light on the so far little understood genetic underpinnings governing species-specific sexual signaling cues encoded in complex chemical profiles.

Abstract ID: 2337
Poster board number:
P072

The genetic basis of hybrid incompatibilities in the Arctic plant *Cochlearia groenlandica*

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Based on morphological assessments, species diversity typically decreases towards the poles. However, we have demonstrated that the Arctic flora contains considerable hidden species diversity in terms of morphologically similar but reproductively isolated

populations within taxonomically well-defined species. Selfing is the predominant mating system in many Arctic plants, and we hypothesize that this may accelerate accumulation of hybrid incompatibilities. To gain insight into the drivers of incipient speciation in Arctic plants, we performed *de novo* genome assembly and genetic mapping / QTL analysis of the selfing Arctic mustard *Cochlearia groenlandica* (2n=14). One plant from Alaska was crossed reciprocally with one from Svalbard, resulting in semisterile F_1 hybrids that were self-pollinated to produce two large F_2 populations for genetic linkage and QTL mapping. The chromosome-scale genome assembly of *C. groenlandica* is 233 Mb and highly contiguous with ~85% assembled into seven chromosomes (consistent with the known base chromosome number). The genome was made for the Alaskan parent and is currently used to resolve the genetic basis of reproductive isolation QTLs identified in the crossing experiment. Three phenotype characters were scored in the F_2 populations: pollen fertility, inflorescence length and fruit weight. Because 25% of the plants in one F_2 population were dwarfed and sterile whereas the reciprocal F_2 population did not show any such extreme phenotypes, we hypothesize that cyto-nuclear incompatibilities are involved.

Abstract ID: 2371
Poster board number:
P073

Sexual dimorphism in lacrimal and salivary glands of the wild house mice

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Mammals, who communicate, advertise and compete by odor cues, project the competition-related sexual dimorphism into olfactory communication and organs facilitating it. Scent gland size dimorphism has been reported in several mammalian species including rodents. In this study, we focused on sexual size dimorphism (SSD) of house mouse submandibular and lacrimal glands, potentially related to sex-limited expression of proteins, previously identified as important mouse communication signals. We studied both wild animals and animals from wild derived strains (WDS) of two house mouse subspecies, *Mus musculus musculus* and *M.m. domesticus*. Our results confirmed SSD in both glands, with larger glands found in males of both subspecies. Significant differences in gland sizes were more pronounced in WDS but correspond to differences found in wild animals. Corroborating patterns were observed by histological analyses of the relative contribution of granulated convoluted tubular tissues in salivary glands. Interestingly, we found subspecies specific differences in the pattern of gland sizes with larger submandibular glands found in *M.m.musculus* and, conversely, larger lacrimal glands in *M. m. domesticus.* We also found differences in the overall protein content in tears as well as in preference for these fluids used as odor cues in two-way

choice tests. All these results indicate potentially different importance of salivary and lacrimal signals in the communication of the two house mouse subspecies.

Abstract ID: 2389
Poster board number:
P074

The evolution of sex roles: new insights from individual-based simulations

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The behaviour of males and females in the context of mating and parenting differ considerably between and within species. By means of individual-based evolutionary simulations, we strive to explain this diversity. Our findings are in striking contrast to the conclusions of analytical models. When the two sexes mating at random and do not differ in any other aspects, our simulations do not predict the evolution of egalitarian care or a line of equilibria, but either strongly female-biased or strongly male-biased care. In longer-term evolution, a population can rapidly switch from one type of equilibrium to the other. This explains the often-reported evolutionary lability of parental sex roles even under constant environmental conditions. If parental investment evolves jointly with sexual selection strategies, again two alternative parental care strategies are possible. In the case of male-biased care, neither female preferences nor male ornaments evolve, while preferences and ornaments do evolve in the case of female-biased care. The simulations suggest that the parental care pattern drives sexual selection, and not *vice versa*. All these results also hold if the parents have a weak synergistic effect on offspring survival; egalitarian biparental care only evolves in case of strong synergy. Throughout, we investigate systematically why the simulation results differ from analytical predictions. It turns out that polymorphisms in care patterns, driven by sexual conflict, play a crucial role. Although these polymorphisms are often transient, they strongly determine the outcome of parental sex role evolution.

Abstract ID: 2415
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P075

Evidence of environment - dependent inbreeding depression in a mixed mating plant

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Inbreeding depression is a major driver of mating system evolution; it is also context dependent. The ecological conditions that most significantly influence inbreeding depression remain poorly understood, however the local competitive environment likely plays a major role. When survival, growth, and/or fecundity are sensitive to intraspecific competition, inbreeding depression may depend on the density and frequency of selfed versus outcrossed competitors—epitomizing soft selection. However, when interspecific competition dominates, the impact of intraspecific conditions on inbreeding depression is

hypothesized to be less important, such that selection against inbred individuals hardens, i.e., fitness depends only on an individual's genetic quality.
Greenhouse experiments were used to test whether inbreeding depression in the mixed-mating, monocarpic plant (*Sabatia angularis;* Gentianaceae) is subject to density- and/or frequency-dependent selection, and how interspecific competition influences these patterns. Selfed and outcrossed individuals were subject to different competitive regimes and followed from germination to flowering.
We found intraspecific competition exerted a negative impact on juvenile size and the impact of interspecific competition was greater than that of intraspecific. Although outcrossed juveniles are significantly larger than selfed individuals at low density, juvenile size equilibrates at high density. Interestingly, frequency-dependent inbreeding depression in juveniles was observed only under interspecific competition. Adult plants exhibited significant inbreeding depression, including frequency-dependent inbreeding depression, across a range of traits.
These results suggest that inbreeding depression is subject to soft selection– even under conditions of interspecific competition—which may contribute to the maintenance of mixed mating in this species.

Abstract ID: 2417
Poster board number:
P076

The effect of recombination on the evolutionary dynamics of populations evolving on neutral networks

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Random beneficial mutations are essential for populations to evolve further. Nevertheless, they typically become increasingly rare once a population has adapted to a static environment. Such static environments can be well represented by fitness landscapes, on which evolution takes place as a hill-climbing process. Since fitness landscapes are high-dimensional objects, adapted populations are usually not trapped on a single local maximum but can move along extended fitness ridges. However, a significant proportion of mutations may then be detrimental, causing individuals to fall off these fitness ridges to remain in this metaphor. Therefore, the population may try to seek regions on the fitness landscape that are particularly flat. From this, the population's mutational robustness would benefit. To study the mutational robustness of evolving populations, we approximate fitness landscapes by neutral networks of highly fit genotypes. Deterministic and stochastic population models show that populations favor mutationally robust regions of neutral networks [1]. We demonstrate that the introduction of recombination strongly enhances this effect based on analytical results for a two-locus landscape and numerical results for different neutral landscape models with multiple loci [2]. Moreover, we study how quickly populations can explore neutral networks and show that intermediate recombination rates lead to an optimal discovery rate of novel fit genotypes on the neutral network [3].
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Abstract ID: 2434
Poster board number:

P077

The role of antennation in mating behavior in parastoid wasp *Aphidius ervi*

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Chemical communication is a vital mechanism for many insect species. *Aphidius ervi* Haliday (Hymenoptera: Braconidae) is a parasitoid wasp specialized on aphids as hosts. In our study, we aim to understand the role of antennation in the mating behaviour of *A. ervi*. Male wasps initiate courtship by mounting, which is followed by positioning their antennae in parallel and smearing them together and copulation if the male is accepted by the female. Specific antennomers were previously shown to have integumentary glands, and a role in secreting chemical compounds from the micropores on these antennomers has been suggested. To gain a better understanding of the role of the antennae, antennal ablation experiments were conducted. Since antennal contact seems indispensable for copulation initiation, the opposite antennae were ablated, forcing the courting couples to smear the remaining oppositely positioned antennae. The results showed that the individuals with oppositely amputated antennae succeeded to copulate as well as the control, in contrast to previously published findings. As an additional study, we observed that if the male is ablated both antennae and the female is intact, the courtship does not initiate; yet when the female is ablated both antennae and the male is intact, mounting and antennation occurs in most of the encounters.

Symposium: S05. A combinatorial view on rapid speciation - the role of ancient genetic variants and hybridisation (id: 38)

Abstract ID: 1310
Poster board number:
P078

The impact of hybridization on gene expression in ZW brine shrimp

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How hybridization between closely related species disrupts gene expression levels across the genome is not fully understood, but is thought to contribute to genetic incompatibilities between them. While expression of F_1 hybrids and their parents has been characterized in various clades, the effect of carrying only some introgressed blocks has not been investigated in detail. This represents an important gap as the long-term fate of these introgressed segments depends on how disruptive they are. In species with XY sex-chromosomes, mechanisms of dosage compensation (DC) often equalize gene expression levels between X-linked genes in the hemizygous sex (eg. XY males) and autosomal genes. It has been postulated that disruption of DC in hybrids may further lower their fitness. While DC does not seem disrupted by hybridization in a few XY taxa in which this question has been answered, we currently do not if this conclusion holds in ZW systems. Here we explore these gaps using the ZW brine shrimp (*Artemia*), in which dosage compensation of Z-linked genes in females was recently documented. *Artemia*

sinica males and *Artemia sp. Kazakhstan* females were crossed to produce F_1 hybrid females, which were then backcrossed with *A. sinica* males. We obtained transcriptomic data from parents and F_2 hybrid offspring, and measured divergence between parents and hybrids at both introgressed and non-introgressed segments, to quantify the global disruption in expression caused by introgression. We further quantified DC in F_2 females with different introgressed blocks, to investigate possible hybrid disruptions of DC and the genomic regions involved.

Abstract ID: 1372
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P079

Bird-of-paradise hybrids, infertile vagaries or drivers of macro-evolutionary change

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In systems with sexual selection the persistent directional female choice has been used to explain rapid evolution and continual change in sexual ornaments. However, as rapid phenotypic radiation requires high levels of heritable genetic variation, occasional introgressive hybridization could potentially be an important mechanism to fuel phenotypic diversification by reshuffling of genetic variants. The Birds-of-Paradise represent one of the most prominent examples of extreme phenotypic radiation driven by strong sexual selection. However, despite complex courtship rituals and extreme male ornamentations, hybridisation is surprisingly well documented within this family, even across genera. As these hybrid combinations are morphologically unique most of them were originally described as distinct species. Today many of these specimens are kept in Natural History collections and have been classified as hybrids based on morphology. In this study we have re-sequenced the genomes of 35 birds-of-paradise hybrids kept in Natural History collections, including almost all known intergeneric hybrid combinations. With access to a chromosome level reference genome (*Lycocorax pyrrhopterus*) and genomes from all species of Birds-of Paradise we identify the parental species of these hybrids as well as investigate potential backcrosses. Our study demonstrates the potential of hybridization across divergent lineages of Bird-of-Paradise and potentially provide direct evidence that intergeneric hybridization is an ongoing process that has the potential to boost genetic diversity. The project integrates state-of-the-art phylogenomics with *museomics* and as such highlights the importance of natural history collections in genomic research.

Abstract ID: 1402
Poster board number:
P080

A wolf in spiders' clothing: genomic-wide screening uncovers admixture between Madeiran wolf spiders

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Seven endemic species of the wolf spider genus *Hogna* Simon, 1885 have been documented in the volcanic archipelago of Madeira. Despite their colourful bodies, large size and widespread distribution across the islands, they have received little attention. A recent study, which integrated molecular markers and morphological information, supported the current delimitation of most nominal species. However, the species pair *Hogna insularum* (Kulczyński, 1899), present in all islands, and the large *H. maderiana* (Walckenaer, 1837), circumscribed to Porto Santo, constituted an exception. Although they are morphologically diagnosable and differ in their preferred habitats, mitochondrial data failed to distinguish them. Of the two main lineages recovered, one was exclusively formed by *H. insularum* haplotypes from Madeira Island, while the second one was a mixture between the remaining *H. insularum* haplotypes and those of *H. maderiana*. To test alternative hypotheses that may explain the observed inconsistencies, we generated double-digest restriction site-associated DNA sequencing (ddRADseq) markers from specimens sampled across most known populations of both species. Our genome-wide analysis revealed the existence of two different groups, but unlike the mitochondrial data, one consisted of *H. insularum* specimens from Madeira and Desertas Islands, while the second one was exclusively of *H. maderiana* specimens from Porto Santo. However, several *H. insularum* specimens from Porto Santo showed similar levels of introgression when compared to the two groups, suggesting hybridization events between the two species on this island. Similar patterns of introgression were also reported in wolf spiders from the Galapagos.

Abstract ID: 1462
Poster board number:
P082

Petunia species in the making: consequences of hybridization between two *P. axillaris* subspecies

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Speciation is a continuous process, and species may take several generations to achieve reproductive isolation. Thus, the term subspecies was conceived to describe a group of geographical, morphological, and genetically divergent populations that still can cross, i. e., hybridize. The two subspecies of *Petunia axillaris* (*axillaris* and *parodii*) are evolutionary lineages that occupy distinct ecoregions in southern South America, but

individuals with an intermediary morphology are found alongside the Negro River in Uruguay. Here we aim to better understand the evolutionary relationships and population dynamics between the subspecies. Therefore, we used genotyping-by-sequencing technology to characterize 222 individuals from both canonical populations and two contact zones alongside the river. Our final dataset contains 5,424 high-quality SNPs. FastStructure and DAPC analyses indicated that each subspecies has a unique genetic component, following morphological and geographical classification. These analyses also revealed several individuals with signs of mixed ancestry, equally observed in canonical and contact zone populations. The ABBA-BABA analysis corroborates that most populations from contact zones have mixed ancestry. NewHybrids suggested that the degrees of hybridization vary along with geographical distribution: recent hybrids occur closer to Negro River, whereas backcross hybrids are more widespread. Fastsimcoal demographic analysis suggests recent and symmetrical gene flow between subspecies. Our results collectively show that the subspecies are in the process of speciation, and populations alongside the Negro River act as the source of introgression. The presence of different classes of hybrids indicates that hybridization was recurrent during the evolutionary process of these taxa.

Abstract ID: 1485
Poster board number:
P083

Hybridization and asexual reproduction in a haploid diploid red alga *Gracilaria gracilis*

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Asexuality (i.e. apomixis and apomeiosis) is strongly associated with polyploidy due to the interbreeding of genetically heterogeneous individuals. This study documents the mixed mode of reproduction of different hybrids between apomictic and sexual reproducing red algae: the *Gracilaria gracilis/Gracilaria dura* species complex.
Rhodophyta life cycle is fundamentally different from those of animals and plants. Multicellular dioecious haploid gametophytes (gamete-producing plants) produce gametes by mitosis. Fertilization of the female gamete (carpogonium) by a spermatia produces a zygote which after a multiplication phase (carposporophyte) develops into a multicellular diploid sporophyte. Sporophytes produce haploid spores by meiosis which germinate to produce new gametophytes. This life cycle provides a unique opportunity to estimate the frequency of hybrid genotypes in diploid sporophytes and meiotic recombinant genotypes in haploid gametophytes. Consequently, the effects of reproductive barriers that prevent fertilization can be distinguished from those that prevent meiosis potentially leading to apomixis.
In this study, we used population genetics approaches to estimate the importance of hybridization, polyploidy and asexual/sexual reproduction in the field. We combined flow cytometry with mitochondrial, chloroplast and nuclear DNA data (microsatellite markers) to better understand the processes initiating apomixis in this species complex. Our results show the importance of asexual reproduction in hybrids that are predominantly triploid and exhibit a mixed reproductive phase (gametes and spore-producing plants).

Moreover, we observed that hybrids are confined to lower bathymetric levels, less subject to abiotic fluctuations compared to parent individuals. Different scenarios describing origin of the different groups in this species complex are proposed.

Abstract ID: 1552
Poster board number:
P084

Eco-evolutionary consequences of costly sexual interactions in hybridizing spider mites

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In some species, costly reproductive interactions owing to incomplete species recognition and hybridization (i.e., reproductive interference) may accelerate speciation processes via reproductive character displacement. This, in turn, is expected to decrease the occurrence and/or strength of negative interactions, thereby facilitating persistence in sympatry. Reproductive interference is thus of great relevance for both speciation research and community ecology, as it may be an important driver of species divergence and distributions. Here, we tested whether evolution of spider mites in sympatry selected for mitigation of reproductive interference, and whether this could occur via reproductive character displacement. We used two closely related species, *Tetranychus urticae* and *T. cinnabarinus*, that readily engage in interspecific crosses despite early (partial fertilization failure) and late (high incidence of hybrid sterility) post-copulatory reproductive isolation. We allowed these species to evolve artificially in allopatry or sympatry for 30 generations before measuring the strength of reproductive interference occurring between mites evolved in either selection regime. We found that despite strong asymmetries in both pre- and post-zygotic isolation, both species suffer strong costs of reproductive interference. Yet, neither of the two species evolved reproductive barriers allowing to lower these costs after evolution in sympatry as compared to allopatry. This finding has important implications for spider mite population dynamics and distribution in the wild, and raises questions about the maintenance of partial isolation in this system, as well as whether other strategies, such as niche partitioning, can serve as alternatives to reproductive character displacement for avoiding reproductive interference.

Abstract ID: 1627
Poster board number:
P085

Whole genome sequencing unravels the genomic landscape of hybrid speciation in alpine butterflies

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Hybridization among closely related species is an important evolutionary force that is increasingly found associated with species diversification and adaptation. Hybrid speciation, in particular, has been identified in many plant and animal species in the past two decades. While this demographic process is often explored through coalescent modeling, the way parental genes segregate in incipient lineages and promote their divergence remain rarely investigated. To tackle this issue, we focus on a recently discovered hybrid species complex of *Coenonympha* butterflies, in which two young species *C. macromma* and *C. darwiniana* originated through hybridization between the two parental species *C. arcania* and *C. gardetta*. We generated whole genome sequence data from sixty individuals to explore the pattern of genetic differentiation, diversity, and selection along their genomes. We characterized the mosaic of parental contributions to the two hybrid genomes and identified regions of high genetic differentiation within the complex, putatively involved in divergent selection and/or reproductive isolation among species. Interestingly, the two hybrid lineages show low overall differentiation with many "islands" of high genomic divergence with their parental species *C. arcania* and high overall differentiation with fewer genomic regions of high divergence with their second parent *C. gardetta*. They also exhibit a slightly different mix of parental genes at various regions putatively under selection, which relates to their combination of parental ecological and morphological traits. With these results, our study provides new insights on the genomics processes associated with hybrid speciation and sheds light on the diversification of these alpine butterfly species.

Abstract ID: 1776
Poster board number:
P086

The genomic basis of hybrid male sterility in *Ficedula* flycatchers

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Identifying genes involved in genetic incompatibilities causing hybrid sterility or inviability is a long-standing challenge in speciation research, especially in studies based on natural hybrid zones. Here we present the first high-probability candidate genes for hybrid male sterility in birds by using a combination of whole genome sequence data, histology sections of testis and single cell transcriptomics of testis samples from male pied-, collared-, and hybrid flycatchers. We reveal failure of meiosis in hybrid males and propose candidate genes involved in genetic incompatibilities causing this failure. Based on identification of genes with non-synonymous fixed differences between the two species and revealing miss-expression patterns of these genes across the various stages of hybrid male spermatogenesis we conclude aberrant chromosome segregation and/or faulty chromatin packing. A lower proportion of spermatids produced by hybrid males implies that a proportion of the aberrant spermatids undergo apoptosis. Finally, we report an overrepresentation of Z-linkage of the revealed candidate incompatibility genes. Our results challenge the assumption that speciation processes are driven by fast evolving genes. We show that changes in genes with highly conserved and central functions may quickly ensure reproductive isolation through post-zygotic isolation. We

hypothesis that given the fast establishment of post-zygotic isolation it is most likely that it is a result of selection upon standing genetic variation resulting on fast lineage sorting of old genetic variation in the candidate genes.

Abstract ID: 1826
Poster board number:
P087

Introgression and incomplete lineage sorting shape the evolution of Eucalypts' rapid radiation

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Species resulting from rapidly radiated clades are especially prone to exhibit variable evolutionary histories from different genomic regions. Eucalyptus subgenus Symphyomyrtus contains about 850 species with lineages distributed across all Australia's biomes. Much of its genetic and morphological diversity arises from the adaptive radiation during periods of aridification and droughts starting about 20 Mya. Bifurcating species tree achieve little resolution in Symphyomyrtus due to introgression, incomplete lineage sorting (ILS) and ongoing speciation. However, discordant phylogenetic signal may reveal processes shaping the genetic architecture of drought adaptations in Eucalypts and the process of speciation as lineages exploited newly formed ecological niches. Here we explore the diverse phylogenetic signal causing discordance in Eucalyptus section Adnataria, a taxa-rich clade, notorious for containing extensively hybridizing taxa. We aimed to assess to which extent introgression and ILS shape the evolutionary history and fuel the diversification process. To address this, we conducted whole genome sequencing for the total 100 taxa of section Adnataria and explore the evolutionary histories of ~900 single-copy genes. We did phylogenetic inferences for the clade and calculated gene and site concordance factors to explore topological variation. Our phylogenomic results show that while internal nodes in the species tree are supported by high bootstrap values, concordance factors indicate a very low and contrasting supports by estimated gene trees and loci revealing extensive reticulation. We conclude that while species are recognizable from morphological and geographical standpoints, their evolutionary background is extremely diverse at different genetic scales giving potential for generating adaptive variation.

Abstract ID: 1855
Poster board number:
P088

Did ancient hybridization fuel the evolution of pelvic brooding ricefishes?

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About 20 million years ago the founder of two endemic radiations of Sulawesi ricefishes (Adrianichthyidae, Beloniformes) colonized Sula Spur from Java or the Asian mainland. One radiation occurred within the Lake Poso *Adrianichthys* and more recently Sulawesi *Oryzias* formed different species in Lakes and Rivers. In *A. oophorus* and the distantly related sistertaxa *O. eversi* and *O. sarasinorum*, a reproductive strategy called "pelvic brooding" has evolved with females carrying an egg cluster beneath the belly. The eggs are connected to the females´ gonoduct via filaments and remain there until the fry hatches. Although they are not each other´s closest relatives, all described pelvic brooding species share a set of morphological traits like elongated pelvic fins and shorter ribs that form a ventral concavity. We investigated by means of a multi-species coalescent (MSC) model and D-statistics whether the parallel appearance of pelvic-brooding in two distantly related lineages is based on introgression of genetic material from *Adrianichthys* species into the Sulawesi *Oryzias* radiation. We found no signatures of gene flow between *A. oophorus* and *Oryzias* species on Sulawesi. However, we found evidence for ancient gene flow between the common ancestor of *O. eversi* and *O. sarasinorum* and the ancestor of the Lake Poso *Oryzias* species. We hypothesize that pelvic brooding is likely a convergently evolved trait in the two ricefish lineages and might have been fueled by the introduction of genetic variation by ancient gene flow.

Abstract ID: 1880
Poster board number:
P089

Ancient hybridization in *Curcuma* (Zingiberaceae) – fuel or brake of lineage diversification?

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It has repeatedly been shown that ancient hybridization can either act as a trigger of evolutionary radiation or, conversely, prevent further diversification of hybrids. These phenomena appear to be widespread in both the animal and plant kingdoms, affecting their evolution enormously, much about them remains to be studied. Here we present an account of several events of ancient hybridization in the economically important plant genus *Curcuma* (Zingiberaceae). We analysed 1094 targeted low-copy genes and plastomes obtained by next-generation sequencing of 37 *Curcuma* species, representing the known genetic diversity and geographical distribution of the genus. Using phylogenetic-network analysis, genome-wide site pattern probabilities and SNAPP, we rejected the hypothesis that the subgenus *Hitcheniopsis* of *Curcuma* arose via massive introgression of the Indochinese lineage Pierreana into a monotypic lineage represented

by the enigmatic species *C. vamana*. On the contrary, we discovered that *C. vamana* arose as an ancient hybrid between two parental lineages: Indian *Curcuma* and Indochinese *Hitcheniopsis*. The timing of the hybridization event was placed in the Miocene, ca 10 Ma, which is ca 1 Ma after the diversification of the parental lineages. The hypothesis that ancient hybridization between distantly related parents prevented further diversification of the descendant was supported over the alternative hypothesis suggesting rapid radiation of the lineage that originated due to ancient introgression. The results raise the question of whether time since diversification of the parental lineages affects further diversification potential, also highlighting the limitations of currently available methods used for hybrid detection.

Abstract ID: 1900
Poster board number:
P090

Evidence for ancient and ongoing hybridization in Iberian freshwater fish from whole-genome data

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Hybridization has the potential to put together genetic variants that evolved in independent lineages into new combinations. Potential for hybridization between allopatric lineages or species arises when barriers to the dispersal of individuals are removed. These processes are particularly relevant in obligatory freshwater fish, where geological changes in the conformation of rivers and lakes can isolate populations over long periods of time or put into contact previously isolated lineages. Here, we investigated the prevalence and consequences of past and ongoing hybridization between two species of Iberian endemic freshwater fish (*S. carolitertii* and *S. pyrenaicus*) across their distributions. Throughout their evolutionary history, the river basins inhabited by these species suffered quite dramatic changes, fuelling multiple periods of isolation and secondary contact. Additionally, they are currently distributed along a latitudinal environmental cline, with increasing temperatures and propensity for drought from north to south. Thus, they provide an excellent system to investigate the role of hybridization and ancient variants in speciation and adaptation. Using whole-genome sequencing we identified three divergent lineages within *S. pyrenaicus* (*S. pyrenaicus* Tagus, *S. pyrenaicus* Guadiana and *S. pyrenaicus* Sado). We identify both ancient and recent hybridization within the group and investigate the distribution of parental contributions in the genome of hybrid populations. We uncover ancient admixture between *S. carolitertii* and *S. pyrenaicus* Guadiana at the origin of *S. pyrenaicus* Tagus. Moreover, we detect recent hybridization between *S. pyrenaicus* Tagus and *S. pyrenaicus* Sado, as well as with *S. carolitertii* from Zêzere river basin.

Abstract ID: 2062
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P091

Re-emergence of a species after the 2011 Tohoku tsunami-induced hybridization

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Hybridization often occurs before speciation is completed. What would be the consequence of hybridization? Hybridization may lead to the emergence of a panmictic population, hybrid speciation, or extinction of one species. It is also possible that the mixed genome is reorganized such that the hybrid population reverts to one parental species with the other parental species genome being purged. Despite the presence of a few examples of such purging after hybridization, it remains unanswered how rapidly purging can occur in nature and what factors contribute to the purging. Here, we investigated the genomic change over nine years of a hybrid population between two stickleback species, freshwater *Gasterosteus aculeatus* and anadromous *G. nipponicus*, whose hybridization was induced by the devastating 2011 Tohoku earthquake and tsunamis. Genomic analysis of 2606 individuals showed that the second generation of hybrids were observed in 2012, suggesting that interspecific hybridization occurred in 2011, the year of the tsunami. Over the nine years from 2012 to 2020, the *G. nipponicus* genome was purged and the hybrid population reverted to *G. aculeatus*. Surprisingly, the majority of purging occurred in the first few generations. Faster purging occurred in an autosome with a newly identified quantitative trait locus for seaward migration. Both ancestral and neo-sex chromosomes, which contribute to seaward migration, sexual isolation, and hybrid incompatibility, also showed higher purging rates of *G. nipponicus* alleles compared to autosomes. These results demonstrate that purging of heterospecific genome can occur within a few generations and barrier loci contribute to this process.

Abstract ID: 2104
Poster board number:
P092

On the hunt for introgression: charting external gene flow into the Lake Malawi cichlid radiation

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Adaptive radiations are suggested to account for a considerable proportion of extant biodiversity and as such provide important model systems for studying the evolution of life and the dynamics of speciation. Classically, reproductive isolation has been considered a key requirement in speciation, but in the new era of genomics, it has increasingly been observed that gene flow between distinct species is widespread among plants and animals. Whilst it is possible that species can form despite the homogenising effect of gene flow, more intriguingly, it has also been proposed that genetic exchange between diverging lineages within a radiation could even favour speciation through the sharing of adaptive genetic variation. However, the evolutionary significance and frequency of such 'adaptive introgression' is still unclear. The incredibly large and young adaptive radiations of cichlid fishes in the African Rift lakes provide a powerful model to assess the adaptive value and evolutionary significance of such introgression. In this study, we construct a more comprehensive picture of the introgression history from external cichlid species into the Malawi clade. We used large scale whole-genome resequencing data consisting of 276 Lake Malawi cichlid species, representing each of the major ecomorphological groups, and 72 cichlid species from the surrounding riverine and lake systems (including Lake Tanganyika and the LVRS). Our results so far have revealed multiple local sites of introgression from various external species, alongside weak genome wide signals of introgression, perhaps indicative mostly of historic gene flow events into the Malawi radiation.

Abstract ID: 2143
Poster board number:
P093

Phylonumtomics uncovers hybridisation and unknown genomic variation of mammal and bird species

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A big conundrum in evolutionary biology is the fact that there are very few spontaneous adaptive mutations. A surprisingly overlooked alternative mechanism to resolve this issue is the acquisition of novel, genetically pre-adapted elements through laterally transferred DNA. Examples of exchanges of genetic material between species are known for prokaryotes and even in eukaryotes through retrotransposal activity. There is also widespread evidence for substantial exchange of genetic material between eukaryotic species through the process of hybridisation. However, we have very limited knowledge about how widespread and frequent hybridisations contribute to the genomic diversification in the animal kingdom and what evolutionary distances they might bridge. Here we address this fundamental knowledge gap by exploring the evidence for class-wide hybridisation using a signature of hitchhiked mitogenomic fossils. For this, we outline a novel genomic approach, called phylonumtomics, that we apply to more than 1000 avian and mammalian genomes, and identify a surprising heterogeneity of laterally acquired DNA across species. We can show that laterally acquired mitoDNA into the nuclear genome can serve as a marker for genomic introgression and raise the possibility of the adaptive potential of such mitonuclear DNA. Lastly, our approach uncovers a substantial fraction of hitherto unknown mitochondrial variation in mammals and birds, illustrating that despite huge sequencing efforts current databases still lack a substantial proportion of the genomic diversity of these animal classes.

Abstract ID: 2369
Poster board number:
P094

Seasonal dynamics of ancient adaptive genetic variants in a stickleback hybrid zone

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Ancient variants of the EDA and ATP1a1a genes, among other genomic regions, are involved in the parallel adaptive divergence of stickleback ecotypes. Accordingly, genetic admixture of sticklebacks should be strongly affected by these genetic traits, but it is not sufficiently known when, where and how these traits become subject to selection. Genome wide comparisons of pure marine and freshwater sticklebacks revealed multiple loci involved in adaptive divergence. To test the roles these candidate loci play in natural hybrids, we analysed their spatial and temporal dynamics in a stickleback hybrid zone. We genotyped 18 candidate loci in 260 adults from parental populations and 852 juveniles collected in June, July and October 2020. 70% of the young of the year and juvenile fish were admixed individuals. Geographical and genomic cline analysis revealed that allele and genotype frequencies from admixed populations changed conspicuously over the season. Overall, the candidate loci fall into two main groups which may be involved in (i) reducing genetic introgression of marine alleles into the freshwater genetic background or in (ii) reducing introgression of freshwater alleles towards the marine genetic background. These contrasting patterns suggest that fitness effects and dispersal differ considerably across the hybrid zone. Our study highlights locus specific roles of ancient adaptive variants, however, their effects are complemented by other less explored genomic regions.

Symposium: S06. Revisiting chromosomal speciation in the genomic era (id: 8)

Abstract ID: 1144
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P095

Chromosomal rearrangements can inhibit speciation by preventing premating isolation

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Chromosomal rearrangements can strongly suppress recombination between the genetic loci they capture, and thus can act as intrinsic barriers to gene flow across a portion of the genome. Nevertheless, the implication of chromosomal rearrangements on

speciation depends not only on their role as intrinsic barriers to gene flow, but also on how they affect the evolution of other barriers to gene flow. Using population genetics theory, we highlight that chromosomal rearrangements suppressing recombination do not necessarily promote strong reproductive isolation between populations. We show that these chromosomal rearrangements also inhibit the evolution of assortative mating preferences that would have reduced gene flow across the entire genome. This is because assortative mating preferences are generally favored when there is a risk of producing maladapted recombinants. By suppressing recombination, chromosomal rearrangements reduce this risk (which is often why they evolved in the first place) and thus inhibit the evolution of assortative mating preferences underlying premating isolation. Therefore, our study emphasize that chromosomal rearrangements can prevent speciation by interacting with other barriers to gene flow. The implication of chromosomal rearrangements on speciation may thus differ across the tree of life, depending on whether the evolution of assortative mate choice occurs or not.

Abstract ID: 1210
Poster board number:
P096

Speciation in a pair of *Brenthis* fritillary butterflies

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Chromosome rearrangements can promote reproductive isolation between populations in two ways. Firstly, fusions can lead to large chromosomes with low recombination rates, resulting in greater linkage between foreign deleterious alleles. Secondly, fixed differences in karyotype may themselves act as barriers to gene flow by suppressing recombination between populations and causing underdominance in admixed individuals. The sister species *Brenthis daphne* and *B. ino* are fritillary butterflies that have evolved a reduced chromosome number through an accumulation of fusions in their common ancestor. Here I use a composite likelihood approach to infer the demographic history of these species from whole genome sequence data. Additionally, I compare genome assemblies of both species to identify potentially fixed chromosome rearrangements. I fit a model where effective population sizes and effective migration rate vary across the genome and test whether: (i) large chromosomes generated by fusions have particularly low migration rates, (ii) differences in karyotype between *B. daphne* and *B. ino* have acted as barrier loci.

Abstract ID: 1355
Poster board number:
P097

Speciation through chromosomal fusion and fission

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Chromosomal rearrangements may hamper gene flow between lineages and so cause, or contribute to reproductive isolation. While the effects of chromosomal inversions on speciation are relatively well-documented, little is known about the impact of chromosomal fusions and fissions. To test whether changes in karyotype numbers resulting from fusions and fissions lead to increased speciation rates, we first established a genome-based phylogeny for the butterfly genus *Erebia*. We then implemented a character state-dependent birth-death model to infer ancestral karyotype changes at a macro-evolutionary scale. Next, we characterized chromosomal changes across the phylogeny as being either anagenetic (speciation along a branch) or cladogenetic (speciation at a branching event). While cladogenetic changes may promote speciation by reducing hybrid fitness, anagenetic changes may do so by suppressing recombination through time. We found a positive relationship between speciation rate and the rate of chromosomal evolution, with the vast majority of karyotype changes being associated with cladogenetic events. We moreover show that younger, more karyotypically diverse clades experienced higher rates of cladogenetic events, which in turn are associated with higher speciation rates. Taken together, our results highlight that there is potential for speciation through chromosomal fusion and fission as an evolutionary driver across the tree of life, especially in clades with diverse karyotypes.

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Poster board number:
P098

The complex phylogeographic history and speciation in subterranean Blind Mole Rats (Nannospalax sp.)

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The small-bodied blind mole rats (BMR - *Nannospalax* sp.) are some of the most cytogenetically diverse mammals, with >70 chromosomal races (CFs) described over their vast distribution area stretching from Egypt and Levant to the Balkans, Anatolia and the South Caucasus. The major question, which remains largely unanswered, is to what degree the various chromosomal rearrangements have contributed to reproductive isolation between different populations living in allopatry and/or parapatry. We have sampled the majority of the known BMR CFs, with Anatolia particularly well-represented, and constructed a detailed phylogeny based on partial mtDNA sequences. While we could see some correspondence between the major mitochondrial clades and the most widely distributed CFs, such as those with the smallest (2n=36/38) and the highest (2n=60) diploid karyotypes in Anatolia, the wide range of karyotypes with intermediate 2n can be found throughout the phylogenetic tree and show no obvious trend. Interestingly, the observed phylogenetic pattern also seems to be poorly correlated with the geographic distances across Anatolia and the Balkans, with clearly monophyletic haplotypes (though different CFs) found on the Aegean island(s) and in the mountains of the South Caucasus. We combine our mtDNA results with the recently published

microsatellite, behavioral and morphological data, and hypothesize on the complex phylogeographic history and the major speciation events within the *Nannospalax* genus. As we are still in the process of obtaining and analyzing the genome-wide ddRAD-seq marker data, we will soon be able to gain better insight into the speciation process in this fascinating animal group.

Abstract ID: 1490
Poster board number:
P099

Sex-specific ancestral fusion between autosomes and W chromosome in *Heliconius* butterflies

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Heliconius are a diverse group of butterflies composed by 48 species and more than 300 subspecies distributed across tropical America. Within the genus, the sara – sapho clade (composed by 12 species) shows unique characteristics such as gregarious and monophagous larvae, pupal mating, and a larger number of chromosomes compared to other *Heliconius*. Here, we re-sequenced 112 individuals from seven species in this clade to investigate their phylogeny, demography, and drivers of adaptation and speciation. Our results revealed the existence of two phylogenetic groups: (i) the sara group (*H. sara,* and *H. leucadia*) and (ii) the sapho group (*H. antiochus*, *H. sapho*, *H. hewitsoni*, *H. congener* and *H. eleuchia*). Interestingly, within the sapho group females showed lower F_{ST} values, lower mean depth and higher heterozygosity than males in some chromosomes. This pattern suggests the occurrence of sex specific W–autosomal fusions: W-chr4 (in females of all species), W-Chr14 (exclusive to females of *H. eleuchia* and *H. congener*), and W-Chr9 (exclusive to females of *H. sapho* and *H. hewitsoni*). Although these chromosomal rearrangements may contribute to speciation and adaptation in the sara – sapho clade, their effect is yet to be discovered.

Abstract ID: 1724
Poster board number:
P100

Conserved chromosomal structure but divergence in centromeric repeats of two hybridizing species

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Despite an increasing number of sequenced avian genomes, relatively little is known about their organization into chromosomes and to what degree changes in the chromosomal structure play a role in speciation. Here, we explored the chromosomal structure of two hybridizing passerine species, the common nightingale (*Luscinia megarhynchos*) and the thrush nightingale (*Luscinia luscinia*), using conventional cytogenetic approaches, immunostaining of meiotic chromosomes, fluorescence *in situ* hybridization as well as comparative genomic hybridization (CGH). Our results show conserve karyotype structures between the two species with the same diploid chromosome number of 2n=84 and the same size for the germline restricted chromosome. A few subtle changes in chromosome morphology were observed between the two species, suggesting that only a limited number of chromosomal rearrangements occurred after the species divergence. However, the interspecific CGH experiment suggested that the two nightingale species might have diverged in centromeric repetitive sequences in most chromosomes. In addition, some chromosomes showed changes in the copy number of centromeric repeats between the species. Further studies of the whole genome sequences are, however, needed to confirm the centromere divergence. The observation of very similar karyotypes in the two nightingale species is consistent with a generally slow rate of karyotype evolution in birds. The divergence of centromeric sequences between the two species could theoretically cause meiotic drive or reduced fertility in interspecific hybrids. Nevertheless, further studies are needed to elucidate the role that divergence of centromeric sequences could play in the nightingales' speciation.

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Poster board number:
P101

Chromosome divergence and hybrid sterility in budding yeasts

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Reproductive isolation, and consequently speciation, builds up from a combination of isolating barriers. We investigated the potential genetic causes of intrinsic reproductive isolation between two closely related species of budding yeast, Saccharomyces cerevisiae and S. paradoxus. F1 crosses between these species are viable but infertile. We find that the primary reproductive barrier is chromosomal divergence, which results in mis-segregation during meiosis due to anti-recombinaton. All chromosomes in Saccharomyces yeast are essential. Thus, a gamete missing a single chromosome is inviable. Build-up of genic incompatibilities, where genes that work well in their parental genetic background do not work well together in a hybrid genetic background, is also thought to be a common mechanism for speciation. We break the chromosomal species barrier by restoring recombination in the hybrid, allowing us to uncover evidence of genic incompatibilities also playing a role in this system.

Abstract ID: 2425
Poster board number:
P102

Did circular DNA shape the evolution of mammalian genomes?

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Extrachromosomal circular DNA of chromosomal origin (eccDNA) can rapidly shape the evolution and adaptation of mitotically dividing cells such as tumor cells. However, whether eccDNA has a permanent impact on genome evolution through the germline is largely unexplored. Here, we propose that a large fraction of the syntenic changes that are found between mammalian species are caused by germline transposition of eccDNA. We have previously shown the existence of eccDNA in mammalian meiotic cells. By reanalysis of available synteny maps, we now find that up to 6% of mammalian genomes might have rearranged via a circular DNA intermediate. Hence, eccDNA in the germline is expected to have large effects on evolution of gene order.

Symposium: S07. Chromosome rearrangements in evolution (id: 949)

Abstract ID: 1172
Poster board number:
P103

High rate and variability in the spectrum of new structural mutations of *Chlamydomonas reinhardtii*

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New structural variation fuels genome reorganisation and is thought to play major roles in evolution, yet the rate of new structural mutations (SM) is largely unknown. Here, we used long-read sequencing of mutation accumulation (MA) lines derived from the *Chlamydomonas reinhardtii* strains CC-1952 and CC-2931 to study the rate and spectrum of *de novo* SMs. We show that the rate of SMs is highly variable between MA lines and strains, yet represents a substantial fraction of the total mutation rate (>5%). Interestingly, the spectrum of SMs is radically different between strains, since nearly all of the chromosome rearrangements and SMs larger than 30 kb were detected in CC-2931. Differences in the SM spectra were largely caused by high heterogeneity in active transposable element (TE) families between strains. Mobile insertions were among the most common type of *de novo* SMs (comprising 21.7% of SMs in CC-1952 and 37.9% in CC-2931), and frequently explained other SMs. In CC-2931, activity of two DNA elements, a Crypton and a newly described type of TE, mediated most inversions and translocations, while in CC-1952 almost all duplications were mediated by a LINE from the *Dualen* clade. However, many other SMs were found, apparently unrelated to TE

activity. Remarkably, CC-2931 showed a high rate of large duplications spanning coding sequences (μ = 4.92x10^{-11}). Our results show that many types of SMs arise at substantial rates, and highlight the potential role of *de novo* SMs and TEs in genome evolution.

Abstract ID: 1293
Poster board number:
P104

From SNPs to SVs: exploring the impact of structural variants on timing emergence of *Clunio marinus*

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Understanding the impact of genomic architecture in adaptive trait evolution has been a major quest in evolutionary biology. Advances in sequencing technologies provide a novel opportunity to address this question in non-model species with exciting traits.
In the midge *Clunio marinus,* timing of emergence is adapted to tides by circadian and circalunar clocks. As tidal regimes differ along the coastline, *Clunio* populations differ in daily and lunar emergence. These are genetically determined and two circadian and two circalunar quantitative trait loci (QTL) were identified. Circadian and circalunar QTLs associated with phase of the rhythm are overlapping and fall in a large non-recombining region. Whether this highlights a pleiotropic role of circadian clock components and if the same genomic regions are associated with other timing phenotypes is still to be determined.
We investigated which loci contribute to the period of the circalunar rhythm and the putative role of SVs in maintaining adaptive emergence phenotypes. First, we performed a genome-wide association (GWA) screen with SNPs called from short-read sequencing data of 13 natural populations differing in period of the circalunar rhythm. Second, we developed a pipeline combining structural variant (SV) calls from the short- and long-read sequencing. We found that in both GWAs, SNPs and SVs fall within known circadian clock genes. Further genotype assessment of these variants will help us explore to what extent circadian genes play a role in circalunar timing.
Hopefully, these efforts will shed light on genomic architecture maintaining adaptive traits and on the virtually unexplored circalunar clockwork.

Abstract ID: 1304
Poster board number:
P105

tRNA scrabble: extensive gene rearrangements in the mitogenomes of bumblebees (*Bombus*)

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Gene rearrangements are widespread in the fast-evolving mitogenomes of bees, providing valuable insights into their evolution. However, bee mitogenome assembly can

be challenging due to the high AT-content and within-individual variation (heteroplasmy) for some species. Bumblebees (*Bombus*) are major pollinators of wildflowers and crops, comprising around 250 species subdivided into 15 subgenera. Their diverse behaviour and ecology make them important model organisms, yet mitogenome structural evolution has been underexplored for this group. Here we assembled 40 novel bumblebee mitogenomes, covering all subgenera and triplicating the number of mitogenomes available for this genus. We found that protein-coding gene order is conserved, but several tRNA gene rearrangements occurred in the bumblebee tree of life, primarily in the cluster located between the control region and ND2. The tRNA rearrangements include translocations, inversions, and tandem duplications/random losses. Phylogenetic analyses show that some rearrangements reflect shared ancestry, with unique translocation events being characteristic of subgenera *Psithyrus* and *Pyrobombus*, for instance. As described for other hymenopteran mitogenomes, the ND5-ND3 junction is a hotspot for tRNA rearrangements, whereas the COX1-ND3 and CYTB-16S junctions are conserved across species. Since nuclear and mitochondrial genomes coevolve to optimise their compatibility, changes on mitogenome architecture can influence mitonuclear interactions. Moreover, adaptive divergence of mitogenomes is usually the first step in animal speciation since it can favour the fixation of novel mitochondrial genotypes between populations and disrupt gene flow in the process. Thus, further studies on mitogenome structural variation may shed light on bumblebee evolution and diversification.

Abstract ID: 1403
Poster board number:
P106

The pangenome of the invasive ascidian Styela plicata. A world of genomic and structural variants

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Invasive species are a major thread to biodiversity and ecosystems. Thus, monitoring genomic features of invasive species is crucial to understand its population structure and environmental adaptation in order to plan future management measures. The solitary tunicate *Styela plicata* is the responsible of one of the most successful and worldwide spread invasions. However, genomic records for this species are limited to two main sympatric mitochondrial COI groups without obvious nuclear structuring. Here we present the chromosome-level reference genome of *Styela plicata*, and the species pangenome using low-coverage WGS of 24 individuals from 6 populations. We observed a high genetic differentiation between North Carolina and the other populations. In addition, we identified several genomic regions across the genome that differed genetically the Atlantic and Pacific populations, and may be responsible for regional adaptation. Furthermore, we also characterized polymorphic inversions in four chromosomes, present in all populations. Regarding mitogenomes, we recovered three major clades, one of them presenting high genetic differentiation, another clade is unique

from North Carolina and the last one presents a large insertion with several partial genes duplicated. Finally, we located some nuclear polymorphisms associated to the each mitogenome, probably related to mitochondrial-nuclear interacting proteins. The pangenome presented here will allow more comprehensive studies on the invasive species *Styela plicata* in the future, and is a starting point for understanding how intraspecific genomic and structural variants are related to population structuring and adaptation processes of species.

Abstract ID: 1617
Poster board number:
P107

Structural variation at *Linum* distyly supergene - cause or consequence of recombination suppression?

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Supergenes are genomic regions harboring multiple tightly linked functional loci that together govern a multi-trait polymorphism under balancing selection. Supergenes often exhibit structural variation, including inversions and large indels, which can cause recombination suppression. Alternatively, such structural variants could accumulate as a result of relaxed selection in low-recombination regions. In this study, we have characterized recombination rate variation around a recently discovered supergene that governs the balanced floral polymorphism of distyly in *Linum tenue*. The distyly supergene harbors structural variation in the form of a large indel. By combining map-based estimates of recombination rate variation and estimates of linkage disequilibrium in natural populations across the *L. tenue* genome, we show that there is a lack of broad-scale recombination suppression around the distyly supergene. We further show that elevated linkage disequilibrium almost exclusively extends to the region of the supergene that harbors structural variation. These results suggest that in *L. tenue*, structural variation at the distyly supergene is likely a cause and not a consequence of recombination rate suppression, a finding that contributes to an improved understanding of the role of structural variation for recombination rate suppression at supergenes.

Abstract ID: 1654
Poster board number:

P108

Strong genomic divergence on new inversions during ecological speciation in *Drosophila*

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During the early stages of speciation, genetic differences tend to accumulate at certain regions of the genome leading to the formation of genomic islands of divergence (GIDs). In theory, this pattern may be due to selection on beneficial alleles contained within the GIDs and/or difference in the rate of recombination due to structural variation. Here, we investigate the possible causes of GIDs in *Drosophila yakuba mayottensis*, a subspecies of *Drosophila yakuba* specializing on toxic noni (*Morinda citrifolia*) fruits on the island of Mayotte. In 2017, we collected *D. y. mayottensis* from three localities in Mayotte and reconfirmed its association with noni fruits. We sequenced the genomes of the three populations in pools and from individual isofemale lines. We did not find evidence for population structure on the island. Comparing these sequences to mainland genomes, we identified 6 GIDs. We assembled a new genome for *D. y. mayottensis* using a combination of Illumina and Oxford Nanopore sequencing methods. We identified ten regions with major chromosomal rearrangements. Two of them that were unique to *D. y. mayottensis* overlapped with the GIDs. Interestingly, no chromosomal inversions have been detected in *Drosophila sechellia*, the only other *Drosophila* species known to be specialist on noni. Despite some similarities at the genic level that we have previously described between the two noni-specialist species, our results indicate that distinct genomic architectures underlie convergent response to common selective pressures in independent lineages.

Abstract ID: 1915
Poster board number:
P109

Emergence of a chromosomal duplication and its adaptive role in a cold-adapted bacterium

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Chromosomal duplication is a frequent mutational mechanism in both unicellular and multicellular organisms. The maintenance of the additional copy in the genome is energetically costly and it can result in physiological constraints. On the other hand, the gene expression imbalance coming from two identical chromosomes might be beneficial and provide selective advantages under stressful environments. Here, we use the non-model bacterium *Pseudoalteromonas haloplanktis* to investigate the emergence of a chromosomal duplication and its impact on fitness. *P. haloplanktis* is a cold-adapted marine species with a genome comprised of two chromosomes (I and II). Because this is a natural isolate, we performed an experiment aiming to adapt it to the laboratory

conditions. Strikingly, whole genome sequencing of a single evolved clone showing a growth increase relative to the wild-type strain revealed the duplication of the entire chrII. To assess the frequency and repeatability of the chromosomal duplication we isolated clones from the endpoint populations of our evolution experiment and performed whole genome sequencing. We also assessed the appearance of additional mutations and evaluated if any of them confers higher fitness than the chromosomal duplication. We find that the chromosomal duplication emerged independently in all the evolved populations in approximately half of the clones. The presence of a second copy of the chrII provides a fitness benefit by increasing the growth rate. Additionally, we identified mutations affecting genes of outer membrane proteins that alter the export of toxic compounds such as antibiotics.

Abstract ID: 2042
Poster board number:
P110

Linking structural variation to gene expression in the Brassicaceae family

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Structural variation, particularly if it involves genes or regulatory elements, is an important driver of phenotypic variation in plants. An increasing number of studies have started to elucidate how structural variation mediates differences in gene expression and phenotype between individuals of the same plant species. The impact of structural variation on such differences between different plant species however, has received comparatively less attention. Here, we address this research question in a panel of different species sampled from different lineages of the Brassicaceae family. A large degree of interspecific structural variation can be expected to be found in this panel, as Brassicaceae have undergone multiple, independent, lineage-specific whole-genome duplication events followed by extensive rearrangements of duplicated chromosomes as the genomes returned to a diploid state. We will generate chromosome-level genomic assemblies based on PacBio HiFi sequencing technology, optical mapping, and Hi-C, and use these assemblies to characterize structural variation in the panel down to nucleotide level. Additionally, we will identify differences in gene expression between panel members through RNA sequencing of their seedlings, and determine whether these can be correlated to differences in the genomic context of genes. Here, we present initial results showing that HiFi sequencing data enables us to reconstruct individual chromosomes with high accuracy.

Abstract ID: 2078
Poster board number:
P111

Structural variation in genomes of two closely related passerine species

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Understanding the genetic basis of species evolution has been a long-standing goal of evolutionary biology. Although the role of genomic rearrangements in this process was first suggested already a century ago, thorough investigation of structural variants in the full diversity of their types and lengths and their connection to adaptive traits or to speciation still presents a challenge. Here we investigate the structural variants among two closely related and still hybridizing passerine species, the common nightingale (*Luscinia megarhynchos*) and the thrush nightingale (*Luscinia luscinia*). Using long-read sequence data and Omni-C chromosome scaffolding, we *de novo* assembled and annotated the genomes of the two species and created a catalog of structural variants occurring between them. With an ensemble of methods for detection of structural variants, we detected over 25 thousand variants. However, the majority of them (~ 90%) were insertions and deletions shorter than 1000 bp. Nevertheless, our catalog also contains several variants spanning more than 10 kbs which might substantially differentiate the genomes of our model organisms. Our results suggest that structural variants might be an important source of genetic variation between species even in taxa with relatively conserved karyotypes and might contribute to species-specific adaptations as well as the origin of reproductive isolation between the species.

Abstract ID: 2091
Poster board number:
P112

Rapid gene content turnover on the germline-restricted chromosome in songbirds

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Birds have a conserved karyotype compared to other vertebrates. It normally has ten macrochromosomes and several tens of microchromosomes. However, in songbirds an extra chromosome exists in the germline. This germline-restricted chromosome (GRC) is eliminated from the somatic cells during early embryogenesis. Despite its apparent indispensability in songbirds, we still know very little about the GRC's genetic composition, function, and evolutionary significance. Here we assembled the GRC in two closely related species, the common and thrush nightingale. We identified 585 and 406

genes on the GRC of each species, respectively, many of them present in multiple copies. Interestingly, the GRC gene content differed dramatically between the two species, with only 192 genes being shared despite only 1.8 million years of species divergence. The chromosome appears to be under little selective pressure, with most GRC genes being present in pseudogenized fragments. Only one gene, cpeb1, had a complete coding region in all examined individuals of the two species and showed no copy number variation. The addition of this gene to the GRC corresponds with the earliest estimates of the GRC origin, making it a good candidate for the functional indispensability of the GRC in songbirds. Our results suggests that the GRC is the fastest evolving chromosome in the songbird genome, showing many structural variations between closely related species and within a species. This contrasts starkly with the conserved bird karyotype.

Abstract ID: 2116
Poster board number:
P113

Wrath detects adaptively important structural variants from haplotagging data in a mimetic butterfly

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Structural variants can play a crucial role in adaptation and speciation; however, their study is limited by our capacity to detect them. Short-read sequencing techniques, although affordable, do not retain linkage information, and the application of long-read sequencing is limited by their cost and higher error rate. Linked-read sequencing has emerged as the alternative, utilising short-read scalability while retaining linkage information. The newly developed 'haplotagging' is a simple, linked-read technique that can be applied to hundreds of individuals at low-cost and has the potential to revolutionise the study of structural variants in wild populations. However, it lacks a tailored, user-friendly protocol for its analysis. We present Wrath (WRapped Analysis of Tagged Haplotypes), a pipeline for the analysis of haplotagging data and the genome-wide detection of structural variants. We apply Wrath to a large population dataset of wild *Hypolimnas misippus*, a tropical species of butterfly that presents polymorphic, mimetic females. Despite the detailed resemblances to its model, selection for mimicry has been hypothesised to be weak, raising the question of how the polymorphism is being maintained. One hypothesis is that structural variation at the locus reduces recombination, which leads to the accumulation of deleterious mutations and selection against homozygotes, enhancing the maintenance of recessive alleles. Using Wrath, we show that two deletions are found at the locus associated with mimicry in this species and validate them using PCR. We demonstrate the easy applicability of Wrath for

haplotagging datasets of large populations and its effectiveness in detecting structural variation of adaptive importance.

Abstract ID: 2285
Poster board number:
P114

Genome rearrangements in the asexual bdelloid rotifer *Adineta vaga* after DNA repair and reproduction

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Bdelloid rotifers are extremo-tolerant microscopic animals, surviving desiccation, freezing and high doses of ionizing radiation. During such stressful conditions, damages to macromolecules accumulate, including DNA, that get repaired upon stress release. Besides, bdelloid rotifers are notorious ancient asexuals that engage in parthenogenetic reproduction without any males or syngamy. How asexual reproduction and genotoxic stresses are affecting genome evolution in bdelloid rotifers remains unknown. Recent studies on new genome assemblies of the bdelloid *Adineta vaga* reported signatures of recombination and large deletions but the underlying mechanism is still unresolved. Here, we studied genome evolution by performing a mutation accumulation experiment (MA) including cycles of desiccation, and a genome repair experiment (GR) exposing *A. vaga* to ionizing radiation. We observed losses of heterozygosity (LOH) indicating that homologous recombination is actively used to repair DNA damage, while also taking place during a modified meiosis in oogenesis. Moreover, we observed chromosome-scale modifications such as deletions and duplications in both the MA lines and the lines exposed to large radiation doses. These results suggest that the genome is dynamic in this parthenogenetic system and that *A. vaga* can survive large chromosomal modifications. We also observed that *A. vaga* only partially repairs large deletions and that HR repair continues over generations. Overall, we show that genome plasticity plays a major role in the extremo-tolerance of bdelloid rotifers.

Abstract ID: 2305
Poster board number:
P115

Background Selection and Mutation Accumulation in Locally Adaptive Inversions

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Chromosomal inversions create genomic regions with increased linkage between the loci they encompass by suppressing recombination within the region when heterozygous. Such a region can be selectively favoured if, for example, it binds together a set of epistatically interacting or locally adaptive alleles, or captures an especially beneficial genetic background. However, any subsequent copies of a new inversion will be fixed for any deleterious mutations that were captured when the inversion initially arose, and, while the inversion is rare, the low rate of recombination also reduces the efficacy of purifying selection. Thus, the accumulation of deleterious mutations could prevent an

adaptive inversion from establishing. Using simulations, we investigate the conditions under which the mutation load of an adaptive inversion prevents its establishment. To do this, we model a two-deme haploid population, connected by migration, in which individuals are undergoing local selection at two loci and can acquire deleterious mutations elsewhere along the chromosome. We track an inversion that captures both the locally adaptive alleles in one of the demes, and attempt to isolate the effects of mutation capture and mutation accumulation to assess the significance of the roles they play in determining the fate of the inversion.

Abstract ID: 2372
Poster board number:
P116

Karyotype evolution in closely related estrildid finches of the genus *Lonchura*

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Avian genome organization is very conserved and shows a very low rate of inter-chromosomal rearrangements when compared to other vertebrates. However, intra-chromosomal rearrangements may be relatively common. To explore karyotype evolution in birds we used antibody-based cytogenetic methods and analysed the karyotypes of five closely related estrildid finches of the genus *Lonchura* in pachytene cells. The karyotypes are rather conserved in the chromosome number, however, we found variation in the centromere position on both macro- and micro-chromosomes suggesting that multiple intra-chromosomal rearangements might have occured between the species. Additionally, we observed polymorphism in the centromere position in both macro- and micro-chromosomes in most species suggesting that intra-chromosomal rearrangements may segregate even within species. Our results suggest that intra-chromosomal rearrangements or repositioning of centromeres can arise over a very short evolutionary time in passerine birds. Because chromosomal structure is crucial for chromosome segregation during meiosis, such changes might affect the fertility of hybrids and thus contribute to reproductive isolation between the species.

Abstract ID: 2442
Poster board number:
P117

Divergent subgenome evolution in the allotetraploid frog Xenopus calcaratus

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Allopolyploid genomes are divided into compartments called subgenomes that are derived from lower ploidy ancestors. In African clawed frogs of the subgenus *Xenopus* (genus *Xenopus*), allotetraploid species have two subgenomes (L and S) with morphologically distinct homoeologous chromosomes. In allotetraploid species of the sister subgenus *Silurana*, independently evolved subgenomes also exist, but their cytogenetics have not been investigated in detail. We used an allotetraploid species in *Silurana*—*Xenopus calcaratus*—to explore evolutionary dynamics of chromosome morphology and rearrangements using a diverse set of cytogenetic approaches (measurements of chromosomal lengths, conventional banding, FISH techniques). We find that the subgenomes of *X. calcaratus* have distinctive characteristics, with a more conserved a-subgenome resembling the closely related genome of the diploid species *X. tropicalis*, and a more rapidly evolving b-subgenome having more pronounced changes in chromosome structure, including diverged heterochromatic blocks, repetitive sequences, and deletion of a nucleolar secondary constriction. Based on these cytogenetic differences, we propose a chromosome nomenclature for *X. calcaratus* that may apply to other allotetraploids in subgenus *Silurana*, depending on as yet unresolved details of their evolutionary origins. These findings highlight the potential for large-scale asymmetry in subgenome evolution following allopolyploidization.

Symposium: S08. Integrative biogeography: Past, present, future (id: 25)

Abstract ID: 1183
Poster board number:
P118

Population genomic of the allotetraploid African clawed frog Xenopus laevis from South Africa.

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The African clawed frog *Xenopus laevis* is native to South Africa and is considered one of the most widespread and high impact invasive amphibians on earth. Although it is a well-established model species that served science since 1896, surprisingly little is known about the genetic diversity of the species in its native environment. Our research aims to establish the ground knowledge about the population structure, genetic diversity, demography and adaptation in wild populations of *X. laevis* in South Africa. Our results show that in South Africa, *X. laevis* forms five differentiated populations based on mitochondrial DNA but only four populations based on thousands of nuclear polymorphisms. The calibrated mitogenome tree suggests that the divergence time between these populations is driven by paleo-climatic changes in aridity, and a

geological uplift of the southeastern Cape. The divergence between populations was followed by gene flow in contact zones.

Abstract ID: 1241
Poster board number:
P119

A novel lineage of Capra discovered in the Taurus Mountains of Turkey using ancient DNA

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Direkli Cave, located in the Taurus Mountains of Turkey, was occupied by Late Epipaleolithic hunters-gatherers for the seasonal hunting including large quantities of wild goats.
We report genomic data from new and published Capra specimens from Direkli Cave and find a novel lineage sister clade to the Caucasian tur species (Capra cylindricornis and Capra caucasica). The lineage is best represented by a ~2.6X genome (Direkli4) which dates to the late 13th-early 12th millennium cal BC, and we report two additional samples with nuclear genomes of this Tur-like ancestry. West Eurasian domestic goats in the past, but not those today, appear enriched for Direkli4 alleles, and we identify genomic regions introgressed in domestic goats with high affinity to Direkli4. This forgotten Capra lineage likely survived Late Pleistocene climatic change in a Taurus Mountain refugia.

Abstract ID: 1272
Poster board number:
P120

Comparative phylogeography of two *Arabidopsis* species in the Carpathians

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The biogeography of Europe was influenced mainly by Pleistocene climatic oscillations and the traces of the evolutionary history of plant species can be inferred from the genetic structure of their populations. Important insights into the spatio-temporal evolution of flora and fauna of the European mountains (especially the Alps) have been provided using (comparative) phylogeography, but we still lack information on plants inhabiting the area below the timberline and/or plants with a wider elevation span, especially from the Carpathians. In our contribution, we will present new findings from the reconstruction of the evolutionary history of two *Arabidopsis* species (Brassicaceae), which have a centre of their diversity in the Carpathians, mainly in the lower (below timberline) mountain ranges, but in several areas, they also reach the subalpine positions. Investigating the evolutionary history of *Arabidopsis arenosa* and *A. halleri* populations by means of multilocus markers (AFLP or SNP) reveals surprising parallels in the evolution of both species. In particular, they confirm the main genetic barrier, already observed in the subalpine species, at the East and West Carpathian

borders, but they also point to the repeated evolution of alpine morphotypes from geographically close foothill populations. In the case of *A. arenosa*, the Carpathians are not only a refugium of rare genetic diversity but also a source of the populations that recolonized the northern parts of Europe.

Abstract ID: 1321
Poster board number:
P121

A museomics approach to determine population dynamics in an endemic New Guinean bird family

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New Guinea, the largest tropical island, is topographically complex and dominated by a large central mountain range, but also has multiple smaller isolated mountain regions along the perimeter of the island. The island is hyper-diverse and harbours an avifauna with many species found only there. The family Melampittidae is endemic to New Guinea and consists of two monotypic genera; *Melampitta lugubris* (Lesser Melampitta) and *Megalampitta gigantea* (Greater Melampitta). Both Melampitta species exhibit scattered and disconnected distributions across New Guinea in the main mountain range and some of the outlying mountains. While the Lesser Melampitta is rather common and found in most mountain regions of the island, the Greater Melampitta is elusive and known from only a few localities in isolated pockets on New Guinea with very specific habitats of limestone and sinkholes. In this project we apply museomics and have resequenced the genomes of the seven known Greater Melampitta samples hosted in museum collections as well as 19 Lesser Melampitta samples across its distribution. We study whether these two species consist of single panmictic populations or multiple distinct populations that may be divergent at the species level. By contrasting the population structure of these two species we also study how very specific habitat requirement, such as in Greater Melampitta, may affect population connectivity. This work will shed new light on the mechanisms which shaped the intriguing distribution of this family and is a prime example of the importance of museum collections for genomic studies of poorly known and rare species.

Abstract ID: 1528
Poster board number:
P122

Zones of secondary contact maintained by temporal isolation through allochrony

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The biogeography of many species is shaped by patterns of recolonization from different glacial refugia following the last glaciation. Where species or lineages meet, they may form zones of secondary contact whose evolutionary outcome critically depend on the level of interspecific gene flow. While zones of secondary contact are common, the factors that maintain them remain often unknown. Here, we investigated the outcome of secondary contact between two closely related lineages of butterflies in the Swiss Alps. We collected specimens over four years from two contact zones together with their allopatric counterparts and obtained phenotypic data from historical specimens. Combining phenotypic and genomic data, we show that the degree of geographic isolation of the contact zones from the allopatric populations scales with the level of interspecific gene flow. We further demonstrate that at the contact zones, the occurrence of the two butterfly lineages alternates between years, providing the first evidence for a classic, yet understudied barrier to gene flow: temporal isolation through allochrony. Taken together, our findings highlight how the interplay between different barriers to gene flow shapes population dynamics and maintains zones secondary contact.

Abstract ID: 1576
Poster board number:
P124

The role of Pleistocene climatic oscillations in the formation of the European crow hybrid zone

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Quaternary climatic fluctuations impact many species in a similar way and may be the underlying forces behind the distribution pattern observed in different organismic groups. In the temperate regions of Europe, populations are forced into refugia during glaciation, creating windows of opportunity for reproductive isolation. During the interglacial period, ice sheet retreats and populations may come into secondary contact, putting the genetic differences accumulated in the diverging populations to the test. One striking biogeographic pattern lies in the European suture zone running through eastern Germany, which is shared by different organismic groups including multiple avian, mammal and plant species. An example is the carrion and hooded crows, *C. corone* spp., which form a narrow hybrid zone along eastern Germany and northern Italy. The all-black carrion crows in Germany are found to be 99.9% genetically identical to the grey-coated hooded crows occurring in the east of the hybrid zone, suggesting that the hybrid zone may not be static and the initial zone of secondary contact may have been dislocated from today's hybrid centre. Our study seeks to reconstruct the demography of the European crows and investigate the roles of Pleistocene climatic conditions in shaping the European hybrid zone. Adding to the genomic data from previous studies, more samples from different localities have been sequenced to obtain a comprehensive representation of the contemporary population. Ancient DNA of crow bones throughout the Holocene and late Pleistocene are also being generated to trace the evolutionary history of the European crows through time and space.

Abstract ID: 1629
Poster board number:
P125

Evolutionary history of the Atlantic cod (Gadus morhua) across space and time

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The economically important Atlantic cod (*Gadus morhua*) is a marine fish species distributed in the Northern Atlantic region with a long overexploitation history. Although historically abundant, a changing climate and continuous fishing activities in the past led to dramatic population declines of Atlantic cod in the present. The genomic consequences of such declines remain unclear. We here use a multidisciplinary approach using ancient DNA methods to investigate past distributions and the impacts of climate change and exploitation on Atlantic cod. Using low-coverage whole-genome data to genotype spatially divergent inversions, we identify the long-term spawning distribution of the North East Arctic cod approximately 4000 years ago. While the distribution of this ecotype shifted northwards during the last century, we find a presence of this ecotype at a more southern latitude than expected highlighting the complexity of reconstructing past marine ecosystems. We further assess the biological origin of archaeological remains of Atlantic cod to trace the extent and expansion of an increasingly globalised trade during the eleventh to nineteenth centuries. Finally, we explore temporally spaced whole genome data to assess any impacts on the genomic composition covering a period of *ca.* 1300 years, providing a long-term genomic perspective for Atlantic cod with potential implications for conservation management.

Abstract ID: 1664
Poster board number:
P126

New mitogenomic data for Lagomorpha enhance the understanding of microevolution in the order

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Lagomorpha comprises two living families, Ochotonidae (pikas) with one genus and Leporidae (hares and rabbits) with 11 genera (seven of them monospecific) and 106 species in total. The leporid *Sylvilagus* (the second most speciose genus after *Lepus*) and some monotypic genera (e.g. *Brachylagus*) lacked robust genomic data until now. We sampled 10–100 years old muscle and skin tissues of museum collections (University of Washington Burke Museum, Seattle, WA, and Field Museum of Natural History, Chicago, IL, USA) to generate complete mitochondrial genomes with custom-designed mRNA probes. Extraction protocols for both modern and ancient DNA were used prior to enrichment and Illumina sequencing. We de novo assembled six mitogenomes of *Lepus alleni* (Mexico), *L. nigricollis*, *Ochotona rufescens* (Afghanistan), *Sylvilagus floridanus*, *S. aquaticus*, and *Brachylagus idahoensis* (USA). We found four misidentified *Lepus*, *Ochotona*, and *Sylvilagus* species acquired from the museums. Further, our study concerning an unidentified *Lepus* sp.

from Iran and Xinjiang (China) indicated the occurrence of *Lepus tibetanus* in Iran and the unusual degree of hybridization within the genus respectively.

Abstract ID: 1698
Poster board number:
P127

Landscape and climatic variations shaped secondary contacts amid barn owls of the Western Palearctic

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The combined actions of climatic variations and landscape barriers shape the history of natural populations. When organisms follow their shifting niches, obstacles in the landscape can lead to the splitting of populations, on which evolution will then act independently. When two such populations are reunited, secondary contact occurs in a broad range of admixture patterns, from narrow hybrid zones to the complete dissolution of lineages. A previous study suggested that barn owls colonized the Western Palearctic after the last glaciation in a ring-like fashion around the Mediterranean Sea, and conjectured an admixture zone in the Balkans. Here, we take advantage of whole-genome sequences of 94 individuals across the Western Palearctic to reveal the complex history of the species in the region using observational and modeling approaches. Even though our results confirm that two distinct lineages colonized the region, one in Europe and one in the Levant, they suggest that it predates the last glaciation and identify a secondary contact zone between the two in Anatolia. We also show that barn owls re-colonized Europe after the glaciation from two distinct glacial refugia: a previously identified western one in Iberia and a new eastern one in Italy. Both glacial lineages now communicate via eastern Europe, in a wide and permeable contact zone. This complex history of populations enlightens the taxonomy of *Tyto alba* in the

region, highlights the key role played by mountain ranges and large water bodies as barriers and illustrates the power of population genomics in uncovering intricate demographic patterns.

Abstract ID: 1706
Poster board number:
P128

Diaspore morphospace disparity among Australasian *Atriplex* L. during adaptive radiation

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Diaspores serve essential roles during plant range expansion and establishment as mediators of dispersal, dormancy and germination. For taxa occupying arid landscapes with unpredictable water availability, successful dispersal and germination in favorable conditions may be especially crucial. The desert and steppe interior of Australia is the site of ongoing adaptive radiation of the dominant chenopod shrubland genus *Atriplex*, a complex of ~70 taxa varying in sexual system, adult life span and growth habit. Among-species fruiting bract morphological variation was examined through multivariate and hierarchical clustering analysis to identify morphogroups and structuring trait variables. Three fruiting bract syndromes were identified: (1) an entirely spongy fruiting bract syndrome with winged appendages and fully united bracts, (2) a fan-shaped and robust tube fruiting bract syndrome without appendages, and (3) an oval-triangular fruiting bract syndrome with herbaceous bracts united at the base and having spongy appendages. The remaining taxa have complex sets of diaspore trait associations and are not well-differentiated from one another on the basis of fruiting bract morphology. Instead, Australasian *Atriplex* occupies a wide diaspore morphospace, deploying many fruiting bract morphological strategies. Australasian *Atriplex* also occupies a wide climatic space, as most fruiting bract traits are not explained by coarse environmental variables and diaspore morphology was not found to predict range extent, indicative of obscure interactions between diaspore morphology and environment. These findings provide morphological support for the rapid diversification of *Atriplex,* alongside other younger lineages occupying Australia's recently aridified interior in a context of niche availability.

Abstract ID: 1745
Poster board number:
P129

Cliff shells: endemicity and radiation in waterfalls of the Western Ghats, India

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Snails of the genus *Cremnoconchus* (cliff shells) – only freshwater members of the marine family Littorinidae – are endemic to the spray zones of numerous west-flowing waterfalls in the Western Ghats (WG), India. Endemicity, specific niche requirements, and transition from marine to freshwater habitat make it an excellent model system to study local adaptation in taxa with limited vagility under rapidly changing environment. However, sound taxonomic information is basal to such studies. Here, we characterize cryptic diversity in *Cremnoconchus* using single gene-based species delimitation analysis and reconstruct its phylogeny. Our results reveal, in addition to the nine currently described species, at least 12 putative species remain undescribed in the region. Spatial isolation due to the patchiness of suitable habitats might have facilitated this diversification. Nuclear and mitochondrial gene-based phylogeny showed that *Cremnoconchus* formed two distinct clades mirroring its geographic distribution wherein one clade was restricted to the northern WG while the other to the central WG. Within the larger Littorinidae tree, the genus was monophyletic. Further, a fossil-calibrated Bayesian time tree suggested that the lineage diverged from its marine counterparts about 90 mya, potentially owing to globally decreasing sea levels. The two sister clades within *Cremnoconchus* separated about 56 mya, coinciding with the formation of the northern WG. Most known species are restricted to a single waterfall, earning the title of point endemics. Consequently, the threat of extinction is quite high for the genus. Results from this study will help understand the existing diversity in this genus and devise directed conservation measures.

Abstract ID: 1758
Poster board number:
P130

Evolutionary history and population dynamics of *Gallus gallus* in Southeast Asia and South Pacific

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The complex geographic and temporal origins of chicken domestication have attracted wide interest in molecular phylogeny and phylogeographic studies as they continue to be debated up to this day. In particular, the population dynamics and lineage-specific divergence time estimates of chickens in Southeast Asia (SEA) and the Pacific regions are not well studied. Here, we analyzed 574 complete mitochondrial DNA control region sequences and identified 158 haplotypes. We documented 85.4% geographically unique haplotypes distributed across major haplogroups except haplogroup C, suggesting high polymorphism among studied individuals. Mainland SEA (MSEA) chickens have higher overall genetic diversity (*Hd*=0.963 ± 0.005; π =0.00782 ± 0.00398) than island SEA (ISEA) chickens (*Hd* = 0.945 ± 0.007; π = 0.00465 ± 0.00398). Phylogenetic trees and median-joining network revealed evidence of a new divergent matrilineage (i.e.,

haplogroup V) as a sister-clade of haplogroup C. Island SEA chickens have a shared genetic affinity of predominant haplogroup D1, a major island haplogroup characterized as Philippine-Pacific sub-clade. The result of the PCoA distinguished population substructure between continental and ISEA chickens along the first two axes which accounted for 52.09% variation. The maximum clade credibility tree estimated the earlier coalescence age of ancestral D-lineage (i.e., sub-haplogroup D2) of continental chickens (3.7 kya; 95% HPD 1,985–4,835 years) while island populations diverged later at 2.1 kya (95% HPD 1,467–2,815 years). This evidence of earlier coalescence age of haplogroup D ancestral matriline exemplified dispersal patterns to the ISEA, and thereafter the island clade diversified as a distinct group.

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P131

Phylogeographic and evolutionary history analyses of *Sus scrofa* in Southeast Asia

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The temporary connections between insular and continental biodiversity hotspots in Southeast Asia (SEA) and the often debated migration events into Island Southeast Asia (ISEA) have influenced the diversity and distribution of the genus *Sus* in these regions. Using large-scale samples (n=450; complete mitochondrial D-loop sequences), we investigated the phylogeography and the population dynamics of pigs in SEA. A total of 149 haplotypes, with a higher overall genetic diversity among SEA pigs (0.976 ± 0.003), were observed than in other regions. Vietnam and the Philippines showed the highest genetic diversity, while Myanmar showed the lowest, with all samples classified only under the D2 haplogroup. Significant population subdivisions were observed among all geographic locations examined. Model-based phylogeny and the MJ networks showed a similar result, confirming that the D7 haplogroup, previously identified in the Indo-Burma Biodiversity Hotspots, and the Philippines, was distinct from all other known haplogroups. Evidence for the Philippine Lanyu-subclade was documented, which may have diverged from the original Lanyu sometime in the Pleistocene. The existence of the D3 haplogroup in Bhutan was also confirmed. All countries, except Thailand, were consistent with the population expansion hypothesis, including major haplogroups D2 and D7. The prehistoric population history analyses suggest a demographic expansion coinciding with the interglacial periods of the Pleistocene that may have spread from Mainland SEA to the rest of the ISEA and the Pacific region. These findings help elucidate the evolutionary history of SEA pigs, an essential for conservation strategies and improvements of economically important genetic resources.

Abstract ID: 1847
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P132

An integrative study of the diversification of dung beetles in the Malay Peninsula and Borneo.

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Diversification via niche partitioning can also be facilitated by sexual selection involving reproductive traits responsible for mate acquisition and fertilization success. *Catharsius* is an ecologically important genus of dung beetles, and recent revisions based on morphological and molecular data identified two distinct species from Borneo and the Malay Peninsula in the *Catharsius molossus* species complex. Rising sea levels after the last glacial period separated tropical rainforests in this region, and *C. dayacus* became mostly restricted to mature rainforests of Borneo whereas *C. renaudpauliani* is generally widespread across plantations and disturbed forests in Borneo and the Malay Peninsula. Both species occasionally overlap in Borneo and can be distinguished by the shape of male pronotal ridge between two thoracic horns which play a role in reproduction. Here, we analyze patterns of genetic variation using nuclear genomic SNP data and mtDNA *COI* markers, together with morphometric analyses of both sexual and non-sexual traits, to explore possible mechanisms underlying recent diversification in *Catharsius*. Our results suggest evidence of introgression from *C. dayacus* in *C. renaudpauliani* from Peninsular Malaysia only and surprisingly not in Sabah where *C. dayacus* and *C. renaudpualiani* overlap. Individuals of the widespread *C. renaudpauliani* from Langkawi, Peninsular Malaysia, Singapore and Sabah, display clear genetic distinction (FST= 0.4) and isolation-by-distance. However, morphological and morphometric trait analyses indicate that these cryptic populations are not significantly different with respect to non-sexual or sexual selected traits, suggesting *C. renaudpualini* may be in early processes of incipient diversification due to drift.

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P133

Biogeography can help to resolve the reticulate history of the the genus *Curcuma* (Zingiberaceae

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Biogeography is the study of the distribution and evolution of organisms through space and time and it generally relies on the purely bifurcating species phylogeny. Instances of hybridization or gene flow, however, may have occurred anywhere along the tree of life, and representing evolutionary history as bifurcating may be erroneous also for downstream approaches. For biogeographical reconstruction, especially hybridizations that occur between phylogenetic internal nodes (sometimes called deep time reticulations, DTRs) are crucial. DTRs were previously detected in different time scales within several well-studied animals and in a few plant groups. Since plants are more prone to hybrid speciation than animals, the occurrence of DTRs might be unexplored in

plants. DTRs were, moreover, documented as possible triggers of lineage diversification and might be a more important process for generating biodiversity than once considered. Here we use the tropical genus *Curcuma* (Zingiberaceae) as a model to analyze DTRs as a possible trigger of species diversification. We estimated phylogenetic networks using SNaQ based on target enrichment data and further explored if our data support hybridization events using coalescent simulations under a machine learning classification. In particular, we test the hypothesis that *Curcuma* subgenus *Hitcheniopsis* is of hybrid origin and that hybridization took place in Indochina. Finally, we used biogeography as an independent test of phylogenetic reticulation, where biogeographic reconstructions from each parental lineage should yield the same or adjacent areas.

Abstract ID: 1905
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P134

First population genetic study of New Guinean Jewel-babblers reveals cryptic diversity

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Understanding the evolutionary processes that shape biodiversity across time and space is a fundamental objective in Biogeography. Biodiversity is not equally distributed around the world and some regions are disproportionately biodiversity rich. The rugged tropical island of New Guinea, for example, is biodiversity rich and home to some 800 bird species of which half are endemic. Moreover, recent research has suggested that New Guinea may have even acted as an 'engine' for avian diversification in the greater Indo-Australian region. However, phylogeographic studies based on comprehensive genomic datasets remain scarce due to the challenges of sampling in remote regions. Here, we use a combination of newly collected specimens and specimens sourced from Natural History Collections to overcome this barrier. We take a whole-genome approach to study the distribution of lineage diversity, population connectivity, and evolutionary history of the Jewel-babblers (*Ptilorrhoa*), an avian group that is widely distributed across and endemic to New Guinea. The four currently recognized species differ in elevational range with both low and highland specialists; Jewel-babblers are therefore well-suited to further investigate possible broadscale patterns in biogeography and diversification. Using whole-genome resequence data for 40 historical specimens and a denovo genome assembly, we discuss the geographic distribution of lineage diversity across the island, the role of elevation in promoting diversification and the discovery of a putative new cryptic species. Our study demonstrates how novel genomic approaches combined with

historical collections can link biogeographic processes and macroevolutionary change in some of the world's most biodiverse and remote regions.

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Poster board number:
P135

Genomic diversity of the bank vole in Scandinavia: the role of multiple colonizations and refugia

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The history of repeated northern glacial cycling and southern climatic stability has long dominated explanations for how current genetic diversity is geographically distributed within temperate species. During northward population expansions, drift-mediated mechanisms (bottlenecks, founder events) have been inferred, resulting in a generalized 'southern richness, northern purity' paradigm. An excellent area to assess this is Fennoscandia, where post-glacial recolonization was restricted to specific routes and time windows. Here, we used high-throughput genomic data to analyze genetic diversity and describe colonization history of the bank vole (*Myodes glareolus*) in Fennoscandia, with more than 800 samples from across the species distribution in Europe. We found that bank voles colonized Fennoscandia multiple times by two different routes; with a minimum of three separate colonizations via a southern land-bridge route from the Carpathian refugium and at least one via a northern route from an Eastern refugium near the Ural Mts. Clustering of genome-wide SNPs revealed tremendous diversity in Fennoscandia, with eight genomic clusters: three of Carpathian refugial origin and five Eastern. Time estimates revealed that two of the Carpathian colonizations occurred before the Younger Dryas (YD), meaning that both survived the YD in Fennoscandia. Results also indicated that introgression between bank and northern red-backed voles took place in northern Fennoscandia just after post-glacial colonization. Therefore, multiple colonizations, temporal and spatial separations and interspecific introgression have shaped bank vole genetic variability in Fennoscandia. Together, these processes drive high genetic diversity in northern populations, directly the reverse of what is found in many other temperate species.

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P136

Recent biogeography of *Argyrodes lanyuensis* along the Taiwan-Philippine archipelago

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The kleptoparasitic spider, *Argyrodes lanyuensis* Yoshida, Tso & Severinghaus, 1998 has been originally assumed to have a microendemic distribution in Lanyu Island, Taiwan. Recently, our study revealed the occurrence of this species in Main Island Taiwan (East) and Philippine archipelago. We inferred the geographic diversification of this species to test (a) Northward, and (b) Southward colonizations. With the use of highly polymorphic SNPs from RAD-seq, we generated a more robust population structure of *A. lanyuensis* as compared with our previous study using mt-COI. We only identified three plausible genetic clusters (K=3; Main Island Taiwan, Lanyu Island and Philippines) of *A. lanyuensis* in STRUCTURE despite the wide investigations conducted in seven paleogeological island boundaries. Similar results were also generated using DAPC, VAE machine learning approach and phylogenetic reconstruction (BEAST and IQTree). Our BFD results suggested highest support for three species model representing the split of Mainland Taiwan, Lanyu and all Philippine populations. The reconstructed biogeographical analysis suggested southward colonization of *A. lanyuensis* from Main Island Taiwan, indicating that Main Island Taiwan is the most plausible ancestral range of this species. Pairwise genetic distance (*fst* and Jost *D*) also supported this analysis which revealed highest genetic diversity between Main Island Taiwan and Lanyu Island. Moreover, GWAS analysis have shown Main Island Taiwan and Philippines with the highest number of significant SNPs. Our study highlights the growing evidence of rare divergence of animal taxa from Taiwan with recent expansion towards the Philippine archipelago suggesting potential differentiation of Philippine population.

Abstract ID: 2025
Poster board number:
P137

A host-driven genetic divergence within a microgeographic pattern: the case of *Argyrodes bonadea*

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Species colonization and distribution patterns are influenced by ecological factors and historical processes such as the cycle of merging and fragmentation of land masses during the repetitive glacial cycles. These factors may result in genetic divergence which

may pave the way toward speciation. Here, we assess the population genetic structure of the kleptoparasitic spider *Argyrodes bonadea* Karsch, 1881 (family Theridiidae) in the Ryukyu island chain, Taiwan, Philippines, and Australia to test the geographic barriers as potential drivers of speciation. A combination of CO1 and RADseq data was used for phylogenetic, ancestral population (RASP) and clustering analyses (STRUCTURE, DAPC, VAE). We employed the Bayes Factor Delimitation to test the different species model hypotheses whereas Pleistocene-driven Hypothesis (PdH) and pre-Pleistocene Hypothesis (PPH) were tested to explain the colonization pattern. Clustering results showed two highly supported lineages (L1: Okinawa1 and Amami; L2: Australia, Philippines, Taiwan, Southern Ryukyu Islands, and Okinawa2) which are further favored by BFD and the DensiTree results. The genetic differentiation observed in the microgeographic island could be attributed to the observed host dependency where *A. c.f. bonadea* in Amami and Okinawa1 is solely hosted by *Cyrtophora* and *Nephila* spiders respectively. Whereas *A. c.f. bonadea* in L2 is seemingly back to its generalist behavior surviving with different hosts. Overall results supported the PPH where North to South colonization is favored as opposed to studies seen in other vertebrates.

Abstract ID: 2071
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P138

Global phylogeography of a wood decay fungus indicates reinforcement on secondary contact

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Fungi are thought to have high dispersal capacity through the massive number of airborne spores they produce, and many morphospecies of fungi do indeed have wide distributions. However, the biological status of these morphospecies have increasingly been called into question by DNA based surveys which show phylogenetically separated and geographically restricted lineages within them. In many cases, crossing studies have also demonstrated the presence of reproductive barriers within fungal morphospecies. In this study, we use population genomic analyses together with *in vitro* crosses of the widespread wood decay fungus *Trichaptum abietinum* to determine the genetic structure within this morphotaxon and infer the processes that have shaped it. To this end, we have whole genome sequenced 350 *T. abietinum* samples from Asia, Europe and North America. Our phylogeographic analyses show six major lineages, one in Asia, two in Europe, and three in North America. The lineages present in Europe are admixing, whereas our crosses show that the North American lineages are reproductively isolated. In Asia a more complex pattern appears, with partial intersterility between multiple sub-lineages. We apply demographic modelling to test whether secondary contact have happened between lineages during the interglacials. Since reproductive isolation in *T. abietinum* is not correlated with overall genomic divergence and appears in sympatry and parapatry, we propose that reinforcement was involved in the evolution of the intersterility barriers in North America and Asia.

Abstract ID: 2105
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P139

Historical biogeography of a multi-host parasite (Cestoda: Ligula intestinalis)

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The tapeworm *Ligula intestinalis* s. lat. (Cestoda: Diphyllobothriidea) is a permanent endoparasite demonstrating a complex life cycle. Globally widespread geographical distribution and multi-host spectrum including dozens of fish species deem *L. intestinalis* a promising model for studying both the vicariant and ecological modes of speciation. We obtained mtDNA and genome-wide SNP data by reduced-represented DNA sequencing (ddRADseq) for the total of 139 *Ligula* plerocercoids collected from 18 fish genera across a broad range representing 21 countries. The result of phylogenetic analyses showed only a few dicrepancies between the two datasets. Both datasets strongly supported the existence of 11 lineages, with the deepest divergence at approximately 4.99 - 5.05 Mya. The result of historical biogeography analyses revealed that the ancestor of the parasite diversified by multiple vicariance events and was widespread through the Palearctic, Afrotropical, and Nearctic between the late Miocene and early Pliocene. All these lineages were either allopatric or parapatric and showed high pairwise FST values, but some also displayed varied levels of historical gene flow. Phylogeographical patterns and migration events among the geographically defined lineages supported our hypothesis of historical isolation in multiple fish hosts. A series of biogeographic and host-parasite events explain the divergence patterns observed, in which speciation and colonization via host-switching and vicariant plus dispersal events happened at different times during the diversification history of both associates, particularly during the Pleistocene. Phylogeographic inference will provide a backbone for testing the hypothesis of a local ecological speciation in several areas of distribution.

Abstract ID: 2120
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P140

Herbarium DNA traces *Phytophthora infestans* strain that caused Irish Famine into 20th-century Europe

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Plant pathogens infecting crops and food plants cause high economic losses and health-related risks. *Phytophthora infestans*, an oomycete that induces late blight on potato and tomato, was introduced to Europe in the 1840s and left a devastating impact as the

causative agent of the Irish Potato Famine soon after. Previous analyses of historical *P. infestans* DNA from 19th-century herbarium records identified HERB-1 as the lineage responsible for the famine. HERB-1 was believed to have been globally replaced by other lineages by the beginning of the 20th century. However, a recent study identified samples belonging to HERB-1 in modern populations from Mexico and South America. This observation raises the question if HERB-1 indeed went fully extinct in Europe. To address this question, we extracted *P. infestans* DNA from seven herbarium specimens of potato collected in Europe across the 20th century. We sequenced two full mitochondrial genomes at 35- and 37-fold mean coverage. Phylogenetic analyses of sequence data from our samples and previously published historical and modern samples revealed that HERB-1 still existed in a potato specimen collected in Switzerland in 1987. Our results thus challenge the belief that HERB-1 went extinct after the 19th-century famine and demonstrate the value of herbarium genomics in informing biogeographic analyses.

Abstract ID: 2152
Poster board number:
P141

Biogeographic history and patterns of gene flow within the Natterer's bats in the Caucasus

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Pleistocene climatic fluctuations greatly affected the distribution and the population divergence of many taxa. During this period, populations were separated and came into contact several times and depending on their level of divergence the extent of their hybridization varied, which might impede further divergence. Therefore, whether taxa came in contact or not is a major factor in species' demographic histories. In this study we investigate the past and the current distribution ranges of two bat species, *Myotis araxenus* and *M. tschuliensis* in the Caucasus, by combining species distribution modelling (SDM) and whole genome sequencing approaches. Our main aim was to investigate the role and the extent of geographic separation in the evolution of hybridization barriers. We used MaxEnt to reconstruct the past distributional ranges of these species, aiming to identify their past range overlaps. In parallel, we used genome-wide SNP data to investigate the levels of the current and the past gene flow between these taxa. We found evidence for rare recent gene flow between these taxa. This suggests that rather effective hybridization barriers have evolved between them. In a next step, coalescent approximations will be applied to evaluate patterns of historic gene flow.

Abstract ID: 2195
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P142

Gene flow in a secondary contact zone of two bat species within the *Myotis nattereri* species complex

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Climatic change has a major impact on the spatial distribution and demographic history of taxa and is therefore a major driver of biological diversification. Populations may become isolated, for example in different glacial refugia, where they evolve independently during periods with unfavorable climatic conditions and may come into secondary contact following range expansion. Investigating contact zones of genetically diverse populations can provide insights for understanding the underlying mechanisms of population divergence, persistence and speciation. In this study, we describe the spatial extent of a hybrid zone and quantify population dynamics between two genetically distinct lineages within the Myotis nattereri species complex. We sampled bats throughout the contact zone and have collected 62 samples from 46 locations across Central and southeastern Europe. Using whole-genome resequencing and a suite of demographic methods, we demonstrate that the degree of admixture varied largely among individuals along a geographic gradient suggesting a lack of intrinsic reproductive barriers. However, notwithstanding the observation of admixed individuals and their dispersive nature, the two lineages still remain highly structured. Overall, we demonstrate how a whole-genome view on the spatial distribution of evolutionary lineages can inform our understanding how biogeography and demography contribute to macroevolutionary change in a well-known European mammal.

Abstract ID: 2200
Poster board number:
P143

Demographic inference of multiple population pairs across the European ranges of two species

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Divergence between species is the product of biogeographic and evolutionary processes. The divergence history is usually inferred with demographic modelling by analysing genomic data from single populations from each species. However, this approach fails to account for spatial dynamics and species interactions. Here, we tested if divergence histories vary depending on geography, using the wood ant species *Formica polyctena* and *F. aquilonia*. We performed whole-genome resequencing of 20 individuals sampled in multiple locations across the European ranges of both species. Then, we reconstructed the histories of distinct heterospecific population pairs using a coalescent-based approach. Our analyses always supported a scenario of divergence with gene flow, suggesting that divergence started in the Pleistocene (ca. 500 kya) and occurred with continuous asymmetrical gene flow from *F. aquilonia* to *F. polyctena* until a recent time, when migration became negligible (2-19 kya). However, we found support for contemporary bidirectional gene flow in a sympatric pair from Finland, where the species hybridise, but no significant contemporary gene flow elsewhere. Our sampling scheme and multiple comparisons approach provided insight into how biogeography can impact contemporary demographic estimates, including effective

population sizes and gene flow. Notably, these inferred differences in recent population sizes and local gene flow between populations may have consequences for the survival and adaptive potential of these populations in the future. This may be informative of how these species may adapt to environmental change. Overall, our approach highlights the impact of spatial dynamics on evolution, particularly the interaction between species via migration.

Abstract ID: 2241
Poster board number:
P144

Genomic Assessment of Scots Pine Expansion in Europe

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Pinus sylvestris (Scots pine) is the most widespread conifer species in Europe, extending latitudinally from southern Spain to northern Finland, and spanning Eurasia longitudinally. During the Last Glacial Maximum, however, the distribution of *P. sylvestris* in Europe was contained in glacial refugia present in southern Europe, in the Iberian, Italian and Balkan peninsulas. The populations in these glacial refugia have played a key role during the following northward expansion of *P. sylvestris*, but their nucleotide diversity has been less studied than in other areas. To understand how glacial refugia may have shaped current genetic diversity of *P. sylvestris* in Europe, we collected genomic data for 20 populations sampled across the continent: from its main glacial refugia in the South to the northernmost parts of its range. Nucleotide diversity using 32k SNPs from exome capture showed low levels of differentiation. We further modeled several hypotheses relative to the northward expansion that could explain the current patterns of genetic diversity by estimating the relative contribution to northern diversity from southern European populations, specifically using rare variants. A better assessment of the recent history of *P. sylvestris* in Europe will provide a valuable resource for improved conservation and breeding plans.

Abstract ID: 2271
Poster board number:
P145

Characterization of molecular diversity of spring fen zoobenthos from two geomorphological regions

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Recent studies on diversity of stream amphipods indicated that the Western Carpathians may have served as an important glacial refugium of freshwater fauna. If this scenario is true, a considerably high molecular diversity can be expected in this biogeographic region also for other aquatic taxa. In our project, we aim to uncover and characterize molecular diversity of benthic macroinvertebrate fauna of calcareous spring fens (a well-studied and hence convenient model community) of the Western Carpathians and for comparison also of the Bohemian Massif, an adjacent region with different geological history. Using a DNA metabarcoding approach, we sequenced a fragment of the COI gene of pooled spring fen invertebrate communities from 21 localities in the Western Carpathians and 8 localities from Bohemian Massif. Here the up-to-date insights about the comparison of molecular diversity of the same habitats in these two areas with different geological histories will be presented. We observed a considerable lack of reference sequences in public databases (Barcoding of Life Database, GenBank) for a large portion of the detected molecular operational taxonomic units (MOTUs), indicating that the studied regions are not yet sufficiently covered by barcoding efforts, and/or suggesting that there indeed may be a considerable unrecognized diversity of macrozoobenthos. We also aim to compare the MOTU diversity with the morphological diversity, already well studied in most of the localities, and to try to detect the spatial variation in changes of molecular/morphological diversities.

Abstract ID: 2374
Poster board number:
P146

Asymmetric lability in habitat shifts underlies the evolution of savanna Miombo trees in Africa

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The Guineo-Congolian region in Africa constitutes the second largest area of tropical rainforest (TRF) in the world. It covered an estimated 15-22 million km^2 during the late Miocene (55-11 Ma) and it has experienced since a declining trend, currently reaching 3.4 million km^2. The overall contraction in TRF area over time is associated to increasing aridification and the replacement of TRF by savanna habitats (e.g., miombo). Here we aim to examine whether rainforest area contraction led to a decrease in net diversification rates linked to increasing extinction, or if it is associated to increasing opportunities for allopatric or ecological speciation during periods of forest fragmentation.

We used a target enrichment approach combined with a complete data set representing all 16 genera within the Berlinia clade (75% species) combined with niche modelling of habitat types. We recovered fully resolved and well supported relationships. Most genera (87.5%) diverged before the Pleistocene and we inferred seven independent shifts to savanna, but with an asymmetric distribution, suggesting a degree of lability to shift habitat in some genera. This indicates the Berlinia clade displays an overall trend of accumulation of species over evolutionary time, suggesting the reduction of TRF area has not decreased net diversification rates. Most habitat shifts to savanna occurred in the Miocene, with no major habitat shifts during the most recent phases of forest expansion-contraction in the Pleistocene. Shifts in habitat from lowland forest to savanna did not trigger diversification rates, but habitat fragmentation might have increased diversification rates through allopatric speciation

Abstract ID: 2380
Poster board number:
P147

Targeted metabarcoding reveals new diversity in marine Myxozoa

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Myxozoa is a unique lineage of highly reduced endoparasitic cnidarians with a complex life cycle. Their intermediate hosts are mostly fish, in which they can cause disease and high mortality. The diversity of Myxozoa is not well known and several new species are being discovered every year. The aim of the current study was to develop a metabarcoding assay targeting Myxozoa and to use DNA extracted from environmental samples to estimate the total diversity of marine Myxozoa.
Water and sediment samples were collected from 54 locations in seven ecoregions across the Atlantic from the temperate South American coast to the arctic Svalbard archipelago. At least 77 OTUs were identified of which few correspond to known species while several are distinct and appear to form independent lineages. In some locations traditional fish screenings were conducted alongside the environmental sampling. Of the 14 species identified during molecular fish screening only three were detected in eDNA samples. This indicates high patchiness and quick dilution of myxozoan spores in the water, or a high detection threshold of the assay.
Our metabarcoding assay revealed a higher diversity of Myxozoa than traditional fish dissections. It is less time and labour intensive and reduces the sacrifice of fish. It is a viable tool for identifying myxozoan diversity especially in yet unstudied areas and can be used for monitoring. Furthermore, it can be used to indicate season and potential host groups for targeted taxonomic surveys leading to the still imperative formal description of new species.

Abstract ID: 2397
Poster board number:
P148

The biogeographic history of the Ethiopian highland Ptychadena

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The Ethiopian highlands grass frogs from the genus *Ptychadena* (Anura: Ptychadenidae) form a monophyletic clade with 12 known species. These species can occur at elevations above 3000 meters and constitute excellent models to study diversification and adaptations to high altitudes. In this study, we sampled around 300 specimens across the broad distribution of this clade and used complete mitogenomes and genome-wide SNP data, associated with phylogenetic analyses, ecological modeling, and biogeographic reconstructions to reconstruct the spatial and temporal history of the species. The analyses allowed a more complete understanding of the contributions of climatic and geological events, as well as eco-physiological dimensions, as drivers of species diversification and adaptation. We also project the species complex climatic niche to the future to investigate evolutionary consequences of distributional shifts and discuss its conservation under a global climate change scenario.

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Poster board number:
P149

Biogeographic affinities of terrestrial invertebrates among Juan Fernández and Desventuradas Islands

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Islands are hotspots of biodiversity and extinction. The Desventuradas Islands, comprised of San Félix and San Ambrosio, are a volcanic archipelago 850 km off the coast of Chile. They are key to understanding the diversification processes which shaped the flora and fauna of other Chilean oceanic islands such as the Juan Fernández Archipelago. But, the biogeographic affinities between these archipelagos are still poorly known. Over the last century, the plant and animal communities present in the Desventuradas have radically changed due to invasive mammal introductions. Here, focusing on terrestrial invertebrates, we: (1) confirm the presence of described endemic species, (2) detect new species records and (3) assess the biogeographic affinities between the Juan Fernández and Desventuradas archipelagos. In September 2018, San Ambrosio was surveyed using different methods. A total of 35 morphospecies were collected. Four endemic species were found, in addition to several previously described higher taxonomic groups with undescribed species. Other nine previously described endemic species were not detected. There was a total of 28 new records, including a new land snail, a new Isopoda and representatives of five spider families. Twelve of all the recorded genera from Desventuradas Islands have known relatives in the Juan Fernández Archipelago. Five of them were not previously known for San Ambrosio, reinforcing the biogeographic affinities between both archipelagos. This research highlights the urgency of surveying islands subject to a multitude of threats, including climate change and invasive species, to generate baseline data and place the island's fauna in a broader biogeographical context.

Symposium: S09. Parallel and repeated evolution in adaptive radiation (id: 16)

Abstract ID: 1133
Poster board number:
P150

How is evolvability affected by niche shifts?

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Understanding the evolutionary potential of populations is key to predicting their ability to cope with changes to their environments, more relevant than ever in a changing climate. A pressing question is to which extent consistent directional selection depletes the variation available to selection, reducing the evolutionary potential. One way to address this question is to leverage niche shifts, exerting known selective pressures and asking how directional selection during adaptation to the new niche affects evolutionary potential. Here, we assess the effect of niche shifts on evolvability in the ancestral and derived host race of the peacock fly *Tephritis conura*. Whereas the ancestral host race likely has experienced stabilizing selection, there has been directional selection favoring a shorter ovipositor length, a later phenology and an ability to process plant tissue from a different host plant in the derived host race. We find that evolvability is lower in the novel host race when compared to the ancestral host race. **P,** when compared between host races largely retains its shape, but the derived host race has a smaller **P**. We also ask if the evolvability is reduced when conditioned on the ovipositor, known to have been under directional selection. Surprisingly, we find that the ovipositor is more autonomous than the other morphological traits measured. This could suggest that the sexually dimorphic ovipositor is more modular. Finally, we find a correlation between evolvability and divergence between populations, suggesting that the variation along the major axes of variation is important for overall evolutionary potential.

Abstract ID: 1197
Poster board number:
P151

Seasonal environments drive convergence in life-history traits across butterfly adaptive radiations

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Earth has repeatedly witnessed climate change events throughout its history that have caused mass extinctions but also resulted in the emergence of novel niches. The global expansion of savannah grasslands during the Miocene (23-5 MYA) is one such dramatic example of climate-driven biome evolution. Colonization of savannahs from ancestral forests has resulted in explosive diversification across the tree of life. However, what adaptations were required to colonize such a harsh environment? An important question but remains underexplored. I use parallel radiations of Mycalesina butterflies from mainland Africa, Asia, and Madagascar, comprising ~310 species to address this

question. Firstly, ancestral state reconstruction using global Mcalesina phylogeny revealed that early forest-linked lineages began invading savannahs around 10-3 MYA. Secondly, focussing on the African radiation, I show that the timing of the evolution of reproductive diapause, a key strategy allowing the temporal escape of the dry season, matches with forest to savannah shifts, and the capacity to undergo reproductive diapause evolved in a habitat-dependent manner. Finally, by rearing replicate pairs of forest and savannah species from the African and Malagasy radiation in a common garden environment and utilizing published data on species from the Asian radiation, I show that savannah species consistently adopt a 'fast strategy' having higher growth rates, higher fecundity, and shorter lifespan compared to forest species across all radiations. These findings demonstrate that adaptations in a suite of life-history traits were crucial in allowing Mycalesina butterflies to colonize and persist in savannahs and may eventually have triggered rapid diversification.

Abstract ID: 1546
Poster board number:
P152

Multiple independent transitions to cave life and molecular diversity in olms (*Proteus anguinus*)

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Convergent evolution is a hallmark of species that transitioned from surface to life underground. The high degree of phenotypic convergence among subterranean species can obfuscate the true number of independent transitions, especially in the absence of close relatives still living on the surface. The olm, *Proteus anguinus*, is a depigmented, eyeless cave salamander that was believed to be a single species distributed along the Dinaric Karst until recently. It was the first subterranean organism scientificall described, and famously featured in Darwin's 'On the origin the species' on character loss. In the mid 90s, an unexpected discovery was made: a population of pigmented olms with distinct eyes. Interestingly, mitochondrial genetic data suggested that these darker olms were nested within lineages of geographically closely distributed depigmented olms. Here, we present a combination of genome-wide SNP data and large-scale mtDNA sampling showing that olms can be distinguished into nine well-differentited genetic lineages. These lineages separated 4–17 mya, and can be considered as distinct species based on species delimitation results. The lineages show no signal of recent admixture and very limited amount of historical gene flow. Biogeographically, the contemporaneous distribution of lineages mirrors hydrologically separated subterranean environments, while the historical separation of olm lineages follows micro-tectonic and climatic changes in the area. The reconstructed phylogeny suggests four independent transitions to the cave phenotype, or alternatively a single transition and one reversal to the surface phenotype. This opens the possibility for future research on the comparative genomics of convergent transitions from surface to caves.

Abstract ID: 1559
Poster board number:
P153

Diversification of a group of songbirds with pervasive phenotypic parallelism

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The independent evolution of similar phenotypes in species that are not each other's closest relatives - phenotypic parallelism - can provide evidence of similar evolutionary solutions to environmental challenges. However, insights into the processes underpinning phenotypic parallelism are still limited. Analyses of genome-wide data help uncover whether phenotypic parallelism occurs mainly through independent mutations and/or incomplete lineage sorting (ILS) of ancestral variation and introgression. Here, we took a phylogenomic approach in wheatears (genus *Oenanthe*), a group of songbirds thought to display pervasive phenotypic parallelism, to corroborate the abundant of phenotypic parallelism by reconstructing the species tree and indirectly infer based on gene tree heterogeneity whether ILS and/or introgression may have contributed to phenotypic parallelism. To this end, we reconstructed the species tree of 50 taxa of wheatears and related genera and estimated gene tree heterogeneity. The species tree provides evidence for the high incidence of phenotypic parallelism in wheatears. We uncover a high prevalence of gene tree heterogeneity that arose from both ILS and introgression. For branches with high gene tree heterogeneity, which are strongest in three wheatear complexes, ILS alone did not adequately explain gene tree heterogeneity. Our results support the role of introgression in these three complexes. The levels of ILS and hybridization in major clade of wheatear diverged around five mya are rather low. The indirect evidence gained from the structure of the species tree and inferred levels of ILS and introgression suggest that the evolution of phenotypic parallelism in wheatears likely included all three possible processes.

Abstract ID: 1600
Poster board number:
P154

Arctic charr in Thingvallatn: a miniature natural laboratory to study repeated evolution

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Parallel divergence along benthic-limnetic ecological axis (feeding on the bottom and in a water column) often occur in freshwater fish. The Arctic charr in lake Thingvallavatn, Iceland, is a textbook example of such diversification, where after colonising the lake some 12 000 years ago, the common ancestor diverged repeatedly in morphology, prey, and habitat use resulting in two benthic (a small and a large) and two limnetic (a small planktivorous and a large piscivorous) morphs. Here we use the Arctic charr system in lake Thingvallavatn as a miniature natural laboratory to address questions on the genomic bases of parallel morphological divergence along benthic-limnetic ecological axis. Although the four morphs represent the classic trophic morphologies associated with benthic and limnetic feeding, their evolutionary origins appear to be complex. Our reduced representation genome sequencing data pointed towards three clear genetic clusters within the lake: the small and large benthic and the planktivorous charr. Our results further indicate that all morphs except for the piscivorous diverged rapidly, shortly after the colonisation of the lake and likely in a scenario of micro-allopatry. The heterogeneous introgression patterns of the piscivorous morph point towards a more

recent divergence and suggest that this morph may be the result of an ontogenetic shift from its limnetic counterpart and/or adaptive hybridisation between the planktivorous and the large benthic. We are currently investigating the genomic basis of benthic-limnetic morphological traits within the lake by using two complementary techniques: QTL mapping and Genome Wide Association Studies (GWAS).

Abstract ID: 1639
Poster board number:
P155

Probabilistic Modeling of Bursts and Gradual Changes of Diversification Rates in Bird Evolution

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Evolutionary biologists have long been searching dated phylogenetic trees for evidence of sudden changes in diversification rates, such as episodes of rapid speciation associated with adaptive radiations. Recent studies have pointed out that small, gradual shifts in diversification rates also occur, and that such gradual processes may explain the observed patterns better than abrupt events. While it is likely that both types of changes in diversification rates occur, whether it is possible to identify sudden shifts against a background of small gradual effects remains an open question. The slow progress in this field is partly explained by limitations in the traditional modeling and inference tools used in phylogenetics. To address these questions, in a recent paper we have shown that universal probabilistic programming offers a powerful and flexible framework for implementing and comparing evolutionary models. Here, using this approach we implemented a new integrated model, including regimes of sudden shifts, gradual shifts, or their combination. The gradual regime, in particular, can associate diversification rate changes with lineage-split events (cladogenetic shifts) or during the intervening intervals (anagenetic shifts). Using an estimated time-tree for all birds, we analyze whether it is possible to identify episodes of sudden, lineage-specific changes in diversification rates while simultaneously controlling for gradual shifts. We also compare the cladogenetic and anagenetic gradual-shift regimes, and whether they can be disentangled. Thus, thanks to probabilistic programming, we created a flexible model that integrates two long-standing views of diversification—*gradual* versus *pulsed*—and argue for its further use in phylogenetics.

Abstract ID: 1863
Poster board number:
P156

Determinism and contingency in the genetic basis of parallel armor plate evolution of sticklebacks

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How predictable is the genetic basis of parallel evolution? Parallel evolution can be caused by mutations at different genes, different mutations at the same gene, or repeated fixation of the same alleles. It remains elusive what deterministic and stochastic factors determine the molecular genetic basis of parallel evolution. Armor plate evolution in sticklebacks is among the most well-known examples of parallel evolution. Repeated plate reduction in several freshwater populations of the three-spined stickleback (*Gasterosteus aculeatus*) in North America and Europe is caused by the repeated use of the same *Ectodysplasin-A* (*Eda*) allele. In contrast, we recently found that independent mutations at both *Eda* and its receptor, *Edar*, caused plate reduction in a Japanese freshwater population. Additionally, we found that plate reduction in *Pungitius sinensis* was caused by independent mutations at *Edar*. Multiple *Pungitius* species share the same alleles likely due to the ancestral polymorphism. Overall, these results demonstrate that *Eda* and *Edar* are hotspot genes for plate reduction. Knock-out experiments of *Eda* and *Edar* showed similar pleiotropic effects, suggesting that stochastic mutation orders may have determined which gene is used for plate reduction in each system. However, we found that different alleles have different effects. Although the low *Eda* allele in North America and Europe is linked with other freshwater-adaptive mutations, making them supergenes, both the Japanese low *Eda* and *Edar* alleles showed little evidence for linkage with other traits. This difference is likely due to the difference in gene flow rates between freshwater and marine environments between geographical regions.

Abstract ID: 1876
Poster board number:
P157

Cave dwelling *Physella* sp. as a model system for studying the loss of pigmentation

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Not much is known about the mechanisms by which species adapt to the peculiar conditions inside of caves. One way of elucidating their adaptative evolution is through

comparative studies, which require finding good model systems that consist of both ancestral and derived forms. The freshwater gastropod *Physella* sp. from Folgelpole Cave, Illinois, USA appears in different phenotypes, ranging from fully pigmented to albino morphs. Hence, it could be a suitable system for studying molecular mechanisms behind the loss of pigmentation, one of the most common traits in cave animals. Using a melanogenic substrate assay we identified that the first step of the melanin synthesis pathway is disrupted in the albino cave morph. To understand the evolutionary underpinnings of the loss of pigmentation, potential pleiotropic effects of melanin production cessation were experimentally examined. We showed that albino snails had significantly higher resistance to anesthesia (AR), controlled by the noradrenergic system, compared to fully pigmented morphs. These results are consistent with the study on *Astyanax mexicanus*, where albino cavefish have higher AR due to shifting a common precursor, L-tyrosine, from melanin to the catecholamine biosynthesis pathway. Anesthesia resistance can be considered a measure of consciousness and alertness, beneficial traits in cave environment, where food and mates are scarce and visual sensation useless. Although the exact molecular cause of albinism in *Physella* has yet to be elucidated, higher AR suggests that the loss of melanin pigmentation could be beneficial for cave invertebrates in the same manner as for vertebrates.

Abstract ID: 1909
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P158

Flying, mating and escaping: diversification of wing shape in *Papilionidae* butterflies

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The diversification of *Papilionidae* butterflies is associated with a striking variation in wing size and shapes. In particular, hindwing tails have evolved multiple times independently. However, the developmental and selective processes involved in the emergence of this conspicuous hindwing variation are largely unknown. Similarly, questions as simple as "*when and exactly how many times did the tail appear?*" are still unanswered today.
Using the collections of the National Museum of Natural History from Paris, we estimated worldwide variations in wing shape and size in Papilionidae, by precisely phenotyping more than 1200 butterflies, from 337 species. Using the well resolved phylogeny of this clade, we used geometric morphometrics and comparative approaches to reconstruct the history of phenotypic diversification. For the very first time, we have taken into account the whole architecture of the wings, not just their outline. By comparing forewing and hindwing shape variation within and among species we aimed at identifying the major evolutionary factors shaping the diversification of these phenotypes. Given the prominent role of forewings in flight performance, we hypothesise that selection on flight behaviour might limit forewing shape variation, while such pressure is likely relaxed on hindwings. We specifically compare forewing and hindwing evolutionary rates, and test for correlation with species diversification in different geographic areas. We finally test for the putative role of natural and sexual selection on the diversification of the wings, specifically focusing on the effect of wing shape variation on flight performance and predator deflection.

Abstract ID: 2136

Poster board number:
P159

Convergence for high trophic position drives functional disparity in crustacean radiation

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The evolution of functional diversity was conceptualized on the premise that traits are hierarchically organized into performance traits and subordinate functional traits. Natural selection acting on the performance traits inevitably affects the subordinate functional traits. Tradeoffs occur when the environment constrains the evolution of underlying functional traits or when the same functional trait builds different performance traits. The tradeoffs can be mitigated when the functional traits integrate into a performance trait through alternative combination, i.e., many-to-one mapping. In such cases, the performance traits that converge in different ecological contexts may drive divergence in the functional traits. We tested this hypothesis in the subterranean amphipod *Niphargus*. *Niphargus* species live in all subterranean aquatic habitats, where they occupy different trophic positions. We assembled a dataset of 40 species from interstitial, 56 species from cave lakes, and 88 from cave streams. Functional and performance traits were inferred from morphology. We hypothesized that the performance trait "trophic position" depends on species agility. Agility depends on two subordinate performance traits, "locomotion speed" and "body shape", calculated from four and five functional traits, respectively. Indeed, "trophic position" positively correlated with "locomotion speed" in all ecological categories. In contrast, correlations between "trophic position" and "body shape" were positive in cave streams, negative in interstitial, and nonsignificant in cave lakes, because stout body enhances swimming in open water but constrains crawling in interstitial. The functional trait space occupied by the three ecological categories only minimally overlapped, suggesting that functional traits diverged when species converged toward higher trophic position.

Abstract ID: 2171
Poster board number:
P161

Unravelling the hidden genetics of Wrinkly Spreaders

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Cooperative behaviors are costly to individual entities but deliver collective-level benefits. An example is mat-formation at the air-liquid interface (ALI) by mutants of the bacterium *Pseudomonas fluorescens* SBW25. The mutants, referred to as "wrinkly spreader" (WS) types, over-produce an acetylated cellulosic polymer. Polymer-over-production is costly to individual cells, but WS mutants are favoured by selection because of benefits (access to oxygen) that accrue to the group of WS cells that together

form the mat. Although much is known about the genetic bases WS mutants, a recent RNA-seq study has revealed a range of previously unknown loci implicated in WS mat-formation. Our goal is to determine whether these loci contribute to colonization of the ALI. And to understand why, despite years of study, these loci have, until now, escaped detection. To this end, we deleted from ancestral SBW25 and from a single WS genotype eight candidate loci, including two operons: a fap operon (PFLU_2696-2701) and a candidate usher operon (PFLU_3900-3906). Gene inactivation did not bring about significant alterations to colony morphology or fitness, thus explaining why the newly identified loci escaped prior detection. Nonetheless, our results indicate that some of the new loci do play minor roles during early stages of mat formation. Much remains to be discovered, but our results thus far indicate that the WS phenotype is far more complex than previously recognized.

Abstract ID: 2193
Poster board number:
P162

The predictable sequence of adaptive radiation in subterranean amphipods

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Adaptive radiation (AR) is an evolutionary phenomenon in which an ancestral species colonizes adaptive zones, free of predators and rich in underexploited resources, and subsequently rapidly diversifies into many ecologically differentiated species. The initial high rates of speciation and diversification may slow down as ecological niches fill up. Theoretically, ecological diversification within AR unfolds predictably, with emerging species initially partitioning among habitats, while diversification in trophic niches within habitats continues longer. We tested this hypothesis using AR of the subterranean amphipod genus *Niphargus*. The genus radiated in southeastern Europe 20–15 Mya, in a series of regional ARs that assembled into one massive AR. Multiple ARs within a single lineage are an excellent model system to test the hypothesis of sequential diversification events. Using functional morphological traits as surrogates for habitat and trophic components of ecological niches, we analysed the sequence of diversification of niche traits over time. We performed analyses at two levels of AR: at the entire genus and on four speciose clades, respectively. Two of these clades diversified predominantly in karst areas with high habitat diversity, while the other two clades diversified in the interstitial with low habitat diversity. Genus-wide analysis indeed suggested that diversification of traits related to habitat concentrated earlier than diversification of traits related to trophic niche. However, at the clade level, sequential ecological diversification was only recovered in two karstic clades, but not in interstitial ones. We conclude that sequential ecological diversification is predictable but habitat-dependent.

Abstract ID: 2392
Poster board number:
P163

What underlies gene reuse in adaptation?

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Is evolution predictable? Convergent adaptations enable us to study the factors increasing evolutionary constraints or reducing the available variation. Here I will use this idea and propose a functional genetics experiment in which I am currently testing the effect of pleiotropy constraints on gene reuse in a case of repeated adaptation. Our model consists of repeated and independent colonization events towards the alpine environment of *Arabidopsis arenosa*. Using selection scans and functional annotation of candidate genes, I selected three, FAR5, MAP18 and PAP1, for a functional follow-up study. I will test the effect of candidate alpine alleles on the fitness of plants by crossing and transplantation experiments. I will take the advantage of incomplete fixation of candidate alleles in an alpine environment and prepare alpine plants homozygous for alpine allele and others for foothill allele and the same scheme for foothill plants. All these plants will be subsequently planted in the alpine and foothill environments and manifestations feasibly affected by the particular genes will be measured. The success of a foothill plant with an alpine allele in the foothill environment will inform us about the deleterious pleiotropic effects because these persist when the benefit that the allele provides in the alpine environment disappears. From the results I want to establish why these genes have been reused. In total, my study should contribute to the knowledge of the effect of pleiotropy constraints on the repeatedly selected genes.

Abstract ID: 2402
Poster board number:
P164

Repeated evolved dwarfism in Arctic charr: patterns of shared and distinct differentiation

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Identifying shared genetic and genomic signals of parallel evolved phenotypic traits is a challenging task. Even if selection pressures are similar under repeated abiotic conditions, variations in genomic backgrounds, demographic history or evolutionary dynamics are expected to generate heterogeneous associations. The extent to which adaptive radiation can be achieved by parallelism is of substantial interest. Adult dwarfism in Icelandic Arctic charr (*Salvelinus alpinus*) has occurred consistently and offers an ideal system to study parallel evolution on different levels and scales. Here we use genomic and morphological data from 25 dwarf populations, and 5 anadromous and 5 generalist resident charr populations as references to investigate the degree of parallelism on both the genotype and phenotype of dwarfism. Analyses of 7,576 single nucleotide polymorphisms (SNPs) generated by ddRADSeq approach confirmed that

dwarf charr populations have evolved multiple times independently in Iceland. Overall, genetic differentiation was lower between dwarf populations and reference populations from the same region than between dwarf populations across different regions. Within geographic regions, dwarf populations in parapatry and sympatry were less differentiated from their corresponding reference population than allopatric populations. Headwater dwarf populations tended to have lower heterozygosity and higher inbreeding than coastal dwarf populations. We will further identify regions of the genome that are associated with divergence between dwarfs and their reference populations, and use geometric morphometrics to compare the head shape of different dwarf populations and search for associations between abiotic factors such as habitat type (e.g. lava spring-fed stream and pond) and phenotypic parallelism.

Symposium: S10. Eco-evolutionary dynamics in changing environments: insights from models, experiments and case studies (id: 961)

Abstract ID: 1055
Poster board number:
P165

Individual variation in a parasite-host system: performance, heritability, and host quality

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Parasite-host systems are characterized by dynamic interactions favouring the evolution of reciprocal adaptations and counter-adaptations. Knowledge on parasite intraspecific variation and trait evolutionary potential, genetic and phenotypic covariance between traits across life stages, and on the intraspecific variation in host characteristics (host quality) is fundamental but lacking. Ticks are ectoparasites where these traits can be investigated. We collected a wild population of tree-hole ticks (*Ixodes arboricola*) and raised two consecutive generations in semi-natural conditions. Ticks were fed on wild great tits (*Parus major*) and individually followed. For larva, nymph, and adult stages we measured performance (e.g. attachment, feeding, moulting, survival, and hatching success) as well as life-history traits (e.g. feeding time, engorgement weight, moulting time, and clutch size). Furthermore, we investigated individual variation and heritability of host quality through tick variation. Heritability estimates of tick life-history traits were generally higher in nymphs than in larvae. Our findings suggest that variation in tick fitness is shaped by variation in tick quality, for which engorgement weight is a good proxy, rather than by life-history trade-offs. As regards host quality, the significant correlation in attachment success between larvae and nymphs on the same host suggests consistent among-host variation for this performance measure. Also, we found a strong heritability for host quality as measured through tick feeding time. Feeding success and survival of larvae was lower on female birds, and nymphal survival was higher on older birds. Our results highlight the importance of individual-based studies in the evolutionary ecology of both hosts and parasites.

Abstract ID: 1158
Poster board number:
P166

Habitat connectivity prevents population structure in a commercially important fish (*Lutjanus jocu*)

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Temporal changes in habitat connectivity affect species distribution, and thus divergence between populations and current patterns of genetic diversity. In the marine environment, species requiring near-shore habitats are among the most sensitive to climate change and are the most exploited by fisheries. Thus, understanding how historical environmental change affect species evolution can potentially assist in adapting current management plans and predicting the impacts due to climate change. We modelled the contemporary distribution of *Lutjanus jocu* (Dog Snapper) and its distribution during the last glacial cycle to understand how natural climatic cycles condition its demographic history and current genetic population structure. During the last glacial maximum, highly suitable habitat was disconnected by regions of lower habitat quality, contrasting with present day habitat suitability that is largely continuous. Thousands of single-nucleotide polymorphisms showed an absence of population structure, consistent with current high habitat connectivity. Coalescence analysis showed that *L. jocu* has experienced a severe bottleneck followed by a recent range expansion, also consistent with our inferred changes in habitat suitability during the recent glacial cycle. Such high genetic connectivity and sensitivity to climate change offers insights into a sustainable management of fisheries, and how this species will react to a changing climate.

Abstract ID: 1291
Poster board number:
P167

Phenotypic robustness differs between queen and worker caste

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The parallels between germline/soma differentiation in multicellular organisms and queen/worker differentiation in social insects were first recognized a century ago (Weismann, 1893). In multicellular organisms, somatic cells have evolved a stunning phenotypic diversity and functional specialization, providing the foundation for complex body plans. Analogously, in social insects the worker caste has evolved remarkably specialized traits and phenotypes, thus allowing for the exploitation of particular ecological niches. Relaxed evolutionary constraints in workers due to indirect selection is

one factor underlying the apparently faster trait evolution in this caste. We hypothesize that reduced phenotypic robustness (i.e. less stringent phenotypic canalization) in workers particularly under aberrant/stressful environmental condition could contribute to the seemingly accelerated trait evolution in this caste. Therefore, we tested whether phenotypic robustness differs between castes by quantifying morphological variation between queens and workers of the ant *Cardiocondyla obscurior* upon pharmacological suppression of HSP90, a central player of the cellular canalization machinery.

Abstract ID: 1340
Poster board number:
P168

The role of niche construction for the adaptability of the red flour beetle, Tribolium castaneum

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Niche construction is an important eco-evolutionary process, where organisms modify their ecological niches by altering the chemical, physical, or biological properties of their environment, which may promote adaptation to changing environments. Niche construction can be particularly relevant for group-living animals that share the same niche, these alterations could influence the level of pathogenic threat that their conspecifics or offspring are exposed to and thus modify the selective environment of both the niche constructors and recipients. Here, to understand the ecological and evolutionary consequences of niche construction, we preformed experimental evolution with red flour beetle (*Tribolium castaneum*) and its natural parasite *Bacillus thuringiensis tenebrionis (Btt)* as a host-parasite model system. Adult red flour beetles modify their environment by releasing quinone-rich secretions which alter their surrounding microflora. We tested the impact of impaired niche construction ability on host adaptation to *Btt* selection by inhibiting the quinone production of beetles via RNAi knockdown. After nine generations of host selection, we found that from the phenotypic readouts, host survival was enhanced in the *Btt*-exposed populations, of which the lines being incubated in conditioned flour had a higher but non-significant advantage when compared to those in non-conditioned flour. Developmental rate difference was only seen between the *Btt*-exposed and control lines exposed to the flour from quinone-less beetles. No differences were observed in fertility and quinone production among all treatments. This work provides urgently needed but rare empirical evidence on the role of niche construction for adaptation.

Abstract ID: 1385
Poster board number:
P169

Do ectotherms adjust their thermal preferences in an urban heat island context?

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Cities are ideal natural laboratories to investigate the response of organisms to rapid global change. A range of abiotic conditions along urbanisation gradients can foster wildlife to cope with contrasted environments within narrow geographical areas. Among the major factors induced by urbanisation, temperature is known to profoundly affect ecology by generating urban heat islands (UHI). Because ectotherms have variable body temperature, they are especially sensible to fluctuating environmental temperatures and thus to harsh urban conditions. Yet, they are able to behaviourally thermoregulate. Mobility is therefore a key mechanism which can lead to contrasted selection pressures on populations at a city scale. In our study, we intend to determine if preferred temperatures differ in populations of two common arthropods collected in contrasting thermal zones: a Lycosid spider (*Pardosa saltans*) and a terrestrial isopod (*Oniscus asellus*). To measure thermal preferences, we used an experimental set up enabling to track the position of individuals along a thermal gradient. This contribution aims to present our results and to answer if mechanisms occur in ectotherm populations, allowing them to cope with altered thermal conditions due to urbanisation, an accelerating global trend.

Abstract ID: 1483
Poster board number:
P170

Eco-evolutionary dynamics of host-parasite systems in complex landscapes

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Global anthropogenic change causes disturbances to natural host-parasite systems leading, for example, to the phenomenon of emerging infectious diseases. Particularly, human disturbances such as habitat fragmentation or the rewiring of dispersal networks can change the spatial context of natural host-parasite systems. Therefore, understanding the eco-evolutionary dynamics of spatially explicit host-parasite systems is critical to global change research. While previous studies have addressed how parasite virulence and host-parasite ecological dynamics feed back onto each other when there is heterogeneity in host contact or spatial structure, the central role of host dispersal and dispersal evolution has been ignored. However, the concurrent evolution of host dispersal and parasite virulence can potentially be modulated by host spatial structure and further impact the ecological dynamics of disease prevalence or host population densities, forming an eco-evolutionary feedback. Thus, in the present study, we seek to understand how host-parasite systems evolve in complex landscapes. We develop an individual-based model of a spatially structured host-parasite system in which host dispersal and parasite virulence can co-evolve in complex landscapes. We first establish our baseline expectation of how host dispersal evolution impacts optimal virulence for a classical regular grid host spatial structure. We further extend our analysis to realistic landscapes represented by random geometric graphs (RGGs) for terrestrial and optimal channel networks (OCNs) for riverine host-spatial structures. We find that the feedback between landscape structure, dispersal and host-parasite ecological dynamics together determine optimal virulence, generating empirically testable predictions.

Abstract ID: 1487
Poster board number:
P171

Learning to cope: the effect of population bottlenecks in the maintenance of complex adaptations

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Adapting to a challenging environment is key for the survival of endangered populations. Fields like Conservation Genetics or Evolutionary Rescue Theory investigate how populations can cope with bottleneck events and environmental change to adapt. However, virtually all models in this field focus on simple traits. Accordingly, our current understanding of how complex traits involved in adaptation are affected by genetic erosion is poor. Here I studied whether and when a complex adaptation, learning, would evolve in a large population and under what conditions this adaptation would persist when the population is experiencing permanent or cyclic bottlenecks. I used an individual-based model where individuals have a neural network capable of learning. First, I found that learning evolved in regimes of environmental change observed to favour the evolution of phenotypic plasticity in previous models. Secondly, I analysed the effect of a permanent population bottleneck on the evolution and maintenance of evolved learning styles. Only when the population size was greatly reduced, network performance declined markedly, indicating substantial genetic erosion of the networks. The degradation of the learning styles was found to be driven by their environmental robustness. Thirdly, I studied the evolutionary implications of cyclic bottlenecks under different environmental regimes but found no effect on the evolution of learning when comparing to stable populations. In conclusion, populations that have evolved a complex trait like learning can maintain their performance during cyclic bottlenecks, and it may require long and harsh bottlenecks to decrease their performance.

Abstract ID: 1500
Poster board number:
P172

The effects of temporal heterogeneity in genetic covariance

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The way environments change may influence the evolutionary dynamics of a population. Consequently, taxa may adapt to how change happens and not just to the effect of change. Here we suggest that trait covariance can evolve as a result of a correlation in changing phenotypic optima of multiple traits over time.. We use an individual-based birth-death model to run simulation experiments and compare the effects of correlation of selective pressures in the evolution of genetic connectivity. Our results evidence that synchrony of selective pressures on different traits can lead to genetic covariance. We could measure how much of the covariance we observed was due to linkage disequilibrium or pleiotropy. This analysis shows that synchrony of selective pressures can cause changes in the genotype-to-phenotype map. These changes in the genotype-to-phenotype map allowed for significantly different mutational effects on phenotypes of populations exposed to different types of changing environments. Our work provides a

new possible way in which G-matrices evolve and how the environment may play a role in shaping complex genotype-to-phenotype maps.

Abstract ID: 1540
Poster board number:
P173

Lead induces sex and development related differential *Mtn* gene expression in two *Drosophila* species

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Lead is one of the most abundant pollutants extensively used all through human history and, with industrialization and exploitation of its ores, its accumulation in the environment has increased over time. As a non-essential heavy metal with high persistence and toxicity, lead has severely negative effects on all organisms, but the adaptation of populations and species in contaminated environments can be through different responses. Metallothioneins (Mtn) are involved in heavy metal detoxification as metal-binding proteins present in all living species, with six isoforms found in the *Drosophila* genus. It is presumed that some of them have higher specificity for certain metal ions, such as Pb^{2+}, but the question arises if there is a specific response related to species, sex and developmental stage. To further corroborate the metallothioneins with an affinity for lead ions, the expression of six *Mtn* genes (*MtnA-F*) was quantified by RT-qPCR in larvae and adult female and male flies of *D. melanogaster* and *D. subobscura* reared on the standard medium and medium enriched with lead-acetate for thirteen generations and lead bioaccumulation was measured in adult flies. Our experimental design allows for the detection of variation in expression of *Mtn* genes in response to lead exposure between species, sexes and developmental stages. Results also show a correlation between *Mtn* gene expression and measured lead bioaccumulation in adult male and female flies of both species.

Abstract ID: 1604
Poster board number:
P174

The metabolic switch? Linking individual physiology and life-history in the Glanville fritillary

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The idea that individuals have finite resources which must be differentially allocated between physiological processes to maximise fitness outcomes underpins the theory of life-history evolution. Yet, while the concept of resource allocation trade-offs is longstanding, our understanding of how physiological mechanisms may mediate such trade-offs is comparatively lacking. An intriguing line of thought suggests that metabolic energy serves as a currency in trade-offs between costly life processes, such as

reproduction and survival, and shape life-history strategies within and across generations. Here, we investigate resting metabolic rate (RMR) as a potential trigger for increased investment in current reproductive effort in the face of reduced life expectancy from increased environmental stress, in line with the terminal investment hypothesis. (*Melitaea cinxia*), reared under common garden conditions, we test for evidence of a 'metabolic switch' that may inform trade-offs by testing for increased RMR in adult males stressed by warmer nightly temperatures (18°C) – a condition associated with reduced male lifespan but increased reproduction (offspring number), compared to males maintained in control nocturnal conditions (8°C) throughout the mating period. Furthermore, we address whether rapid investment in current reproductive effort via increased offspring number compromises offspring quality (larval development rate, fat deposition), and assess how these trade-offs operate under varying stress exposure (alternating 18° – 8°C nocturnal temperatures). Our results contribute to a more informed understanding of how physiological responses may shape evolutionary theory and a detailed overview on how life-history trade-offs operate under different environmental stress contexts.

Abstract ID: 1674
Poster board number:
P175

Context-dependent tradeoffs and population dynamics across life histories

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Demographic tradeoffs are central to life-history theory and play an important role in driving life-history diversity. They arise from a finite amount of available resources that need to be allocated among different functions by an organism, and this allocation typically depends on the individual and environmental context. Surprisingly, little is known about how context-dependent tradeoffs at the individual level affect population dynamics across different life histories. Here, we develop an individual-based simulation to incorporate environmental context-dependent tradeoffs at the individual level between key demographic rates. We use this model to simulate population dynamics for various life histories across the slow-fast pace of life continuum. We found that the population dynamics of slower life histories are relatively more sensitive to changes in the patterns of context-dependent tradeoff expression, regardless of the tradeoff considered. Additionally, we found that the impact on population dynamics depends on which tradeoff is considered; context dependence in intra-individual and intergenerational tradeoffs had opposite effects on growth rate variability. Our work highlights that the context-dependent expression of different tradeoffs at the among-individual level can influence pace of life, ultimately affecting population dynamics, with within-cohort selection being a key mechanism acting on individual heterogeneity within and covariation among demographic rates.

Abstract ID: 1735
Poster board number:

P176

Fitness consequences of heatwaves in Drosophila melanogaster

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Varying temperatures and their ecological consequences are a major driver of adaptive evolution and generation of biodiversity. However, because of global climate change, temperature fluctuations are becoming more severe and frequent. This includes more widespread, longer, and more intense heatwaves. Such extreme weather events can have damaging effects on organisms and cause species declines, extinctions, or range shifts across ecosystems. Animals such as insects are especially affected because their physiology and metabolism depend directly on the temperature around them. Studies on the consequences of climate change for biodiversity tend to focus on where and how species can survive. However, the persistence of a species depends not only on survival, but also on reproduction. Fertility is often more sensitive to heat stress than survival because gametes can get damaged. Here, I propose an experiment in *Drosophila melanogaster* to assess (i) how heat stress during the developmental and/or adult stage affects male fertility, (ii) how well males recover after such stress. We found interaction of larval and adult heat stress causes significant damage on gametes. This study addresses the genetic variation in the ability of males to cope with different thermal conditions, including its fitness costs and benefits.

Abstract ID: 1827
Poster board number:
P177

Realized niche breadth evolution driven by reproductive interference and resource competition

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Climate change causes distribution changes, leading to secondary contacts among closely related species, which are likely to share similar mating signals and resource requirements. Reproductive interference creates positive frequency dependence, whereas resource competition (if between-species one is weaker than within-species one) creates negative frequency dependence. When both reproductive interference and resource competition act, positive frequency dependence dominates when one or the other species is rare, but negative frequency dependence dominates when the two species are equally abundant; local coexistence can be contingent upon initial conditions. When there is spatial heterogeneity (e.g. multiple host plants of herbivorous insects) and organisms can distinguish habitat types, habitat preferences can evolve so that individuals avoid habitats that are predominantly occupied by the other species. This process involving eco-evolutionary dynamics can lead the two interacting species to show different realized niche breadths. My simulation model shows that asymmetric realized niche breadths can stochastically evolve even when the two species have symmetrical parameter values. Relaxing the assumption of symmetrical parameters can increase the likelihood of the evolution of realized niche breadth difference. These results

cast a doubt on the role of tradeoff in local adaptation in shaping realized niches, with empirical implications.

Abstract ID: 1932
Poster board number:
P178

Phenotypic response of flowering plant to limited access to natural pollinator community

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Plant–pollinator interactions are essential for plant reproductive success and pollinator food supply. However, the current dramatic decline in pollinators threatens the existence of many wild and cultivated flowering plants. Understanding if and how plants respond to changes in their pollinator community therefore is urgent and of fundamental interest. We use an experimental evolution approach to *in situ* track the dynamics of phenotypic and genetic changes in *Brassica rapa* induced by limited access to natural pollinators. Specifically, we implemented the following three treatments over six generations in common garden: i) hand-pollination, ii) full access, and iii) temporally limited access to natural pollinator community. Changes in fitness components (fruit set, seed production, germination rate) and phenotypic traits (flower morphology, volatiles compounds) are tracked, and all populations will be re-sequenced to estimate allele-frequency changes along the genome. Here, we report on the phenotypic response and changes in fitness observed over the first four generations of the experiment. After a strong initial decrease in estimated fitness in the populations subject to the limited-access to pollinators, the total number of seeds and the germination rate increased in the third generation. This early recovery of the plants' reproductive success implies a rapid evolutionary response, most likely from standing genetic variation. While our finding suggest that flowering plants have the potential to adapt rapidly to changes in their pollinator community, future research is needed to confirm the generality of these results.

Abstract ID: 2006
Poster board number:
P179

Rapid seasonal thermal adaptation in Chironomus riparius

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Effects of seasonal or daily temperature variation on fitness and physiology of ectothermic organisms and their ways to cope with such variations have been widely studied. However, the way multi-voltines organisms cope with temperature variations from one generation to the next was, until this point, not well understood. In the context of global climate change, the way those species cope with the seasonal temperature variations provide a good insight on their reaction range in case of exceptional temperature event. To investigate this, a multi-voltine midge *Chironomus riparius* (Meigen, 1803) was used as test species. The possibility of

phenotypical plasticity was tested with a common garden approach. After three generations, significant mortality rate differences led the conclusion that the population responded rapidly to climatic variation via adaptive mechanisms more than via phenotypic plasticity. An Evolve and Resequence (E&R) study was therefore performed to infer *C. riparius* evolutionary potential for rapid thermal adaptation. We exposed populations of C. *riparius* sampled *in naturae* to three temperatures and to cyclic varying temperature for more than two years in parallel to the genomic monitoring of a natural population. Life-cycle fitness tests and genomic analyses revealed strong, genome-wide selective response in all laboratory replicates. This confirmed a selective response to identical selection pressure(s) most likely induces by the laboratory conditions. However significant variations in SNPs frequency were observed following the temperature cycles in laboratory as well as change in haplotypes trajectories following exceptional temperature events *in naturae,* highlighting the evolutionary potential of natural populations.

Abstract ID: 2022
Poster board number:
P180

Allochrony in the Moorish gecko as a behavioral syndrome: an ecological and genetic study

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Personality is a universally recognized concept according to which animals possess defined ethological patterns. Behavioral syndromes represent variants of eco-ethological patterns allowing individuals to access resources in different ways within a population. Eventually, the onset of different behaviors may set reproductive barriers promoting speciation. The research goal is to test possible behavioral syndromes in the Moorish gecko (*Tarentola mauritanica*) by adopting both genetic and ecological approaches. In the study population, individual exhibit phenological divergence in their activity levels, being exclusively diurnal or nocturnal. The genetic structure of the population was assessed by microsatellites. The ecological divergence was estimated by analysing: the ability to mimic the substrate (Background Color Matching), morphology, and phenological pattern, after a six-months captivity period under uniform conditions, when diurnal and nocturnal geckos were kept separated. Diurnal geckos did not differ from nocturnal ones at neutral loci, but phenological difference was significant between the two groups as regards the evening and night hours, thus showing phenology was in some way individually fixed. Diurnal geckos showed greater luminance and lighter saturated colour than nocturnal ones according to BCM. The two groups did not show appreciable differences in color adaptability, suggesting that differences in the absolute values of luminance and saturation are due to the structure of the integument shared by individuals. The results obtained contribute to shed light on the medium-long term consequences of a behavioral syndrome matching clear temporal segregation. The observed divergence between the two groups may relate to micro-evolutionary processes worthy of further deepening.

Abstract ID: 2068
Poster board number:
P181

Genomic insights into the muskox' history of surviving against all odds

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The muskox plays a key role in the Arctic tundra ecosystem by managing the plant communities through grazing and being a prey to predators. The muskox also has close ties to the humans in the region and it has served as an important source of food throughout history, but particularly to some cultures like the Independence I culture people. While the muskox' ability to survive in extreme conditions proved a successful strategy that allowed the species to survive until present, genetic studies suggest that this evolutionary strategy comes at a cost. Here, we analyse genomes from 107 muskoxen from Canada and Greenland, as well as an ancient ~20,000-year-old genome from Siberia to assess the impact that the complex phylogeograhy had on the present-day genetic variation of muskoxen. We find that the genetic makeup of muskoxen is defined by a history of isolation and gene flow, and in particular strong genetic drift and loss of genetic diversity. As a result, the modern muskox is among the least diverse mammals, on par with the notoriously homozygous species like the cheetah, Channel Island fox, Iberian lynx, baiji, or vaquita. Yet, it does not show immediate signs of inbreeding depression and the population trend is considered stable. Our results provide some insights into the possible reasons why muskoxen seem to thrive in spite of depleted genetic variation.

Abstract ID: 2198
Poster board number:
P182

Effect of host plant species and insecticides on the evolution of genetic diversity of a crop pest

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For agricultural pests capable of attacking different plant species, crop distribution and selection pressure imposed by insecticide use are two key constraints imposed on their evolutionary trajectory. Here, we assessed the contribution of host-based genetic differentiation to the dynamics of resistance alleles to three insecticide modes of action in *Myzus persicae*. This major aphid pest is infamous for its ability to resist to multiple insecticides. Two distinct samplings were conducted: reference sampling on identified crops and continuous random sampling for 7 years using a suction trap. All aphids were genotyped at 14 microsatellite markers and four insecticide-resistant loci. We analyzed the genetic structure of these populations using an individual-centered approach. Four well-defined genetic clusters were found in the aerial samples, three of which could be linked to specific crops. We found a sharp differentiation between peach and herbaceous individuals. Within the individuals sampled on herbaceous hosts, two distinct genetic

clusters were identified, one of which seems to be more strongly associated with tobacco. The fourth group was only found in the aerial samples and display strong genetic difference with other groups. The 4-loci resistance genotypes showed a strong association with the four genetic clusters, indicative of barriers to the spread of insecticide resistances. The 7-year continuous random sampling revealed a rapid turnover in aphid genotypes and associated insecticide resistance patterns. This study highlights the importance of considering landscape-scale population structure to identify the risk of emergence and spread of insecticide resistance for a particular crop.

Abstract ID: 2218
Poster board number:
P183

Predicting the genetic signatures of dry-season aestivation of malaria-transmitting mosquitoes

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Sub-Saharan malaria-transmitting mosquito populations exhibit strong seasonal dynamics with huge temporal population size variation. Very often these populations re-establish and expand rapidly with the first rain after a prolonged period of dry season. It is a great challenge to understand their survival during the dry season. One popular hypothesis is that aestivation, a form of dormancy, helps them persist in the arid conditions. With little direct evidence, the aestivation model remains as controversial as the other hypotheses proposed. Through computer simulations we aim to establish the expected genetic signatures under aestivation and some selected alternative hypotheses, such as continuously-reproducing (seasonal) and migration models. Genetic signals like change in allele frequency, heterozygosity, relatedness, linkage disequilibrium, are explored. In particular, the discrepancy between longer- and shorter-term population size estimates may be one of the consequences of aestivation. These quantitative findings provide valuable resources for future population monitoring, parameter estimation, and experimental design.

Abstract ID: 2242
Poster board number:
P184

Limits to adaptation and fragmentation of a species' range

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I explore the limits of adaption to spatially and temporally changing environments, assuming hard selection, and allowing for evolution of genetic variance. I focus on the propensity of a species' range to fragment due to a failure to adapt to the changing conditions. Does the cohesion of the species across its range change with the distribution of dispersal, for example under a combination of local and long-distance dispersal?

Abstract ID: 2248
Poster board number:

P185

Demography modeling: understanding the ABC of *Ophrys* orchids radiation

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The sexually deceptive *Ophrys* orchids attract pollinators in a species-specific manner. They mimic the females of the pollinator species with floral traits such as scent, color, and shape, to induce pseudocopulation with the male pollinator. This interaction is a form of reproductive isolation, which leads to species divergence, thus speciation. It is estimated that the *Ophrys* species originated ~5 Million years ago (Mya) in the Mediterranean basin. During the Quaternary period several glacial-interglacial events and climate oscillations took place, which led to a species-rich radiation event in the last ~1.2 Mya. It is also known that during this period *Ophrys* experienced a pollinator-shift from the solitary bees *Eucera* to the *Andrena* genus. We are interested in the origins of the radiation within the *Ophrys* genus, as genomic studies show being in early stages of speciation. Our goal is to find demographic patterns within endemic sympatric populations from Southwest Italy that comprises 4 species: *O. exaltata, O. garganica, O. incubacea and O. sphegodes*. The approach presented uses the power of Approximate Bayesian Computation (ABC) modeling applied to Genotype-By-Sequencing data from 127 individuals. This is a flexible approach where we simplify possible ancestral scenarios into a model to approximate the likelihood function, using population genomics statistics and simulations. Overall, this work is a step forward to understand the micro evolutionary patterns across this genus.

Abstract ID: 2398
Poster board number:
P186

Understanding plant evolution mediated by interactions with pollinators and herbivores

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Plants and insects share a deep evolutionary past, and their ecological interactions like pollination and herbivory have been crucial in their reciprocal diversification. However, the lack of integration and experimentation in pollination and herbivory has hindered our progress in the physiological, ecological, and evolutionary processes and mechanisms linking ecological interactions and plant evolution. We addressed this challenge by adopting an integrative trait-based experimental evolution approach combined with behavioral assays under controlled and common garden settings. We used Brassica rapa as a model system and carried out two experiments of 8 and 5 generations under greenhouse and common garden respectively, and quantified evolutionary changes in morphological, chemical, life-history, and mating system traits. Our experiments showed that pollination and herbivory together contributed more to trait evolution than did their single effects and that the physiological and ecological herbivore-induced tradeoffs have far-reaching consequences in the evolution of self-compatibility and autonomous selfing

in initially predominantly outcrossing experimental populations. These findings represent a significant contribution to our understanding of how exactly ecological interactions might favor and restrict rapid plant (trait and plasticity) evolution and diversity, particularly under current global change.

Abstract ID: 2405
Poster board number:
P187

Eco-evolutionary dynamics in an insect community

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Increasing evidence indicates that evolutionary processes can occur over short time scales and have cascading effects on the ecological dynamics of populations and communities. Moreover, eco-evolutionary dynamics may operate across a range of spatial scales, from local patches to regional habitat mosaics. A major assumption is that non-evolutionary factors are more important in determining ecological patterns and dynamics at larger spatial scales, such as community species composition and interaction dynamics than local evolutionary processes. Prior research on the eco-evolutionary dynamics of the stick insect *Timema cristinae* demonstrated maladaptation to its host plant resulted in different intensities of avian predation, which affected the abundance of both *Timema* and coexisting plant-arthropods. We define maladaptation as the proportion of *Timema* individuals that display the less cryptic of two color morphs, given the host plant species occupied by each morph. However, this study was based on a local population at a scale of a few square meters. Whether this process occurs at larger spatial scales is unknown. Here we examine the effects of cryptic maladaptation of *Timema* on arthropod communities at a 100x larger spatial scale across a mountain range. Our results show that maladaptation of *Timema* along an elevational gradient affects arthropod abundance and population dynamics. Furthermore, we found that arthropod species within a community exhibit a heterogeneous response to maladaptation, which results in different community composition and thus affects arthropod dynamics. These results highlight that eco-evo dynamics occur at broader spatial scales and are important in determining spatial ecological patterns.

Abstract ID: 2433
Poster board number:
P188

Coalescent effective population size: between the stepping stone and the island model

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The effective population size Ne is often regarded as the size of an idealized population, which undergoes the same effects of drift or inbreeding as the regarded one. In the field of coalescent theory, it is equivalent to the expected coalescence time of a random lineage pair in this population. My focus is on the coalescent effective population size in the continuum between the one-dimensional circular stepping stone model and the island model. I show how the coalescent effective population size changes when a certain

fraction of migration goes to the neighbouring demes and the rest of the migrants disperses globally. I explore this concerning the percentage of local/global migration for different migration rates and numbers of demes in the population (while keeping the total population size constant). The formula for the effective population size of a more general migration model is used to describe the behavior of the effective size in the continuum. To represent the expected coalescence time of the stepping stone and island model, I use mathematical formulas as well as the population genetics simulator msprime.

Symposium: S11. Adaptation and evolution across environmental gradients (id: 26)

Abstract ID: 1005
Poster board number:
P189

Non-optimal phenotypic plasticity evolves under assortative mating: new theoretical predictions

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The comparison between patterns of genetic and phenotypic variation across environmental gradients is commonly interpreted as informing about non-optimal phenotypic plasticity. Co-gradient variation where genetic variation enhances phenotypic variation would signal too weak plasticity. Counter-gradient variation where genetic variation conversely opposes the direction of phenotypic variation would signal hyperplastcity, i.e. too strong plasticity. Here, we present both analytical and simulation results of quantitative genetics models suggesting that assortative mating can often result in the evolution of non-optimal phenotypic plasticity and the maintenance of genetic divergence despite strong gene flow. Assortative mating describes a pattern of mating where individuals with similar phenotypes mate together more often than expected by chance. Assortative mating has been described for many quantitative traits in both animals and plants. Our models predict that the sexual selection and non-random gene flow generated by assortative mating result in the evolution of (i) co-gradient variation, (ii) combined with, either too weak phenotypic plasticity, or, more surprisingly, hyperplasticity, depending on the intensity and distance of gene flow along the environmental gradient. These novel predictions suggest caution when making inferences about the adaptive value of phenotypic plasticity from the comparison of patterns of genetic and phenotypic variation across environmental gradients.

Abstract ID: 1045
Poster board number:
P190

Dispersal plasticity driven by variation in fitness across species and environmental gradients

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Dispersal plasticity, when organisms adjust their dispersal decisions depending on their environment, can play a major role in ecological and evolutionary dynamics, but how it relates to fitness remains scarcely explored. Theory predicts that high dispersal plasticity should evolve when environmental gradients have strong impact on fitness. Using microcosms, we tested in five species of the genus *Tetrahymena* whether dispersal plasticity relates to differences in fitness sensitivity along three environmental gradients. Dispersal plasticity was species- and environment-dependent. As expected, dispersal plasticity was generally related to fitness sensitivity, with higher dispersal plasticity when fitness is more affected by environmental gradients. Individuals often preferentially disperse out of low fitness environments, but leaving environments that should yield high fitness was also commonly observed. We provide empirical support for a fundamental, but largely untested, assumption in dispersal theory: the extent of dispersal plasticity correlates with fitness sensitivity to the environment.

Abstract ID: 1072
Poster board number:
P191

Parallel genomic architecture of adaptation in Littorina saxatilis along shore levels

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Understanding the ecological and physical factors driving intraspecific divergence and the origin of species is the “holy grail” of evolutionary biology. Parallel ecological divergence can occur in heterogeneous environments, showing different patterns at the genotype level under parallel phenotypic evolution. In this study, we focused on the genomic basis of temperature adaptation in the marine snail *Littorina saxatilis* in response to low-shore and high-shore from different latitudinal locations to understand the spatial distribution of adaptive genetic variation. We tested whether the same set of loci underlie shore level temperature adaptation in different geographical locations. We used pooled whole-genome resequencing for determining the allele frequency variation among locations. We found that while some genomic regions showed location-specific patterns, others are likely to contribute to adaptive divergence across locations. We also found overlap between these regions and candidate chromosomal inversions. Chromosomal inversions can increase differentiation across large stretches of the genome and control divergent phenotypes, which can be associated with local adaptation in the presence of gene flow, favouring rapid parallel adaptation to heterogeneous environments. Chromosomal inversions can play an important role in adaptation and speciation as has been seen in other polymorphic species.

Abstract ID: 1116
Poster board number:
P192

Effect of heat and drought at southern range limits on plant performance

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Climate has been long known to impact species distribution. However, it is not always clear which aspects of the environment are the most restricting (Hargreaves et al., 2014). A recent literature study documented that cold ends of species' distributions were most often affected by temperature, whereas warm ends of many species were shaped by moisture and temperature, apart from biotic interactions (Paquette & Hargreaves, 2021). Many species seem to withdraw from their warm end of distribution associated with climate warming (Rumpf et al., 2018), suggesting that warmer or hot-dry conditions reach levels outside of the ecological niche. In a greenhouse experiment, we tested whether the effects of heat and drought expected at warm range edges under climate warming were deleterious to plant performance, as well as if and how the effects interacted. We exposed one center and four range edge populations of the North American plant *Arabidopsis lyrata* to heat and drought, as it is increasingly experiencing these conditions at the southern range edge under climate change, and studied their effect in separation and in combination on plant traits and plant performance. Differences were tracked as reaction norms in response to stress treatments from the germination until reproduction. In the poster we present the results of this study, highlighting interaction effects between heat and drought on performance and the role of plastic trait changes.

Abstract ID: 1119
Poster board number:
P193

Evolutionary constraints at low-latitudinal range edges under climate change

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Warm edges of species distribution have been shown to be under particular threat by climate warming as range retractions are commonly observed. It is unclear why many populations cannot adapt to and long-term persist under warmer, dryer, or hot-drier conditions. Theory suggests that changes in the selection regime and genetic limitations can play an important role in setting range limits: Selection regimes may contribute if environmental gradients become too steep or are multivariate. Genetic limitations may include low genetic variation for environmental tolerances, or genetic correlations antagonistic to the direction of selection. In a greenhouse experiment, manipulating temperature and watering, we investigated how genotypic variation for growth and performance changed from no stress to univariate to combined stress, and the presence of trade-offs among stress tolerances. We raised full-sib plants of 120 families of a genetically diverse central population of *Arabidopsis lyrata* under average southern edge conditions, as well as under heat or drought as can sometimes occur, or combined heat and drought. By tracking growth, development, and allocation strategies we produced genetic variance-covariance matrices (G-matrix) within and across experimental environments. We will present results that shed light on the role of stress on evolutionary

potential in multi-trait space, the presence of trade-offs in coping under multiple stressors, and their effect on adaptation at warm range limits.

Abstract ID: 1154
Poster board number:
P194

Limited dispersal and spatially varying selection among European populations of sea lamprey

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Sea lamprey *Petromyzon marinus* is an anadromous and semelparous fish without homing behaviours. Despite being a freshwater, free-living organism for large part of their life cycle, its adulthood is spent as a parasite of marine vertebrates. Here, we performed the first genome-wide characterization of sea lamprey´s genetic diversity in their European natural range. The objectives were to investigate connectivity among river basins and explore evolutionary processes mediating dispersal during the marine phase. We sequenced 186 individuals from 8 locations spanning the North-eastern Atlantic coast and the North Sea with ddRAD-sequencing, obtaining a total of 30910 SNPs. Population genomic analyses reinforced the existence of a metapopulation encompassing freshwater spawning sites within the North-eastern Atlantic and the North Sea, though the prevalence of private alleles at northern latitudes suggested some limits to the species' dispersal. Seascape analyses revealed candidate loci associated with abundance of some host species were located in a genomic region coding for variable lymphocyte receptors, an adaptive immunity tool unique to jawless vertebrates, and to *MARCH* proteins, family of E3 ubiquitin ligases also involved in the regulation of immune responses. Abiotic factors such as [PO_4^{3-}], dissolved [O2], and T°C were found to be associated with candidate loci involved in myo-inositol synthesis, a pathway linked to osmoregulation, and to other genomic regions involved in organismal homeostasis. The identification of adaptive seascapes in this ancient species, especially linked to primitive adaptive immune responses, is important to understand the evolutionary pathways early in vertebrate evolution.

Abstract ID: 1255
Poster board number:
P195

G x G interactions between algal and zooplankton clones isolated during the spring season

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According to the Plankton Ecology Group (PEG) model, seasonal phyto- and zooplankton dynamics in lakes are explained by a change in phytoplankton community composition determined by abiotic and biotic factors. Consumer-resources interactions are central to this model as zooplankton dynamics depend on the quality and quantity of food while also influencing algal succession. Phyto- and zooplankton dynamics have

been analysed mainly at an interseasonal and interspecific scale and we are lacking information on the potential key role played by intraseasonal and intraspecific variations in phytoplankton and their consumers. To test for this variation, we isolated clones of the diatom *Asterionella formosa* and clones of the major consumer *Daphnia longispina* from Lake Constance. We checked for differences in interaction strength by conducting time-shift experiments where we combined clonal populations of the algal and *Daphnia* isolates from the beginning (March) and end of the spring season (June) and measured ingestion rates of *D. longispina*. With this experiment we tested the prediction that *Daphnia* clones isolated in March and June differ in their filtration rates, as they experienced different food quality and quantity. Specifically, *Daphnia* clones from March are predicted to have high filtration rates as they are adapted to low algal densities of mainly undefended preys (according to the PEG model). Isolates from June are predicted to have low filtration rates as they are adapted to high algal quantities of mostly defended prey. The results of our experiment suggest that intraspecific variation occurs during the seasonal dynamics of consumers and their resources.

Abstract ID: 1452
Poster board number:
P196

The forces maintaining a balanced inversion polymorphism

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Inversions suppress recombination in heterozygous state, allowing linked, potentially adaptive alleles to be coinherited as a 'supergene'. Yet, reduced recombination also prevents purging of deleterious alleles which accumulate on both inverted and non-inverted chromosomes. In *Drosophila melanogaster*, the *In(3R)P* inversion polymorphism varies clinally and segregates at intermediate frequencies at low latitude on multiple continents. However, little is known about the evolutionary forces that maintain this balanced polymorphism. Possible explanations include associative overdominance, epistatic or negative frequency-dependent selection. Here we begin to address this long-standing issue by using 2500 diallel crosses involving 50 wildtype chromosomes and measuring proxies of pre-adult survival. We found that inversion homokaryotypes had reduced chromosomal viability as compared to non-inverted homokaryotypes and heterokaryotypes, which survived equally well. Inversion homokaryotypes also had lower egg-to-adult viability. Our results suggest that the inverted arrangement harbours a higher recessive load and might thus enjoy highest fitness when relatively rare, potentially consistent with negative frequency-dependent selection. We further analyse genomic data to investigate the forces that maintain this balanced polymorphism.

Abstract ID: 1532
Poster board number:
P197

Effects of temperature and an invasive predator on genetic and phenotypic variation in damselflies

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Understanding and predicting how organisms respond to environmental changes, with a particular emphasis on those mediated by human activities, has become a major concern in conservation biology. Here, we studied the effect of two environmental factors related to human disturbance in multiple life-history traits of a freshwater insect, the damselfly *Ischnura elegans*, further exploring the transcriptomic basis of their response. For this, we used damselfly individuals of different origins, low-latitude (southern Poland) and high-latitude (southern Sweden) populations, to consider the existing variability in life-history strategies. Damselfly larvae were exposed to two experimental treatments in a crossed design, to mild warming temperature, fitting climate change trend according to IPCC RCP8.5 scenario, and to an invasive alien predator cue, the spiny-cheek crayfish. During the experiment, we measured several phenotypic traits (growth rate, development time, body size and weight) and preserved samples for a gene expression analysis. Using multivariate statistics, we demonstrated that especially growth rate and weight of individuals from different latitudes were affected in a different way by mild warming temperature and by the invasive predator cue, revealing complex relationships linking phenotype and environment. The gene expression analysis provided insights into the gene regulatory network and metabolic pathways underlying these phenotype-by-environment interactions.

Abstract ID: 1653
Poster board number:
P198

Investigating local adaptation of wild olive tree to climate change across a north-south gradient.

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Global change is impacting ecosystems and is a challenge for plant species evolution. Local adaptation is one of the evolutionary mechanisms allowing populations to cope with selective pressure. Here, we investigate local adaptation to climate change of an iconic perennial Mediterranean species, the wild olive tree *Olea europaea* subsp *europaea*. According to previous phylogeographic studies, this species is structured into east and west genepools. Focusing on the west Mediterranean populations, we are exploring a large variability of climatic conditions in a north-south gradient in order to detect genomic variants associated locally to climate. Here, we describe the sampling approach used to define 27 wild olive populations with 15 individuals each (11 from south France and Corsica, 9 from Spain and 7 from Morocco) selected according to temperature and precipitation parameters. Using genomic data (SNPs) from a capture sequencing experiment of 55,000 genes, we are analyzing genetic structure, searching for selection signal and performing genome environment association (GEA) analyses. We expect to figure out past climate impacts on wild olive tree by searching positive selection signal and detecting genomic variants associated to current climate, across the overall gradient but also at regional scales. The

understanding of local adaptation of olive tree to present climates assists us to anticipate its response to the current global change. In perspective, it would also help to forecast the impacts of future climate on olive tree diversity.

Abstract ID: 1730
Poster board number:
P199

Adaptation to climatic variation in the native and introduced ranges of a cosmopolitan plant

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Climate change and the global spread of invasive species are currently two of the most significant threats to the maintenance of biodiversity worldwide. Yet it is still poorly understood how species adapt to rapidly changing climates or if invasive species can become more problematic by adapting to a novel environment. We conducted a large trans-continental common garden experiment in North America and Europe to understand whether a cosmopolitan plant can adapt to spatiotemporal variation in climate in its native or introduced ranges. Individuals from 93 populations of the plant species *Trifolium repens* (white clover) from both its native (Europe) and introduced (North America) ranges were planted in four experimental common gardens located in northern (Montpellier, France) and southern (Uppsala, Sweden) Europe (i.e., native range) and northern (Toronto, Canada) and southern (Louisiana, USA) North America (i.e, introduced range). We recorded plant sexual and vegetative fitness in each common garden and assessed whether plants are best adapted to local climates, whether populations show evidence of rapid adaptation to recent climate change, and if the strength of local adaptation is greater in the native range than the introduced range. Results suggest white clover does exhibit adaptation to local climate, but also that plants from historically warmer climates than that of the northern common gardens exhibit the greatest fitness, indicating that white clover is not adapting quickly enough to withstand the effects of recent climate warming.

Abstract ID: 1750
Poster board number:
P200

The power of museomics to dissect the genetic basis of winter coat colour polymorphism in stoats

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Identifying genetic variants associated with phenotypic polymorphisms involved in environmental adaptations provides powerful means to understand whether species can cope with rapid environmental changes. Seasonal change from summer brown to winter white coats is one of the most remarkable adaptations to seasonal environments, allowing camouflage year-round in environments with seasonal snow. Such adaptations are threatened by continuing and future decreases in snow cover. Yet, this trait is polymorphic within species, with individuals from regions with less winter snow presenting a brown coat year-round. Such variants may provide the ingredients for future adaptation to climate change. Here, we dissect the genetic basis of winter colour polymorphism in the stoat, Mustela erminea, a small carnivoran with circumpolar distribution. We sampled specimens with scored winter coat colour in biological collections from natural history museums, originating from Ireland, where stoats remain brown in winter, and from winter coat colour transition zones in Great Britain and Central Europe. Whole genome resequencing data was collected, and population genomics analyses dissect how demographic history and structure are related to the distribution of winter coat colour morphs. We scan the genome for association with winter coloration using divergence and admixture mapping, and identify associated genetic variants. Scans for patterns of selection will allow understand whether past adaptation underlies the persistence and distribution of the alternative morphs in the natural populations of the species. Our study dissects the genetic basis of a relevant phenotypic polymorphism, which will then be used to develop predictive models of adaptation to climate change.

Abstract ID: 1762
Poster board number:
P201

The genetics of plant-plant interactions in *Arabidopsis thaliana*

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The phenotype of an individual is not only affected by its own genes, but also by the genes of its conspecifics through social interactions. The theoretical framework of Indirect Genetic Effects (IGE) allows to describe how such interactions affect heritable variation and response to selection. While many studies have documented IGE and their evolutionary consequences in animals, little is known on the importance of IGE in plants. We grew 98 natural accessions of *Arabidopsis thaliana* in a competition experiment with the aim of quantifying the contribution of IGE to heritable variation in different plant traits. In our experiment, flowering time and rosette diameter were not affected by IGE, but significant IGE variation was found for aboveground biomass with a strong negative correlation between direct and indirect genetic effects. A Genome-Wide Association Study (GWAS) identified five major effect loci with significant IGE on plant biomass. Using large-scale genomic data, we located IGE variants within the native range of the species and show that alleles with positive IGE (i.e., alleles increasing neighbor biomass) mostly occur in North Scandinavia and relict populations from Spain and North Africa. Genome-Environment Associations (GEA) and complementary population genomic analyses suggest that IGE loci are primarily associated with climatic adaptations. Overall,

our results suggests that intraspecific interactions are dominated by competition in *A. thaliana*, and that climatic adaptations have important effects on plant-plant interactions.

Abstract ID: 1792
Poster board number:
P202

Nutrient limitation influences moss-associated nitrogen fixation across a subartic gradient

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Moss-associated cyanobacteria have been show to contribute greatly to the nitrogen (N) pools of pristine ecosystems. Moisture and temperature are the most important abiotic factors directly influencing the rates of biological nitrogen fixation (BNF) in mosses. However, the availability of some macro and micronutrients can also be correlated to changes in those rates, and this is linked to the functional role of nutrients involved in the nitrogenase enzyme complex. To identify the effects of nutrient availability on BNF we conducted an experiment with mosses in a subarctic ecosystem, in which we applied N and phosphorous (P) along an elevation gradient in Abisko, Sweden. Nitrogenase activity in mosses was assessed via the acetylene reduction assay (ARA) at different time points after the additions. Our results show that N additions rapidly reduce BNF rates associated with mosses, however, P additions lead to variable results. Further, the effects of nutrient additions depended on the positioning along the elevation gradient in the subarctic; reflecting differences in nutrient availability and thereby, limitation. Our findings show how the availability of essential macronutrients (i.e. N and P) can play a fundamental role in promoting or inhibiting BNF in mosses, and that time frame, and seasonality, can be significant in modulating the response of BNF to nutrient availability.

Abstract ID: 1797
Poster board number:
P203

Postglacial history and local adaptation of the wood decay species *Trichaptum abietinum* in Europe

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The postglacial migratory history has been thoroughly analyzed for European animals and plants, but not so for fungi. In this study, we conducted population genomics analyses of a widespread forest fungus in order to unveil its postglacial colonization history in Europe, as well as to test for signals of local adaptation to different climates or substrates. Our study species, *Trichaptum abietinum,* is a common wood decay fungus of coniferous wood with a wide distribution in boreal forests covering large climatic gradients. Altogether 145 specimens across Europe were collected, from which we isolated haploid (monokaryotic) cultures that were genomes sequenced for population genomic analyses. Principal component and Admixture analyses indicate two or three glacial refugia, one Eastern Eurasian, one south-European and tentatively one West-European refugium resulting in genetically distinct groups in the European samples. Eastwards and northwards proliferation from these refugia following the last glacial retreat could have led to several suture zones in continental Europe. This pattern also

resembles the history of the host trees spruce and pine. Together with separate postglacial distribution histories, genetic adaptation to diverging climatic conditions dividing continental and coastal areas is suggested to be an additional causal factor for the observed genomic division in the European samples. Further analysis will model historical population dynamics and gene flow in addition to closer investigations of possible adaptation to local conditions in the different groups.

Abstract ID: 1846
Poster board number:
P204

A mostly-microendemic assemblage of tiny microhylid frogs on a mountain in northern Madagascar

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The genus *Stumpffia* Boettger, 1881 (Anura: Microhylidae: Cophylinae) contains some 43 species, most described in the last 10 years, thanks to intensive fieldwork and taxonomic effort. The new picture of the diversity of these frogs is revealing interesting evolutionary scenarios. We present new data on the Stumpffia assemblage on Montagne d'Ambre, a volcanic mountain in the north of Madagascar. A visit to the west slope of the mountain, never before studied herpetologically, added a new record of *S. mamitika* for the mountain, bringing the total number of species occurring on the mountain to seven, four of which are apparently micro-endemic to the mountain. Furthermore, four of these species (*S. mamitika*, *S. angeluci*, *S. huwei*, and *S. maledicta*) belong to a single clade, and may have speciated in situ as a microendemic radiation. We provide new data on the elevational structure among all of the locally occurring *Stumpffia* species, and bioacoustic differences among their advertisement calls, as a first step toward understanding how they are differentiated, and thus how they may have arisen as separate species in the first place.

Abstract ID: 1864
Poster board number:
P205

Genomic basis of local adaptation in the European barn owl (*Tyto alba*)

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Widely distributed species face heterogeneous environmental conditions which may lead to differential adaptation among populations. In the Western Palearctic barn owl (*Tyto alba*), plumage colour varies along a South East-North East cline in Europe due to selection. However, other traits and genomic regions of this non-migratory raptor species may also be under the influence of different spatial selective pressures. Taking advantage of whole-genome sequencing from 74 European barn owls from 9 populations, we scan the genome to reveal traces of selection. A landscape genomics approach also shows that some of the genomic variations are significantly associated with environmental conditions at the continental scale, supporting the putative influence of the abiotic conditions in the local adaptation of the species. In parallel, we pinpoint a

large non-recombining genomic region showing a very different pattern of diversity that the rest of the genome. In this 15 Mega-bases region, we identified two distinct haplotypes distributed among populations, with one indicating signs of selection in the two southern populations of Italy and Portugal. If the function of this region remains unclear, altogether, our findings show how population genomics may help to detect tracks of selection at the genomic level, and how species facing a wide range of heterogeneous conditions locally adapt to their environment.

Abstract ID: 1912
Poster board number:
P206

Intensity of pathogen-imposed selection for disease resistance varies along an elevation gradient

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Disease resistance is highly polymorphic in natural plant populations. Variation in disease prevalence may favor diverse immune responses by changing the selective pressure for resistance through space and time. Theory predicts the intensity of biotic interactions to change along elevational gradients, yet the extent to which this generates spatially heterogenous selection for disease resistance is not known. Here, we study how the prevalence of infection by the fungal pathogen *Podosphaera plantaginis* on its host plant *Plantago lanceolata* changes across a 1100 m elevation gradient in the Swiss Alps. Using both a field reciprocal transplant experiment and a controlled inoculation experiment we study how resistance and infectivity as well as patterns of local adaptation change along the elevational gradient. We observe a striking decline in disease prevalence towards higher elevations. Further, our experimental results indicate higher susceptibility in plants originating from the high elevation populations where infection risk is low. Jointly our results suggest that the intensity of pathogen-imposed selection may change with altitude, with direct consequences for how disease resistance is spatially distributed.

Abstract ID: 1998
Poster board number:
P207

The genomic basis of temperature adaption of Littorina saxatilis across small scales

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The question of how organisms adapt to their environment has long fascinated evolutionary biologists. Understanding the potential ways that species might adapt to future conditions is essential in predicting species persistence in the context of climate change. The rough periwinkle, *Littorina saxatilis* (Olivi), is an intertidal snail and an ideal

model organism for the study of local adaptation across environmental gradients of small scales. *L. saxatilis* can show genomic and phenotypic variations across shore levels, which can differ in environmental conditions such as temperature, humidity, salinity. In this study, I will highlight *L. saxatilis* as a promising model for temperature adaptation by 1) reviewing literature based on adaptive phenotypic responses of *L. saxatilis* related to temperature; 2) presenting results on phenotypic differences of between *L. saxatilis* from different shore levels, focusing on several promising but under-explored trait, such as heart rate and activity level. Snails were sampled from Norway, Spain and Sweden. Phenotypic differences between snails of different shore levels were compared across a latitudinal gradient, revealing how temperature differences shape behavior and physiological phenotypes in *L. saxatilis*; and 3) conducting QTL mapping of adaptive traits and differential expression analysis to investigate both genomic and transcriptomic genetic basis of local adaptation across latitudinal gradients and shore levels. This study will contribute to the genetic basis of temperature adaptation in *L. saxatilis* across shore levels from three different countries.

Abstract ID: 2037
Poster board number:
P208

The story of *Proasellus* (Isopoda, Crustacea) - cave colonization ensured by the plastic response?

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Some taxa successfully adapted to caves across diverse geographic and temporal scales, while others have a few or no cave-dwelling representatives. This implies that groups that gave rise to numerous cave species have some preadaptations which allow them to colonize, survive, and eventually fully adapt to the subterranean environment. We ask whether phenotypic plasticity could be an underlying mechanism that enables successful cave colonization in the early stages as it was shown for the cavefish *Astyanax mexicanus*? Genus *Proasellus* has invaded caves multiple times independently. As a model system, we selected a widespread surface species *P. coxalis* which is also known to form cave populations. To understand which adaptations evolve in subterranean species in this genus, we used a closely related cave species *P. anophtalmus*. We exposed one randomly selected group of both species to complete darkness (DD) and the other group to a normal light-dark photoperiod (LD) as controls. After four months in the experiment, DD and LD cohorts differ in gene expression, but *P. coxalis* showed a more pronounced plastic response (3024 DEGs) compared to *P. anophtalmus* (491 DEGs). At the phenotypic level, differences between DD and LD *P. coxalis* (first generation hatched in the experiment) indicated better general fitness in DD conditions (growth rate, fecundity, survival) while some traits (body pigmentation, metabolic rate) changed in the nonadaptive direction. Our results indicate that phenotypic plasticity may be a general mechanism for adaptation to the darkness of caves.

Abstract ID: 2044
Poster board number:
P209

Transposable elements and environmental niches interaction in the Cape Floristic Region

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Non-coding repetitive DNA (repeatome) is an active part of the nuclear genome, involved in its structure, evolution and function. It is dominated by transposable elements (TEs) and satellite DNA and is prone to the most rapid changes over time. The TEs activity presumably causes the global genome reorganization and may play an adaptive or regulatory role in response to environmental challenges. We applied this assumption for the first time to plants from the Cape floristic hotspot to determine whether changes in repetitive DNA are related to responses to a harsh but extremely species-rich environment. The genus *Pteronia* (Asteraceae) serves as a suitable model group because it shows considerable variation in genome size at the diploid level and has high and nearly equal levels of endemism in the two main Cape biomes, Fynbos and Succulent Karoo. First, we constructed a robust phylogeny based on multiple low-copy genes that served as a phylogenetic framework for detecting quantitative and qualitative changes in the repeatome. Second, we performed a comparative analysis of the environments of two groups of *Pteronia* differing in their TEs bursts. Our results suggest that the environmental transition from the Succulent Karoo to the Fynbos is accompanied by TEs burst, which is likely also driving phylogenetic divergence, despite the overall poor resolution of the phylogeny due to rapid radiation. We thus hypothesize that analysis of rapidly evolving repeatome could serve as an important proxy for determining the molecular basis of lineage divergence in rapidly radiating groups.

Abstract ID: 2121
Poster board number:
P210

Environmental effects on the genetic architecture of fitness components in an hermaphrodite

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Understanding how environmental change affects genetic variances and covariances of reproductive traits is key to formulate firm predictions on evolutionary responses. This is particularly true for sex-specific variance in reproductive success, which has been argued to affect how populations can adapt to environmental change. Our current knowledge on the impact of environmental stress on sex-specific genetic architecture of fitness components is still limited and restricted to separate-sexed organisms. However, hermaphroditism is widespread across animals and may entail interesting peculiarities with respect to genetic constraints imposed on the evolution of male and female reproduction. We explored how food restriction affects the genetic variance–covariance

(G) matrix of body size and reproductive success of the simultaneously hermaphroditic freshwater snail *Physa acuta*. Our results provide strong evidence that the imposed environmental stress elevated the opportunity for selection in both sex functions. However, the G–matrix remained largely stable across the tested food treatments. Importantly, our results provide no support for cross-sex genetic correlations suggesting no strong evolutionary coupling of male and female reproductive traits. We discuss potential implications for the adaptation to changing environments and highlight the need for more quantitative genetic studies on male and female fitness components in simultaneous hermaphrodites.

Abstract ID: 2196
Poster board number:
P211

Genetics of adaptation to local climate

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Insect populations in seasonal environments often show local adaptation in photoperiodic plasticity for life cycle regulation including timing of winter diapause. The critical photoperiod (CPP) is defined as the photoperiod where half of a population enters diapause and the other half continues non-diapause development. Adaptive variation among populations in CPP is common but the genetic background and architecture is often not well known. Studies across several species, however, suggests that CPP may be associated with genes on the sex chromosomes. Earlier research on distantly related populations of the Speckled wood butterfly, *Pararge aegeria* have shown that population differences in CPP are associated with genomic regions both at the Z-chromosome and autosomes. To further explore this, we performed reciprocal crosses between two closely related populations of this species with known differences in CPP to explore if genetic variation on the Z-chromosome may be generally associated with population differences. We assayed F1 hybrids for sex-specific differences between the two reciprocal crosses in CPP. Although both reciprocal crosses show CPP's that are intermediate to the two original populations, there was no indication of sex-specific differences between reciprocal crosses. This suggest that local adaptation in CPP between these two populations have primarily evolved by selection on genes on the autosomes. In combination with the earlier results this indicate that population difference in CPP can evolve by alteration of different genetic elements. These studies also form the basis for a more detailed exploration of the genetic background to adaptive variation in CPP using functional genomics.

Abstract ID: 2216
Poster board number:
P212

Testing for the mechanisms of balancing selection maintaining 6Pgdh polymorphism in the bulb mite

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Genetic variation is required for adaptation, but its maintenance is a major puzzle in evolutionary biology. The focus of this study is environment-dependent balancing selection, where the fitness of genotypes depends on the spatio-temporal variation of the environment, maintaining genetic variation in heterogeneous environments. Specifically, we investigate Phosphogluconate dehydrogenase (6Pgdh), a sexually selected gene in the bulb mite *Rhizoglyphus robini*. The gene has two alleles (S and F), that differ by a single nonsynonymous change, where the S-bearing males achieve higher reproductive success. We use experimental evolution to test whether temperature or sexual selection intensity (manipulated by sex ratio) are the factors underlying balancing selection. Firstly, mites were evolved at different temperatures under equal sex ratio (24°C, 20°C, 18°C,) and at different sex ratios (male biased, equal sex ratio, female biased) at 24°C. Both temperature and sexual selection intensity affected the strength but did not reverse selection on 6Pgdh (the S allele was favored in all the treatments). Then, we test for the effect of lower temperatures and temperature (18°C vs. 12°C) by sex ratio (female biased, equal sex ratio) interaction in a fully factorial crossed design. We also checked the change in F-frequency after one generation at higher ranges of temperatures and observed a slight (but not significant) increase in F-frequency at 8°C and decrease at 24°C. Our results suggest that both temperature and sexual selection intensity contribute to selection on 6Pgdh.

Abstract ID: 2263
Poster board number:
P213

Parallel subfunctionalisation of isoforms of photosystem II subunit PsbO in plants

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Photosystem II is a multi-protein complex embedded in thylakoid membranes. By using light energy, it is splitting water and providing electrons for photosynthetic electron transport chain. PsbO (manganese-stabilising protein) is one of its extrinsic subunits that is required for water splitting in plants.
Many plant species express two *psbO* genes, resulting in two slightly different PsbO protein isoforms. Interestingly, we found that the duplication of *psbO* gene occurred many times independently. In spite of this, the level of protein divergence is similar in different species. Moreover, the paralogous PsbO isoforms differ on similar positions of the protein structure. This suggests that similar subfunctionalisation of PsbO isoforms occured paralelly in various plant lineages. We supported this hypothesis experimentally by complementation of *Arabidopsis thaliana psbo1* mutant with *psbO* genes from *Solanum tuberosum*.
Moreover, to better understand the functional differences between PsbO isoforms, we analysed transcriptomic data available for *Arabidopsis thaliana*. The ratio of PsbO1/PsbO2 is very stable during various experimental perturbations. However, transcriptomic data from natural accessions show dependence of PsbO1/PsbO2 ratio on climatic conditions, indicating that a relative increase in *psbO2* gene expression is typical for accessions from locations with higher probability of photorespiration.

Abstract ID: 2289

Poster board number:
P214

Genomic patterns of differentiation and signals of selection along multiple hybrid zone transects

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A fundamental question in evolution is how divergent populations are maintained despite gene flow. Analyses of hybrid zones ideally help understand the genetic basis of such genomic barriers, as well as spatial allele frequency patterns and the interaction between selection, dispersal and environmental factors. However, studying only one hybrid zone means that it is difficult to determine whether patterns of variation are generated by selection or by genetic drift.
To address the patterns of parallelism of genetic barriers, we have used two transects in the snapdragon (*Antirrhinum*) hybrid zone in the Spanish Pyrenees. Previous work has identified several major-effect loci controlling flower colour differences between yellow and magenta subspecies. Genomes scans based on PoolSeq revealed evidence for selection at these loci in one transect across the hybrid zone. Here, we test for parallelism in genomic signatures of selection by analyzing linked-read sequence data (haplotag sequencing) collected from two separate transects. We validate population-scale imputation and phasing of linked-read sequences using parent-offspring trios and genotypes from SNP arrays. We characterize patterns of differentiation and signature of selection along the genome as well as across transects to explain the similarities and dissimilarities between them.

Abstract ID: 2309
Poster board number:
P215

Evolution of thermal mismatch between host and parasite in a temperature gradient experiment

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The degree of (mis)match between host and parasite ecological niches is an important determinant of the geographic ranges of the interacting players. To date, we still know little about how adaptation to environmental conditions change this match between niches, and how this feeds back on epidemiology and coevolution. These questions are particularly relevant in the context of global climate change. We are currently running an experimental evolution project on parasite and host (co)adaptation in metapopulations located on a temperature gradient, from permissive (23°C) to stressful (33°C). Using experimental microcosms of the protist *Paramecium caudatum*, we track the capacity of two bacterial parasites (*Holospora undulata* and *H. obtusa*) to spread into the gradient. Our main goal is to assess the evolutionary capacity of host and parasites to adapt to high-temperature stress and the possible consequences for life-history and interaction traits (virulence/resistance). We will present data on the long-term epidemiological dynamics along the gradient, and show results from a first cross-infection assay at different temperatures, testing for potential trade-offs between host temperature adaptation and the evolution of resistance to the parasites.

Abstract ID: 2310
Poster board number:
P216

Modelling reaction norms with few assumptions

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Reaction norms describe the phenotypic expression of a genotype over a range of environments. In evolutionary theory, these are typically modelled using very specific shapes, such as straight lines or logistic (S-shaped) curves. This may lead to wrong conclusions when the assumptions being made are too restrictive. Here we present a novel method to model smooth non-linear reaction norms with very few *a priori* assumptions about shape, using restricted cubic splines – a type of function defined piecewise by polynomials. We present an example of an optimal non-linear reaction norm obtained analytically, where a hypothetical single celled organism is able to vary its metabolic investment into processing different nutrients which themselves vary in digestibility. To simulate this example reaction norm, we use a restricted cubic spline based on k independent gene values. Each simulation consisted of a starting population of 1,000 individuals with a horizontal reaction norm defined by 5, 10 or 20 genes, which were then allowed to evolve freely for 300,000 generations. All populations achieved a shape very similar to the optimal reaction norm, independently of the number of genes used. Moreover, a lower number of genes does not lead to faster adaptation. Here we show that modelling smooth non-linear reaction norms is possible without constricting their shape.

Abstract ID: 2420
Poster board number:
P217

Climate-driven natural selection across protein-coding and cis-regulatory genetic variation

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How do genetic polymorphisms steer climate adaptation? While extensive theory and data in human genomics posit that complex adaptive traits are primarily driven by changes in gene expression networks, study of coding variants in the plant model *Arabidopsis thaliana* finds hundreds of loss-of-function alleles involved in adaptation. However, the relative contributions of regulatory and protein coding variation to fitness in *A. thaliana* in ecologically-relevant conditions remains unknown. To assess the impact of natural selection in *A. thaliana*, we utilized fitness measurements from ~500 diverse accessions grown under high and low precipitation at two common garden field sites within the species' native range and quantified short-term natural selection on ~11 million variants across the genome. We annotated the variants via: 1) functional effect

predictions and cis-regulatory information from existing RNA-seq and DAP-seq datasets, 2) a machine-learning model developed to identify cis-regulatory variants likely influencing chromatin accessibility and gene expression, and 3) because DNA methylation differences contribute substantially to variation in *A. thaliana* adaptive traits, we used bisulfite sequencing datasets to annotate gene body and genome-wide methylation. We assessed the impact of selection across variant annotations, and performed enrichment analysis of variant types, functions, and gene ontologies. We find that nonsynonymous mutations, while less common overall, have an outsized contribution to fitness relative to regulatory mutations, and that the influence of methylation is context dependent, contingent upon methylation type and genomic region. This work advances our understanding of the architecture and functional nature of adaptive genetic variation.

Symposium: S12. Resurrection ecology as a tool for the study of rapid evolution (id: 42)

Abstract ID: 1165
Poster board number:
P218

Trait and fitness variation in a resurrected phytoplankton population from two periods

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Aquatic ecosystems underwent major changes in the last decades. Cultural eutrophication followed by periods of attempts to revere this are probably the most significant and prominent examples. The phytoplankton species composition tends to follow these changes with losses and gains of taxa as well as changes in the dominance of species depending on the environmental conditions. However, some species persist at similar frequencies independent of the environmental conditions. We hypothesize that the persistence of some species is mediated by evolutionary adaptation to different environments. To test for this, we resurrected and isolated multiple clonal lines of *Chlamydomonas* sp. from Lake Constance sediment, associated with either eutrophic or re-oligotrophic conditions in the lake. We characterized and compared competitiveness and defense as two major trophic traits of these isolates and linked these to fitness under controlled laboratory conditions. Specifically, we followed the growth and yield of 14 isolates from each period in low and high phosphate conditions in the presence and absence of predation by *Brachionus calyciflorus*. We found significant differences in traits between isolates and that the trait ranges differed when isolates from the different time periods were compared. In addition, isolates with similar trait combinations for defense and competitiveness differed in fitness when tested in the different environments (phosphate and predator). The observation of differences in heritable trait variation and differential translation into fitness responses suggests that adaptive evolution may play a role in the resilience of *Chlamydomonas sp.* to major environmental changes.

Abstract ID: 1480
Poster board number:

P219

Back to the past: rapid adaptation in *Viola arvensis* using resurrection ecology

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Insect pollinators decline has been reported in various parts of the world, thus inducing changes in selective pressures on entomogamous plants. As plants need pollinators for their reproduction, pollinator decline may impact plant reproductive system. We hypothesized that pollinator limitation may induce plant evolution towards less attractive flower and higher capability of selfing in self-compatible entomogamous. This set of traits is called the selfing syndrome. Using resurrection ecology, the aim of our work was to study the evolution of phenological, floral and fitness traits in a common annual weed. We thus studied four populations of the Field Pansy, *Viola arvensis*, from the Parisian basin (France), as four independent replicates of evolution. We grew up populations issued from seeds collected in 90'-2000 and their descendants collected in 2021 in common environment. Phenotypic traits were measured in 2021, the refreshing generation, and in 2022, the test generation. We also used population genetics tools to estimate realized selfing rates *in natura*. Microsatellites markers revealed an increased of realized selfing rates between 90's and 2021. Phenotypic measurements showed a shift of corolla length, corolla width, consistent with the evolution of a selfing syndrome. Such evolution towards selfing syndrome raises questions about the future of plant-pollinators interactions and on a potential breakdown of this interaction.

Abstract ID: 1481
Poster board number:
P220

Thermal plasticity of resurrected and contemporary populations of *Hypericum perforatum*

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Environmental change forces species to adjust to new conditions. Adjustment can occur through phenotypic plasticity or evolutionary adaptation, or both. While phenotypic plasticity can allow species to rapidly respond to changes in the environment, evolutionary processes are often slow, especially for species with long generation times. To estimate species' abilities to cope with change, the relative roles of plasticity and adaptation need to be quantified. Among the most powerful approaches for measuring and distinguishing between such changes are allochronic study-setups. One prominent

example of such an approach is resurrection studies. We present the first results from a large resurrection experiment on Hypericum perforatum. Seeds from 14 populations collected in five locations between 1984 and 2021 were germinated and grown across four temperature conditions in greenhouse compartments during winter 2021-22. We expected to find contemporary populations displaying greater performance at hotter temperatures compared to their historic counterparts. To date, we have collected data on vegetative traits, germination and flowering phenology, and will collect data on flower abundance, flower size and seed set to evaluate fitness. Our preliminary results indicate no difference in early vegetative traits between the historic and contemporary populations but show differences in the average germination and flowering phenology with the historic populations overall showing later phenology. Such patterns could indicate that rapid evolution has indeed occurred, and that even for a perennial plant species, climate change introduces high enough selective pressure for evolution to play a role in adjusting to new climatic conditions.

Symposium: S13. Evolutionary ecology of chemically-mediated species interactions in plants (id: 936)

Abstract ID: 1041
Poster board number:
P221

How did the preemptive counter-defense become superior? A modelling study

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Various herbivorous insects prefer the toxic plants of the Brassicaceae family as their hosts. Glucosinolates (GLSs) are the defense compounds of Brassicaceae, which are hydrolyzed by myrosinases at the onset of herbivory and produce toxic isothiocyanates (ITCs). ITCs are detrimental to the feeding insect herbivores. The feeder insects have evolved specific adaptations against ITCs to cope with the detrimental effects. These adaptations are called counter-defenses. Insect herbivores of Brassicaceae are categorized into two different types according to their counter-defense techniques. The first category includes the specialist feeders with preemptive counter-defense. These insects prevent the GLSs from being hydrolyzed to ITCs. On the other hand, there are the generalist feeders with responsive counter-defense, where the ITCs have been formed, but counter-defended as soon as detected. Experimental results suggest that the preemptive counter-defense is more efficient. This can be explained by the comparatively low free ITCs content in the gut of specialist larvae. Now, the question is, how does preemptive counter-defense always lead to a lower amount of free ITCs than responsive counter-defense? To answer that, the dynamics of both counter-defenses are needed to be studied. Assuming that a feeder insect is exposed to ITCs until its lifespan is over, we proposed deterministic models to analyze the progression of free ITCs with respect to the two counter-defenses, and quantify the effect of ITCs in a specialist and

generalist insect, respectively. The model explains how the decrease in the level of ITCs is achieved, which helps to understand the benefit of preemptive counter-defense.

Abstract ID: 1097
Poster board number:
P222

Correlations between attraction and defence plant chemistry – what is the true target of selection

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Floral scent and chemical defense compounds are complex plant traits predicted to vary among populations due to local selection from interacting insect species as the compounds emitted can attract efficient pollinators or repel unwanted visitors. There is ample evidence for interspecific variation in compound composition and emission rates, but many studies involving plant chemistry and how it mediates plant-insect interactions tend to focus on either insect attractants or repellants separately. In plant chemistry, this unilateral approach is problematic since plant chemicals that attract or repel insects often share biosynthetic pathways and could therefore be correlated or constrained. In order to determine true targets of selection (i.e. floral scent or plant defence compounds etc.) it is important to investigate to what extent these compound groups are correlated and constraining the evolution of the other. We have investigated floral scent, green leaf volatile and glucosinolate composition and emission rate in 35 populations of the perennial herb *Arabis alpina* and investigated to what extent the compositions of the different compound groups are correlated. With this, we hope to gain insight into what group of chemicals is the true target of selection, and if pollinator-mediated selection is indeed the most likely explanation of the among-population variation in floral scent in this species.

Abstract ID: 1270
Poster board number:
P223

Flower size, not floral scent, may function as an honest signal in a generalist-pollinated perennial

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In flowering plants that produce a concealed reward, pollinator foraging preferences may generate selection for traits that are correlated with rewards and thus serve as “honest signals.” The strength of selection for honest signals could vary across traits and populations, due to variation in pollinator communities, pollinator preferences, or plant mating system. We investigated whether flower size and floral scent could function as an honest signal of floral rewards and be subject to pollinator-mediated selection in *Arabis alpina*, an arctic-alpine herb. An emerging model system for ecological genomics and the evolution of life history traits, *A. alpina* exhibits variation in flower size, floral scent, and plant mating system, and is visited by a diverse array of insects. We examined variation in relationships between flower size, floral scent, and nectar volume in plants from 29 populations in a greenhouse common garden. We also estimated pollen limitation, which is related to the opportunity for selection, in 12 natural populations. We found that both across and within self-compatible and self-incompatible populations, larger flowers generally produced more nectar. In contrast, volatile emission rate was not associated with nectar volume. Pollen limitation was detected in six populations. Our results suggest that selection for floral traits that serve as honest signals of floral rewards can vary across trait types and populations. Aspects of floral morphology may be particularly likely to function as honest signals because of phenotypic integration and modularity of floral structures, while floral scent may function primarily as a long-distance pollinator attractant.

Abstract ID: 1644
Poster board number:
P224

Temperature-induced plasticity and reciprocal selection in a plant-pollinator-herbivore system

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Global warming increases temperatures in many habitats, possibly disrupting plant-insect interactions because plant and insect physiology are strongly influenced by temperature. To understand how plants and insects (co)adapt to global warming, we need to study how temperature influences their interactions and the underlying chemical traits. We investigated how temperature changes the interaction between the field mustard (*Brassica rapa*) and its pollinating herbivore, the small cabbage white (*Pieris rapae*), using cold (average 23C) and hot (average 26C with weekly 30C day) greenhouse environments. Butterflies visit flowers of mustard to feed on nectar and thereby provide pollination, but also lay eggs on the plant, which hatch into hungry caterpillars. We show that temperature changes both the mutualistic and antagonistic interaction strength of the plant-pollinating-herbivore interaction. Butterflies visited more flowers in the hot- compared to the cold environment. Despite this, plant fitness increased less per butterfly visit in the hot- compared to the cold environment. In contrast, butterfly fitness was correlated with flower visitation and butterflies laid more eggs in the hot environment. Interestingly, plants were able to tolerate herbivory better in the cold environment, while

herbivory had a stronger negative effect on fitness in the hot environment. Combining trait and fitness measurements in both temperature environments, we show that temperature changes reciprocal selection between plants and butterflies, including chemical plant traits such as flower scent, colour, and defence chemistry (glucosinolates). Therefore, temperature-induced plasticity in the interaction between a plant and its pollinating herbivore likely reshapes their coevolutionary trajectory.

Abstract ID: 1670
Poster board number:
P225

Floral volatile variation in an Andean orchid pollinated by euglossine bees across landscape

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The study of the reproductive biology of plants is one of the most interesting aspects of tropical ecology. Many processes and mechanisms that maintain populations depend on their complex interactions with pollinators, and therefore, in plants with some degree of allogamy, floral traits are important for reproduction. Among these traits, aroma production has been documented for several angiosperm species, with the Orchidaceae family being the most investigated. We studied intraspecific variation in four populations of an Andean orchid species to identify how environmental factors influence the diversification of the floral volatile composition of this plant in which aroma mediates its obligate interactions with euglossine bees for successful pollination. Floral fragrance analyzes for volatile compounds were performed by gas chromatography/mass spectrometry at the intra- and inter-population level. In general, little variation was detected and floral fragrances were mainly composed of 2-(4-methoxyphenyl) ethanol and 2-methoxyphenol. This finding suggests that stabilizing selection may be occurring. In addition, these compounds attracted a single species of eglossine bee. Such pollinator specificity could be an important mechanism of reproductive isolation between this orchid and other sympatric species. Longer-term studies that include different seasons are necessary to understand the evolutionary and functional ecology of these complex floral traits.

Abstract ID: 1734
Poster board number:
P226

How does metal hyperaccumulation protect *Noccaea caerulescens* from the herbivore *Pieris brassicae*?

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Heavy metal hyperaccumulating plants such as *Noccaea caerulescens* actively filter specific heavy metals out of the ground and store them in aerial parts. The Elemental

Defence Hypothesis implies that higher concentrations of heavy metals in these plants can be useful as a defence against pathogens and herbivores such as *Pieris brassicae. Studies have shown that P. brassicae* caterpillars prefer plants with lower concentrations of zinc or nickel, but it is unclear if they detect differences in the metal concentration of the plant via 1) changes in the scent, 2) the taste, 3) the surface structure or 4) the visual appearance of plants. This study tested an involvement of the olfactory and gustatory response of *P. brassicae* caterpillars feeding on *N. caerulescens* plants grown on different concentrations of zinc and nickel. We conducted feeding choice experiments distinguishing olfactory and gustatory cues, analysed scent and glucosinolate (a class of herbivore defensive compounds) profiles and measured accumulated zinc and nickel concentrations to identify changes in the VOCs or glucosinolates that differ along with metal concentrations. While no significant differences in the plants' VOC profiles were detected, we found significant positive and negative correlations between leaf zinc or nickel concentrations respectively and specific glucosinolate levels, which directly related to differences in the olfactory and gustatory response of *P. brassicae* caterpillars. Our results thus reveal a potential link between metal hyperaccumulation, glucosinolate production and the plants' interaction with herbivores and uncover a potential mechanism underlying the Elemental Defence Hypothesis.

Abstract ID: 1748
Poster board number:
P227

Patterns of variation in a novel defence reveal evolutionary drivers of chemical diversification

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Phytochemical diversity can result from coevolutionary cycles, as specialization in herbivores imposes diversifying selection on plant chemical defences. Plants in the speciose genus *Erysimum* (Brassicaceae) produce evolutionarily novel cardenolides as defences on top of ancestral glucosinolates, allowing plants to escape a diverse community of specialist glucosinolate-adapted herbivores. This gain-of-function thus provides a unique opportunity to identify the selective drivers of phytochemical diversification. The annual plant *Erysimum cheiranthoides* is widely distributed across Eurasia, and sampling of natural genotypes from the full range of its distribution reveals substantial qualitative as well as quantitative among-genotype variation in the novel cardenolide defences. In contrast, glucosinolates variation is exclusively quantitative and independent of variation in cardenolides, suggesting different selective pressures acting on the two types of defence. Both defences also vary substantially within-plant, with evidence for species-specific responses in the feeding behaviour of different *Erysimum*-associated herbivores. By linking variation in the ancestral and novel defences of this species to performance of its current and past herbivore community, we can thus conclude that ancestral glucosinolate defences are most likely maintained by selection from generalist herbivores, whereas novel cardenolide defences have enabled the plant to specifically target more specialized, glucosinolate-resistant herbivores. Even in this unique plant system with a functionally entirely novel defence, the diversity of selective pressures imposed on the plant by its herbivores thus prevents an ancestral defence to become obsolete. Therefore, the substantial phytochemical diversity found within virtually all plants is likely similarly favoured and maintained by selection from the plant's natural enemies.

Abstract ID: 1939
Poster board number:
P228

Evolution of chemical defenses in Salicaceae and the plant-herbivore arms race

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Plants and insects are involved in a complex coevolutionary arms race. The pressure by insect herbivores is thought to support diversification and escalation of plant defenses, giving rise to the plethora of plant defensive metabolites. Previous studies suggest that macroevolutionary trajectories in plant chemistry depend on the nature of prevailing selection pressures and can include other trends than escalation. Plant families with large geographical distributions covering variable environmental conditions are ideal systems for investigating the macroevolutionary trends in plant defenses. The willow family (Salicaceae) include ca. 55 genera with geographical distributions ranging from tropical forests to arctic tundra. In addition to common secondary metabolites such as flavonoids and tannins, members of the Salicaceae produce family-specific salicinoids that are effective against many generalist insects. Previous studies in temperate Salicaceae suggested that some species lost salicinoids and employ other defense strategies instead. This is probably because several temperate herbivore species have adapted to use salicinoids as feeding cues or for self-defense against predators. However, little is known about defensive roles and diversification of salicinoids in the tropical Salicaceae. We will combine a high-resolution Salicaceae phylogeny based on whole genome sequencing with detailed metabolomics surveys to investigate the evolution of chemical diversity in Salicaceae, with an emphasis on salicinoids. This study system will help us reveal how the diversity of individual metabolite groups arises and declines during the plant-insect arms race and explain why and how plants switch to alternative defensive strategies.

Abstract ID: 2079
Poster board number:
P229

Floral scent variation partly explains visitor variation within populations of *Arum maculatum*

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Floral scent is important for pollinator attraction by affecting pollinator identity and frequency of visits. It varies among and within plant species, but little is known about how inter-individual variation in floral scent affects the abundance and composition of floral visitor assemblages within populations. We address this question by investigating floral scent and visitor assemblages in two previously well-studied populations of *Arum maculatum* from Austria (JOS) and northern Italy (DAO). This deceptive plant species has a hyperdiverse scent and relies mainly on this phenotypic trait for pollinator attraction (Psychodidae and other Diptera). Both scent and floral visitor assemblages vary not only among, but also within *A. maculatum* populations. By correlating data on floral scent and visitor assemblages, we show that intrapopulation variation in floral scent partly explains variation in visitor assemblages. The quantity of the emitted floral scent correlated positively with visitor abundance in both populations, but explained visitor composition only in the southern (DAO) population, where strongly scented inflorescences attracted more sphaerocerid flies. However, in each population, the composition of floral scent did not correlate with the composition of floral visitors. Our study, for the first time, sheds light on the importance of inter-individual variation in floral scent in explaining floral visitor assemblages at the population level.

Abstract ID: 2127
Poster board number:
P230

Autopolyploidy and pollination divergence in *Dianthus broteri*: a transcriptomic aproach

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Polyploidy, defined as the acquisition of more than two sets of chromosomes, is one of the most important mechanisms in plant evolution. Autopolyploids would originate after a whole genome duplication event, causing changes in genomic structure, gene expression and regulation. This plasticity might cause phenotypic variation among ploidy levels, promoting ecological divergence between newly formed autopolyploids and parentals. We propose the autopolyploid complex *Dianthus broteri,* a carnation species with four different cytotypes (2x, 4x, 6x and 12x), whose populations present disjunct distribution from the South to the East of the Iberian Peninsula. In this research we focus on biotic factors, studying differences in dominant aromatic compounds between ploidy levels, capturing scents and analyzing them by gas chromatography. These differences might be due to changes in the expression and regulation of genes involved in floral scent production due to polyploidization, which have been studied carrying RNA differential expression analyses between the four cytotypes. Shifts in aromatic compounds could lead into changes in pollinator spectrum, as shown by previous studies and pollinator censuses, where high specialization in dodecaploids is observed, as well as differences between other polyploids levels. These differences might allow

autopolyploid levels in the *D. broteri* complex achieve their establishment by ecological divergence.

Symposium: S14. Ecological drivers and evolutionary consequences of within-population colour variation (id: 7)

Abstract ID: 1317
Poster board number:
P231

The role of opsins in search image tuning in the damselfly *Ischnura elegans*

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The damselfly *Ischnura elegans* is characterized by female-limited colour polymorphism, with one morph (andromorph) that mimics the blue colouration of males, and two other morphs (gynomorphs) exhibiting female-specific green or orange colouration. The learned mate recognition (LMR) hypothesis suggests that the presence of multiple female morphs reduces males' ability to recognize any one morph as a suitable mate, reducing the effects of male-mating harassment on females. Males, in turn, are predicted to improve their mate-finding ability by forming search images for the most common female morphs. Behavioural experiments provid some empirical support to the hypothesis males bias courtship towards more common morphs, however, it is not known whether changes in the peripheral visual system act to tune male search images. In this study, we quantify changes in opsin gene expression between the eyes of immature and mature male *I. elegans* from populations varying in female colour morph frequencies. We further test whether male opsin expression changes during adult development and across populations. We then assay the spectral absorbance of short and long-wavelength opsin proteins found in the ventral eye using in vitro heterologous expression and spectroscopy. Finally, we examine whether the male visual system is tuned to female body coloration and whether opsin expression correlates with female morph frequency across populations. Overall, our results examine the extent to which peripheral visual adaptations act as a mechanism to improve female detection and aim to empirically test sensory-based predictions of the LMR hypothesis to explain female polymorphism in this well-studied insect group.

Abstract ID: 1575
Poster board number:
P233

All that glitters is not iridescence–devising a measure of iridescence that links color to optics

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Many color traits in nature are known to vary within and between populations. While several studies have explored differences in pigmentary traits (e.g., carotenoid or

melanin pigmentation), little attention has been given to variation in structural colors, such as iridescent coloration. This is likely in part because iridescent colors are difficult to categorize and measure. To identify the underlying nanostructure requires time-consuming microscopy work. Moreover, while measures such as saturation and brightness can be directly related to mechanism (pigment concentration) for pigmentary colors, no such clear mechanistic relationship exists for iridescent colors. This makes it difficult to find the genetic underpinnings of color differences in iridescent colors. To solve this problem, we developed a method to quantify variation in iridescent feather nanostructures using cross-polarization imaging. Importantly, this method captures not only variation in intensity of the color but is directly related to the nanostructural order in the feather barbules, tying color to mechanism. It allows researchers to infer feather nanostructures from camera imaging alone, providing a fast way to quantify iridescencent nanostructures. Since many insects produce iridescent colors using similar principles (multilayer interference), it is likely that this method could be applied more widely. We hope that this method can be a first step towards unravelling variation in iridescent coloration in nature.

Abstract ID: 1582
Poster board number:
P234

Integration of signaling traits during social interaction in a colour changing lizard

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During social interactions, animals display various static and dynamic signaling traits that are mediated by the neuroendocrine system. For an animal to respond appropriately to a social context, all the traits involved in generating an optimal response should be suitably coordinated. The extent to which these trait components are correlated determines the direction and outcome of social interaction. We aim to understand the correlations between various static and dynamic traits expressed during aggressive interactions using *Psammophilus dorsalis* as a model. Using wild-caught lizards, we staged male-male interactions and recorded their responses using a digital video camera to quantify behaviour and a modified multi-spectral camera to quantify colour (hue, chroma, brightness, speed of colour change). Blood samples were taken before and after the experiments to measure baseline and social stress-induced hormone levels. During male-male social interactions, males displayed a suite of behaviors such as, head bob, attack, bite and mount. They also undergo dynamic colour change with yellow and UV colours on their dorsal and orange on lateral body region. We show that though colour and behavior are both signals of aggression, they can act independently, such that behaviourally more aggressive individuals do not necessarily display brighter and more saturated colours. Testosterone and corticosterone levels also change because of social interaction and are potential mediators for components of the complex signaling suite. Identifying relationships among these traits is essential to understand the evolution of suites of complex traits as well as alternate social strategies of individuals in a species.

Abstract ID: 1712
Poster board number:
P235

Coexistence of male colour morphs in an African annual fish

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African annual killifishes of the genus *Nothobranchius* are species rich clade with pronounced sexual dichromatism and intraspecific variation in male nuptial colouration. Many species are represented by two distinct male colour morphs. We combined data from natural populations with experimental test to understand temporal dynamics, drivers and consequences of red and yellow male morphs in *Nothobranchius furzeri*. We found strong geographic features of morphs distribution, relative interannual stability of morph ratios within populations where the morphs were sympatric, no difference in the survival, and no association between morph ratio and environmental characteristics in particular wild populations. In the laboratory, we found no role of sexual selection in maintenance of polymorphism. Females were choosy but individual females did not consistently select males of one or other colour morphs. Males of neither colour morph were more successful in male-male contest over access to females. We conclude that genetic drift is the most likely explanation for the distribution and maintenance of two distinct colour morphs in this species.

Abstract ID: 1889
Poster board number:
P236

Look under the leaf: effect of artificial light at night on duckweed colour

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One side of a leaf is always more exposed to light then the other. If you increase the amount of light on the plant the leaf colour may change. Potential mechanism is via increased production of pigments. These pigments protect the leaves from being damaged by UV light in nature. However, little is known if leaf colour polymorphism can be induced by unnatural changes to light exposure, such as these associated with urbanisation. The aim of my experiment was to test response of duckweed Landoltia punctata to artificial light at night. 80 replicates were randomly assigned to Control and another 80 to ALAN group. Control group experienced natural photoperiod, while ALAN group were also exposed to LED light at night. After 49 days, photos of the bottom sides of the leaves were taken using a digital camera. Leaf colour polymorphism was quantified from the images using an R package pliman. Duckweeds from the ALAN group had darker pigmentation underneath their leaves, relative to the Control group plants. It is possible that the leaf colour polymorphism resulting from response to artificial light at night is based on an existing pre-adaptation to strong sunlight experienced in natural habitats. Also, counterintuitively, in this duckweed species, the light-induced colour polymorphism is hiding on the dark side of the leaves, not directly exposed to excess light. Overall, this work highlights how studying human-induced exposure to artificial light at night can contribute to our understanding of colour variation within and between populations.

Abstract ID: 1968

Poster board number:
P237

Huge flower color polymorphism in *Iris pumila* L: previous studies and current research

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Huge flower color polymorphism found in natural populations of *Iris pumila*, endangered species inhabiting the Natural reserve of Deliblato Sand, Serbia, enables the identification of genetically distinct clones and makes this species a superb object for genetic polymorphism studies. Evolutionary biology studies of the dwarf bearded iris were conducted and published by the researchers from our department in the last four decades with special emphasis on evolutionary ecology and ecological genetics. However, these studies had several important limitations. Subjectivity in visual identification led to inconsistencies in defining color morphs. In our current research, variability in flower color is precisely accessed by reflectance UV-enhanced spectroscopy in the field, removing subjectivity in visual identification and influence of surrounding light conditions. Those specters reveal both discrete and continuous variation and will be followed by pigment HPLC analysis providing insights into the biochemical basis of flower color polymorphism. Limitations of previous studies also included smaller samples restricted to the flowering peak. Therefore, we are now also conducting a long-term study of the dynamics of color-morph frequencies using digital photography (including ones taken by drone), involving several complete flowering seasons on selected spots (covering over 4000 square meters and including tens of thousands of flowers) in undisturbed *I.pumila* natural population. This approach could reveal how precisely determined color-morph frequencies change both temporally and spatially in their natural habitat in the face of changing environments and vegetative succession and in perspective the role of natural selection vs. random events in maintaining flower-color polymorphism.

Abstract ID: 1992
Poster board number:
P238

Becoming pale in the city: a strategy of the European garden spider to adapt to city life?

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Urbanization can impose strong selection pressures on living organisms. One of these pressures is the increased environmental temperature due to human construction, habitat fragmentation, loss of vegetation and alteration of the water cycle in urban areas (Heat island effect). A way to reduce heating consists of changing the body temperature by adjusting body colouration. Darker surfaces absorb more light energy, that gets transformed into heat, than lighter surfaces, and thereby allow organisms to adapt to the suboptimal higher temperatures, or inversely to heat up faster in cold environments. We tested the hypothesis that the European garden spider, *Araneus diadematus,* is adapting

to this heat stress by developing a paler body colouration. The species is known for its profound intra-specific colour variation in the distinctive white cross pattern (structural colouration) and brownish background abdomen (pigmental colouration). We conducted a large-scaled sampling campaign to collect on average twenty female spiders along an urban-rural gradient consisting of 81 sampling locations at two spatial scales. All spiders were quantified in detail for different size and colour traits. We additionally studied heritability of these colour patterns in a common garden experiment and we compared populations within and outside city centers. We demonstrate a strong variability in colouration in line with putative adaptations to urbanisation and further show how the scale dependence and heritability of the different components allows us to infer the adaptive nature of these phenotypic changes along urban-rural gradients.

Abstract ID: 2146
Poster board number:
P239

Cryptic ultraviolet color variation in the polymorphic common wall lizard

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The common wall lizard, *Podarcis muralis* (Laurenti, 1768) is an emerging model for the study of color polymorphisms. It shows remarkable intrapopulation variability in ventral coloration with up to five morphs that, unlike other color polymorphic lizards, have not been shown to differ consistently in physiology or behavior. Here, we show that the white color morph in adult *P. muralis* comprises two ventral colors. One type reflects in the near ultraviolet (UV+), which is similar to the phenotype of newborn and juvenile lizards. The second type has reduced reflection in the UV range (UV-). To describe this variation, we analyzed the ventral spectra of 3786 adult individuals from multiple populations in the Pyrenees and Italy. We used a combination of visual modelling, light and transmission electron microscopy, and whole-genome sequencing to understand how this variation arises. Our results show large interpopulation variability in the proportion of these two white forms. UV+ coloration is less common in Italian populations. Visual modelling indicates that both phenotypes can be categorically discriminated by conspecifics.

Ventral skin of UV+ and UV- individuals possess the same set of dermal chromatophores, but iridophores are more abundant in UV- lizards. However, genomic scans did not identify any region underlying variation in the white morph, suggesting that phenotypic differences between white individuals are not generated by direct genetic control. A plausible scenario is that environmental constraints could shape iridophore ontogeny, preventing some individuals from developing an UV- phenotype as they mature.

Abstract ID: 2187
Poster board number:
P240

Piecing together the *Heliconius* wing pattern: Identification of colour elements used in mate choice

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Mating cues may be comprised of several individual elements, which act independently or in combination to attract a suitable partner. Each element may also act in other contexts, such as predator defence or camouflage. In *Heliconius* butterflies, wing patterns are comprised of several individual colour pattern elements, which advertise the butterflies' toxicity to predators. These wing patterns are also mating cues, and males predominantly court females with the same wing pattern as their own. However, it is unknown whether males base this preference on the full wing pattern or only individual pattern elements. We compared preferences of male *H. erato lativitta* between female models with the full wing pattern and those with some pattern elements removed. Preference in *H. erato lativitta* were equally strong between the full wing pattern model, and the model with the yellow forewing band removed, indicating that this element is not essential to the mating signal. Wing pattern preferences contribute to pre-mating isolation between two other *Heliconius* taxa, *H. erato cybria* and *H. himera*, so we next compared preferences for the same models in these species. *H. erato cyrbia* and *H. himera* showed strong differences in preferences, also related to the yellow forewing band. We conclude that mating preferences within *Heliconius* are not based on the full wing pattern, and that pre-mating isolation between species may be driven by differences in preference for individual wing pattern elements. This suggest that the evolutionary constraints imposed by contrasting selection pressures may not act equally across the whole pattern.

Abstract ID: 2220
Poster board number:
P241

SPIN*-CITY: the role of spider colour in adapting to urban heat islands.

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Cities are anthropogenic areas that differ markedly in (a)biotic characteristics compared to the surrounding countryside. Urban centers can heat up considerably due to the urban heat island effect (the use of building materials that trap heat, the loss of plants, wind and water) leading to specific thermoregulatory challenges, especially for ectothermic animals. Thermal melanism theory predicts that this increased temperature prompts an evolutionary response leading to paler individuals in urban areas that can stay cooler compared to their darker counterparts.
The European garden spider (*A. diadematus*) exhibits a remarkable, continuous colour variation, ranging from pale to dark individuals and resulting from an interplay of pigmentary background colour (likely melanin) and structural colouration (white spots consisting of guanine crystals). We sampled spiders in 14 European and North American cities along an urban/rural gradient in an ongoing and international collaborative effort (https://www.spiderspotter.com/en/info/for-scientists). These results demonstrate high variability in the response of background colour and a more consistent signal of smaller white spots which is likely mediated by city specific characteristics. Interestingly, these spiders use a potentially long range, passive dispersal mechanism in which they float on silk threads and are carried by the wind (ballooning), indicating high levels of gene flow between urban and rural areas.
We discuss how the thermoregulatory effects of colouration and the passive, long-range dispersal might play a important role in the maintenance of colour variation.

*SPIN means spider in Dutch

Abstract ID: 2224
Poster board number:
P242

Consequences of mobbing and predation on camouflage abilities and use of space in tawny owls

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Animal colouration has been selected through time since it is involving loads of different functions. For instance, intraspecific colour variation is often associated with camouflage or protection. Our study species, the tawny owl (*Strix aluco*), shows a melanin-based polymorphism with two colour morphs: brown and grey. This species is ideal to study changing camouflage effects due to environmental variation since the reddish-brown morph has lower survival and is more conspicuous in snowy (light) conditions compared to the paler grey morph. We ran two distinct experiments involving a series of treatments with captive-reared tawny owls (*Strix aluco*) to disentangle if the morphs differently choose to perch in a matching background, if they use space differently and if their response to predator and mobber cues depend on their perception of conspicuousness during roosting. We found that grey tawny owls are more prone to roost in front of a matching background than brown ones. Mobbing and predator cues triggered a behavioural alertness response similarly in both colour morphs. Our results suggest that the two morphs exploit their space the same way but use their camouflage abilities differently, which may affect detectability by mobbers and predators.

Abstract ID: 2229
Poster board number:
P243

Genetic control of colour in the tropical seastar *Linckia laevigata*

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Heritable colour polymorphisms (CPs), where alternate colour morphs occur within a single species and are genetically controlled, provide an unparalleled opportunity to rigorously assess the role colour plays in the evolution of species. However, until now there was little possibility of investigating CP in marine invertebrates as the pigments responsible for colours in this group are rarely known and even less is known about their synthesis or inheritance.
The iconic seastar *Linckia laevigata* is a rare exception to this rule. This seastar with its attractive appearance and rainbow of colour morphs is a 'poster child' for tropical reefs in the Indian and Pacific Oceans. It occurs as a variety of colours including yellow, orange, grey and purple but is best known for its royal-blue morph. Blue pigments are extremely rare in the animal kingdom, and as a result this species is prized by the aquarium trade and is in the top ten most traded marine invertebrates. Exceptionally the pigments responsible for the iconic blue coloration of the seastar *Linckia laevigata* have not only been identified as carotenoproteins, but we have obtained full-length sequences of the gene responsible for the protein moiety.
In this talk we present the first data to show whether there is a link between variation in the colour gene and visible colour. Our data will provide the opportunity to further investigate the effect of colour on adaptation, ecology, geographical range and speciation in *Linckia* and more widely in other species.

Abstract ID: 2307
Poster board number:
P244

Is shell colour polymorphism in Littorina associated with chromosomal inversions?

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Shelled molluscs are known for displaying diverse colour patterns, which are often polymorphic within and/or between population and species. Understanding the evolutionary mechanisms involved in the origin and maintenance of colour polymorphisms in molluscs, the largest phylum in the marine realm, is thus of ultimate importance to shed light on phenotypic diversification. Although different pigments have been identified in molluscs, the genetic basis and evolutionary processes underlying shell colour remain largely unknown, mainly when compared with vertebrates. Aiming to fill this gap, we started characterizing the genetic basis of colour polymorphism in marine gastropod species of *Littorina*, which show highly variable shell colour morphs within and among populations. Whole genome sequencing was implemented for two pools of sympatric individuals (yellow and dark brown) from a *L. fabalis* population characterized by a stable shell color polymorphism compatible with negative frequency dependent selection resulting from disassortative mating for colour. Differentiation between these *L. fabalis* colour morphs was higher within a large genomic region encompassing a polymorphic inversion that includes a QTL for colour in *L. saxatilis*. This contrasts with the pattern observed in a population of its sister species *L. obtusata*, where higher differentiation between colour morphs in that same genomic region was not found. Altogether, this suggests that chromosomal inversions (supergenes) may be involved in the maintenance of shell colour polymorphism in some but not all *Littorina* populations/species. The evolutionary processes underlying the association between inversions and shell colour and how this varies between *Littorina* species will be discussed.

Abstract ID: 2355
Poster board number:
P245

Relationship between seed dispersal and flower color variation in Anemone coronaria

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Anemone coronaria is a geophyte that shows a geographic flower color pattern along Israel. In the north part of the country there are color-polymorphic populations of red, purple, pink and white flowers, while in the south only red-populations occur. Preliminary observations on flowers showed a preference of pollinators (bees and flies) to purple and white flowers, compared to red ones. This might be an indication that color polymorphism in *A. coronaria* is maintained by a combination of diverse pollination systems. Additionally, abiotic environmental factors (soil, water availability), which vary along the gradient, may also play a role. Another important trait for population dynamics, is seed

dispersal, which has been rarely studied in relation to flower color variation. Here we investigate whether seed dispersal abilities of *A. coronaria* differ between polymorphic vs. monomorphic populations along an aridity gradient in Israel. Considering wind speed and direction, seed traits and surrounding vegetation, we applied a mechanistic model (WALD) to estimate seed dispersal distance and the probability of long-distance dispersal (LDD) for both mono- and polymorphic populations. Considering these parameters, we calculated a connectivity network between ~30 populations (mono- and polymorphic) along Israel. We expect two possible scenarios: **a)** degree of connectivity between all populations (mono- and polymorphic) is the same; **b)** higher degree of connectivity is found between only mono or only polymorphic populations. These results might provide insights regarding the role of seed dispersal on maintaining flower color variation in *Anemone coronaria*.

Abstract ID: 2362
Poster board number:
P246

Dissecting proximate causes of variation in melanin-based colouration in the house sparrow

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Whether melanin-based plumage colouration accurately reflects a bird's quality is still controversial. Observations of numerous physiological and biochemical aspects of environmental and individual's condition gave rise to a wide range of unsolved research questions. To better understand potential mechanisms behind the observed variation in plumage colouration, we shifted our attention from a commonly measured high-level expression of colour to low-level physiological phenomena by targeting the microstructure and direct pigment content of the feather. In a well-studied bird model system, the house sparrow (*Passer domesticus*), we combined an experimental manipulation of birds' physiological condition and availability of resources that are key to the production of the studied colouration (phenylalanine and tyrosine (PT). We found that feathers from sparrows fed with the control diet had noticeably lower values of brightness, suggesting an increased absorption of visible light and higher quality of the ornamental "blackness" in comparison to those sampled from birds fed with a PT-reduced diet. The assumption was confirmed by analysing lower-level phenomena. Electron paramagnetic resonance (EPR) spectroscopy detected higher melanin concentrations in samples from the control than the PT-reduced group. Our multi-level analysis excluded mechanisms such as barbule density and melanosomes' distribution, clearly pointing to the finest-level proxy of colour: the concentration of melanin in melanosomes themselves. Together, these results strongly suggest that despite melanins being manufactured by birds endogenously, the efficiency of melanogenesis can be noticeably limited by diet. As a result, the birds' plumage colouration is affected, which may entail consequences for an individual, e.g., in social signalling.

Symposium: S15. Rapid evolution of color patterns (id: 954)

Abstract ID: 1124
Poster board number:
P247

Evolution and development of wing colour patterns in ithomiine butterflies

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Increasing our knowledge of genetic architecture and developmental processes causing phenotypic differences between organisms aids our understanding of how evolution gives rise to the huge diversity of organisms found in nature. Diversity in certain groups of toxic butterflies, among others *Heliconius* and ithomiine butterflies, can be directly linked to selective forces shaped by predation and aposematism where different co-localizing species are known to mimic each other. The genetic basis for pigmentation patterns in *Heliconius* is well-studied, however, the genetic basis of colour patterns in ithomiine butterflies remains largely unknown. Identifying the genes underlying the ithomiine colour patterns will provide the opportunity to investigate the repeatability of discoveries in *Heliconius* across longer evolutionary timescales. I study the genetic architecture of wing patterns in several species of ithomiine butterflies to elucidate the genomic changes that control morphological variation and diversification. GWAS analysis identified that Cortex, the gene that controls the presence or absence of a yellow band in *Heliconius*, also controls a yellow band pattern in *Mechanitis* butterflies. I am now investigating the expression pattern of this gene through antibody staining and in situ hybridization, as well as functionally validating the GWAS results through genetic modification using CRISPR-Cas9.

Abstract ID: 1544
Poster board number:
P248

Plumage coloration misrepresents relationships in a recent avian radiation

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Among passerine birds, the wagtails (Motacillidae, genus *Motacilla*) offer striking examples of rapid evolution of male plumage. One outstanding question is to understand whether similar phenotypes reflect shared ancestry, or other evolutionary processes (e.g. retention of ancestral polymorphism, evolutionary convergence, introgression). However, efforts to understand the processes underlying plumage evolution have been hampered by difficulties in reconstructing the wagtails' phylogenetic and demogaphic histories. Here, we use complete genome sequences to resolve the phylogenetic relationships of the "black-and-white" wagtails, a group of five species including the extremely phenotypically variable White Wagtail (*Motacilla alba*). Our findings demonstrate that high levels of ancestral allele sharing among species obscure their phylogenetic relationships. Furthermore, we found at least one introgression event, from the White Wagtail into the African Pied Wagtail (*M. aguimp*), which creates additionnal genealogical conflicts at the root of the clade. Overall, the reconstructed phylogenetic

tree shows that the “black-and-white” wagtail species diversified through rapid initial splits, and that species with similar plumage phenotypes are not closely related, suggesting that plumage characteristics evolved either through retention of ancestral polymorphism or evolutionary convergence. Finally, a closer investigation of the White Wagtail’s subspecies support that two geographically adjacent populations with strikingly similar coloration patterns were not closely related, suggesting a complex phylogeographic scenario and a role of hybridization in plumage evolution.

Abstract ID: 1705
Poster board number:
P249

Genomic Analysis of Host Association and Coloration in Clownfishes

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Clownfish and anemones are among the most charismatic examples of mutualism in the animal kingdom. Anemone host usage by clownfish species was recently updated and interestingly exhibited patterns of host associations based on coloration patterning. Clownfish species that are orange/yellow are hosted by *H. magnifica*, species that are dark orange/red are hosted by *E. quadricolor*, and those that are darker with contrasting colors and bands are Generalist (hosted by 3+ anemone species). Evolutionary convergence based on coloration and host usage within different clades of the clownfish phylogeny might be one of the drivers of adaptative radiation creating higher diversity in clownfish. Using a phylogenomic approach, we analyzed all the orthologous protein-coding genes between the damselfish and the clownfishes (15,229 genes). We estimated the rate of non-synonymous vs. synonymous substitutions for each branch of the tree by mapping the substitutions at each site. We then tested for each gene if the switches of host association across the clownfish phylogenetic tree were associated with changes in dN/dS values. We highlight possible candidate genes that could be important in the clownfish-sea anemone mutualism and could be involved in the specific association with certain types of hosts. We further examined genomic regions that showed elevated levels of divergence between the type of host used. Our results show potential genes associated with host switches in clownfish both at the genomic region and the protein-coding genes, which gives us insights into the genomic mechanisms driving host association.

Abstract ID: 1710
Poster board number:
P250

Clownfish’s host-phenotype trait complex is a product of convergent evolution.

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Clownfishes and their association with sea anemones represent one of the most iconic examples of mutualism in the animal kingdom. The group also reflects many of the telltale characteristics of classic adaptive radiation. 28 species of which 24 evolved

during the last 5 million years forming associations with up to ten different sea anemones species, resulted from one speciation event triggered by the acquisition of mutualism with the venomous sea anemones (Litsios, *et al*. 2012). Nevertheless, the mechanisms involved in the evolution and diversification of the clade are not yet understood. Studies on coloration and morphology have advertised the importance of these traits in the evolution of the clade. However, the mechanism that links host association and phenotype, explaining the evolutionary trajectory of clownfishes remains a mystery. We hypothesize that host selection is coupled with phenotypic traits such as coloration and morphology, forming a trait complex that has shaped the radiation of the clade. Here, we redefined the host associations of clownfishes based on > 4000 photographed observations. We analyzed coloration patterns and morphology of 207 images of several populations of clownfish species distributed along the Indo-Pacific. Then, we integrated host selection, coloration, and morphology into macroevolutionary models. Our results provide evidence of the relationship of host selection with morphology and coloration patterns, exhibiting signatures of host-phenotype convergent evolution and detecting critical host transitions that triggered character displacement in sympatric lineages.

Abstract ID: 2123
Poster board number:
P251

Convergent loss of ommochrome pigmentation in cave-adapted isopod crustaceans

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Albinism or pigment loss is an adaptation to a subterranean lifestyle and one of the prime examples of convergent evolution. It occurs in diverse cave-adapted animal groups regardless of the type of pigment they contain. The causes of melanin loss have been described in only a couple of cave-dwellers, while the mechanisms of albinism as a consequence of any other pigment deficiency are completely unexplored. Ommochromes are tryptophan derivates and a less studied class of pigments found in a wide range of invertebrates. Our research was focused on related crustaceans of the order Isopoda. Using a biochemical approach to extract and detect ommochromes in conjunction with liquid chromatography coupled to mass spectrometry (UPLC-MS) the type of biological pigments in surface isopods was determined. We identified for the first time and to the best of our knowledge ommochromes in three groups of surface isopods: families Sphaeromatidae (Flabellifera) and Trichoniscidae (Oniscidea) and the genus *Proasellus* (Asellota). Additionally, we quantified the precursors of ommochrome synthesis in closely related surface and cave species. Our results suggest that the disruption of ommochrome synthesis is preferentially at the beginning of this anabolic cascade since we observed the accumulation of tryptophan in cave dwellers. These results suggest that isopods are a good model to study the molecular mechanisms underlying albinism as a consequence of ommochrome deficiency. To resolve that issue, we will look for the expression changes and possible inactivating mutations in the candidate genes using a comparative transcriptomic approach on several pairs of surface-cave relatives.

Abstract ID: 2129

Poster board number:
P252

Understanding wing patterns in Central asian Hawkmoths

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Colouration and its variation in the animal world has fascinated scientists since the beginning of natural history studies. This holds particularly true for butterflies and moths, the Lepidoptera, as their sheer wing-pattern diversity has been the centre of many research projects. Essentially, wing patterns were and still are key to differentiate most species of Lepidoptera. However, the sole usage of these features to delimit some groups of closely related species, such as *Hyles* hawkmoths, has turned out to be misleading. Predator avoidance, mate recognition and sexual selection, but also abiotic factors and genetic drift in more or less isolated populations of the same species drive wing pattern differentiation. Furthermore, and in particular with the Palaearctic *Hyles*, hybridization is a frequent phenomenon and intermediate phenotypes, such as transitional forewing patterns, occur regularly. Our study, which combines and walks along the vicinity of population- and phylogenomics with these moths, strives to understand the genetic basis of the wing patterns and their evolutionary pathways.

Abstract ID: 2133
Poster board number:
P253

Constrained evolution of dorsal plumage color contrasts with flexible evolution of ventral feathers

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When selection acts differently on dorsal versus ventral coloration, ancestral covariance between these traits should break down, leading eventually to independent modules of trait evolution . Here, we compare the evolution of feather color across 11 body regions for Australian songbirds (Meliphagoidea). We find evidence for three modules of covarying color regions. Among these modules, color of flight feathers and dorsal plumage is highly conserved compared to ventral plumage, which evolved numerous contrasting color patterns at a 3-20 times faster rate. While both dorsal and ventral plumage are correlated with the degree of vegetation (NDVI), dorsal plumage color is more similar to satellite photos of background substrates. Dorsal plumage color is thus constrained by its function in background matching. Overall, differential selection on ventral and dorsal colors likely maintains these as distinct modules over evolutionary time scales – a novel explanation for dorsoventral contrast in pigmentation.

Abstract ID: 2149
Poster board number:
P254

Hyles (Lepidoptera: Sphingidae) karyotype and high quality genomes as basis for wing pattern studies

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FISH analysis of the karyotype revealed n = 29 chromosomes in *Hyles euphorbiae*. The *H. euphorbiae* genome was PacBio sequenced and amended by Hi-C Illumina data yielding a 504 Mb assembly with a scaffold N50 of 18.2 Mb and 99.9% of the data being represented by the 29 largest scaffolds, corroborating the haploid karyotype. Hi-C data was also used for chromosome-level scaffolding of the published *H. vespertilio* genome, leading to a second assembly (651 Mb) with scaffold N50 of 22 Mb, 98% in the 29 largest scaffolds representing the chromosomes. The larger *H. vespertilio* genome size was accompanied by a proportional increase of repeats from 45% in *H. euphorbiae* to nearly 55% in *H. vespertilio*.
In both *Hyles* species, the three wing pattern genes, *optix, wingless/wint-1* and *cortex*, were found on chromosomes 23, 4 and 17, respectively. Peaks of divergence surrounding *wingless/wnt-1* and *cortex* provide candidate genomic areas in which wing patterns are determined in this genus.

Abstract ID: 2382
Poster board number:
P255

Phylogeny drives color pattern resemblance in Müllerian mimics

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Müllerian mimicry is one of the major drivers of butterfly color pattern diversity. It results from strong selection for resemblance exerted by predator while learning to avoid unpalatable or toxic species. Mimicry provides spectacular cases of adaptive phenotypic evolution and mong the strongest selection coefficients measured. However, within a given mimicry ring, a wide range of levels of resemblance can be observed, from really coarse to nearly perfect mimicry. The persistence of perfect and imperfect resemblance within the same selective context is a challenge to our understanding of mimicry selection, of adaptive optima, and of evolutionary paths and paces leading to stable equilibria. We here tackle this problem both from a theoretical and an empirical point of view using natural mimicry communities. We modeled the effect of the shape of mimicry selection on the evolution and coexistence of perfect and imperfect mimicry. We then analyzed wing pattern ressemblance in a real community of butterfly Müllerian mimics, using a tool specifically designed to compare color patterns quantitatively and comprehensively. Contrary to Batesian mimicry, where model species are often known, it is more difficult to define perfect and imperfect mimicry in Müllerian communities. We developed a method based on pattern generation and randomization to measure and compare phenotypic variance at the scale of a mimicry community. In a phylogenetic framework, we showed that, imperfect mimicry prevails in real communities, and that

phylogeny drives the level of resemblance. Our combined approach suggests that particularities in evolutionary trajectories could explain cases of perfect mimicry.

Symposium: S16. Predator cognition and the evolution of prey defence strategies (id: 938)

Abstract ID: 1001
Poster board number:
P256

Chemical defense acquired via pharmacophagy can lead to herd protection in a sawfly

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Predation is an important selection pressure acting on organisms, with organisms showing diverse anti-predator strategies to combat it. One such widespread strategy is chemical defense in which organisms either synthesize or extrinsically acquire defensive chemicals. An interesting aspect is the intraspecific transfer of such chemicals and whether such chemicals acquired from conspecifics can also serve as defense against predation. Here, we used adults of the turnip sawfly, *Athalia rosae*, which can acquire neo-clerodane diterpenoids and potentially other compounds ('clerodanoids') via pharmacophagy when having access to the plant *Ajuga reptans*. We show that clerodanoid access mediates protection against predation by mantids for the sawflies, both in a no-choice feeding assay and a microcosm setup. Even indirect access to clerodanoids, via nibbling on conspecifics that had access to the plant, resulted in protection against predation by mantids albeit to a lower degree than direct access. Furthermore, sawflies that had no direct access to clerodanoids were less consumed by mantids when they were grouped with conspecifics that had direct access. Most, but not all, of such initially undefended sawflies could acquire clerodanoids from conspecifics that had direct access to the plant, although in low quantities. In summary, our results demonstrate that clerodanoids serve as effective chemical defense that can be acquired by pharmacophagy as well as by intraspecific transfer between adults. Moreover, the presence of chemically defended individuals in a group can confer protection onto conspecifics that had no direct access to clerodanoids, suggesting a 'herd-protection' effect.

Abstract ID: 1132
Poster board number:
P257

Recognition of predator calls is socially transmitted across territory borders in wild birds

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Eavesdropping on predator calls to assess predation risk is ubiquitous in birds and other sound-oriented taxa. However, the mechanisms through which individuals acquire the ability to recognize that specific sounds are signals of a threat remain poorly explored. Earlier work focusing on visual and olfactory predator recognition has suggested that animals often learn such behaviors socially i.e., from others. Yet, the role of social learning in auditory predator recognition remains untested under natural conditions. Here, I tested whether an ability to recognize predator calls in free-living birds can be socially transmitted among conspecifics occupying adjacent territories during the spring breeding season. In a playback experiment, I found that Wood Warblers (*Phylloscopus sibilatrix*) can learn to recognize unfamiliar, complex sounds (samples of punk rock songs) as putative predator calls by associating the appearance of unfamiliar sounds with alarm calling reaction of conspecific neighbors. Moreover, I found that once learned soon after nestlings hatching, the anti-predator response of Wood Warblers was then retained until the end of nestlings rearing period. Jointly, these results demonstrate social learning as being at the forefront of predator–prey interactions, providing one of the mechanisms underlying the widespread abilities of animals to rely on predator vocalizations when assessing predation risk, and point towards the positive role of individuals' social environment in the acquisition of vital, fitness-enhancing skills even in otherwise territorial animals.

Abstract ID: 1306
Poster board number:
P258

Quantification of mimicry resemblance in butterflies using feature extractor of deep neural network.

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Studies on Mullerian/Batesian mimicry have a serious technical limitation in evaluating the model – mimic similarity in a quantitative way, which is particularly problematic, for example, when we are going to discuss the possible role of "imperfect mimic" as an evolutionary origin of the "perfect mimic" comparing the similarity in appearance between the model and its mimics. Deep neural networks that have been trained for image classification tasks can also be used for the measurement of similarity between two images. Metrics generated by the feature extractor of pre-trained deep neural networks have been shown to represent the similarity based on human perception, and the method requires relatively little engineering effort. Here we tested the validity of a feature extractor, LPIPS, in the task of the quantitative estimation of similarity between mimetic/non-mimetic pairs of butterfly specimens. The distances deduced by LPIPS were consistent with an experimentally confirmed mimicry system, the female-limited Batesian mimicry in *Papilio polytes* (model: *Pachliopta aristolochiae*), suggesting that LPIPS can be used to provide an index of similarity between butterfly specimen images. When LPIPS was applied to other species pairs for which mimicry is argued (e.g. tiger Danaus mimicry of *Argyreus hyperbius*), it suggested that some pairs are less similar than currently considered. These results demonstrated that the feature extractor of pre-trained deep neural networks can be used as a tool for the unbiased evaluation of mimetic relationships.

Abstract ID: 1507
Poster board number:
P259

Evolution of antipredator response in a complex life cycle

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An organism is expected to use all its potential to avoid its predator. However, the organism faces multiple selection pressures simultaneously. Due to the interplay of these forces, we see an optimised response shaped over many generations. Animals with complex life cycles provide an exciting system to study the evolution of antipredator responses across life stages because such life history can pose manifold selection pressures on a trait. Given their differences in morphology, physiology and functionality, that which is beneficial at one stage might not be the best solution for another stage. We test contrasting hypotheses for the evolution of antipredator response in a complex life cycle of *Aedes aegypti* where the larval and pupal stages share the same habitat and experience very similar predation risk conditions. One hypothesis is that pupae should mount an enhanced antipredator response if larvae have already experienced predation cues. However, the pupal stage is motile and non-feeding. It depends on the resources accumulated during the larval stage for its functions. Therefore, alternatively, pupae might mount a reduced response in the presence of a predator, given that larvae have already experienced a starvation vs predation trade-off. To test these hypotheses, we reared larvae with and without predation cues and later exposed the naive pupae to the same cues to check for their antipredator response. We also performed a survival assay where we released these naive pupae in the presence of an actively feeding predator to test the fitness payoffs of their antipredator response.

Abstract ID: 1522
Poster board number:
P260

Shimmering response in *Apis dorsata* are triggered by dark stimuli moving against a bright background

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Due to the absence of physical barriers, the open-nesting giant honeybee *Apis dorsata* has evolved a spectacular collective defence behaviour – known as "shimmering" – against predators, which is characterised by travelling waves generated by individual bees flipping their abdomens in a coordinated and sequential manner across the bee curtain. We examined if shimmering is visually-mediated by presenting moving stimuli of varying sizes and contrasts to the background (dark or light) in bright and dim ambient light conditions. Shimmering was strongest under bright ambient light, and its strength declined in dim-light. *A. dorsata* shimmered only when presented with the darkest stimulus against a light background, but not when this condition was reversed (light stimulus against dark background). We suggest that this is an effective anti-predatory strategy in open-nesting *A. dorsata* colonies, exposed to high ambient

light, as flying predators are more easily detected when they appear as dark moving objects against a bright sky. Moreover, the stimulus detection threshold (smallest visual angular size) is much smaller in this anti-predatory context (1.6° - 3.4°) than in the context of foraging (5.7°), indicating that ecological context affects visual detection threshold.

Abstract ID: 1563
Poster board number:
P261

Variability of a cooperative defense behavior in social pine sawflies

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To determine the evolutionary potential of cooperative traits, we need to identify the genetic and environmental sources of their phenotypic variation upon which selection acts. In addition to collecting phenotypic data from wild and lab-reared populations, this also requires using quantitative genetic and molecular methods. By doing so, we studied the sources of variation in a cooperative behavior using the socially behaving pine sawflies *Diprion pini* and *Neodiprion sertifer*. During the larval stage both species feed and defend gregariously in groups of 20-100 individuals. They are specialized on pines from which they sequester defensive compounds for their defense. When attacked, the larvae raise their head and regurgitate a resinous fluid in concert which makes them less profitable for predators and parasitoid wasps. The advantage of this system is that there is natural variation in the benefits and costs of cooperation as well as in the expression of this behavior. We can also quantify the individual contribution to cooperation. This gives us the possibility to measure correlations between investment into cooperation and other life-history traits and to identify potential phenotypic and genetic constraints. We discuss how these results will increase our understanding of the mechanisms shaping cooperative behaviors.

Abstract ID: 1683
Poster board number:
P262

Innate reactions of birds to mimetic hoverflies and their hymenopteran models

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Hoverflies (Syrphidae) belong to textbook examples of Batesian mimicry, but experiments testing reactions of natural predators to hoverflies and their hymenopteran models are still scarce. We tested the effect of potential innate avoidance on reactions of avian predators towards hymenopterans and their hoverfly mimics belonging to wasp-like, bumblebee-like, and honeybee-like mimetic rings. As naive predators, we tested

hand-reared juvenile great tits (*Parus major)* lacking any experience with either hymenopteran or dipteran prey. The birds were divided into four groups, each tested in a multiple-choice trial with a different combination of frozen insect specimens, namely: (1) bumblebee, bumblebee-mimicking hoverfly, and non-mimetic hoverfly; (2) honeybee, honeybee-mimicking hoverfly, and non-mimetic hoverfly; (3) wasp, wasp-mimicking hoverfly, and non-mimetic hoverfly; (4) bumblebee, honeybee, and wasp. The prey was presented to birds simultaneously on the natural background of a green leaf, and we recorded the order in which the three prey items were handled by the birds, duration of handling, and frequency of aversive reactions. Birds from the bumblebee and honeybee group had a tendency to handle the mimetic hoverflies first, followed by the models, and leaving the non-mimetic control as the last choice. By contrast, neither birds from the wasp group or birds tested with the three hymenopteran models showed any preferences. The results do not indicate any strong innate avoidance of the hymenopteran models and/or their hoverfly mimics. Instead, the reactions of juvenile birds appeared to be guided by a preference for larger prey combined with a slight bias against some hymenopteran models.

Abstract ID: 1692
Poster board number:
P263

Snakes as mediaeval knights in ring armour: Antipredatory strategy in sand boas (Erycidae)

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We trace the evolution of the morphological structures essential for the mechanical defence of the body in sand boas (Erycidae). Those fossorial snakes with cylindrical bodies and blunt heads have short tails, which are usually indistinguishable from the head. Caudal vertebrae are enlarged and highly modified. Sand boas are known for their tail displays, which are probably an antipredator strategy. The altered shape of the tail, the unique caudal vertebrae and the tail displays suggest that the tail plays an important role in the antipredator repertoire of sand boas. Our study examined the tail morphology of 7 sand boa species and 20 other snake species from different families using microcomputed tomography (μCT). We detected the presence of dermal armour (osteoderms) in three sand boa species. This is the first description of dermal armour in snakes. The ancestral state reconstruction revealed one origin of caudal vertebrae modification and up to three independent origins of osteoderms within a single fossorial family of Erycidae. We did not find a similar pattern in any other examined snake species. Nevertheless, similar structures are known from unrelated clades of squamates like gerrhosaurids and geckos. This supports the view of underlying deep developmental homology. Osteoderms support the defence of the sand boas as ring shirts of the mediaeval knights. We interpret it as another component of the rich antipredatory strategy of sand boas. This project was supported by the European Regional

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Poster board number:
P264

Weapons or deterrents? Exploring the mode of nudibranch chemical defence against predators

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Defensive chemicals are used by plants and animals to reduce the risk of predation through different mechanisms, including toxins that cause injury (weapons) and unpalatable or odiferous compounds that prevent attacks (deterrents). However, whether effective defences are both toxins and deterrents, or work in just one modality is often unclear. In this study, our primary aim was to determine whether nudibranch defensive compounds acted as weapons (in terms of being toxic), deterrents (in terms of being distasteful) or both. Our secondary aim was to investigate the response of different taxa to these defensive compounds. To do this, we identified secondary metabolites in 30 species of nudibranch molluscs and investigated their deterrent properties using antifeedant assays with three taxa: rock pool shrimp and two fish species. We compared these results to toxicity assays using brine shrimp and previously published toxicity data with damselfish. We found no clear relationship between palatability and toxicity, but instead demonstrate how defensive compounds can be classified into categories based on these two defensive properties. Overall, responses to secondary metabolites were similar between fish and shrimp, except for isonitriles, which were highly unpalatable to shrimp but weakly unpalatable to fish. Our results pave the way towards better understanding how animal chemical defences work against a variety of predators. We highlight the need to disentangle weapons and deterrents in future work on anti-predator defences to better understand the foraging decisions faced by predators, the resultant selection pressures imposed on prey and the evolution of different anti-predator strategies.

Abstract ID: 1747
Poster board number:
P265

Birds select for higher mimetic accuracy in ant-mimicking spiders and true bugs

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Spiders and true bugs have the highest incidence of ant-mimicry among arthropods. At the same time, there is a considerable variation in mimetic accuracy within both taxa, which can be partly explained by selection from different types of predators. Passerine birds, visually-oriented predators of spiders and insects, may represent an important predator group potentially selecting for higher mimetic accuracy, but studies focused on their response to ant mimics are surprisingly scarce. We compared responses of great tits (*Parus major*) to three myrmecomorphic species – an accurate ant-mimicking spider *Leptorchestes berolinensis,* inaccurate ant-mimicking spider *Zodarion rubidium*, and accurate ant-mimicking damsel bug *Himacerus mirmicoides*. To assess the effect of specific experience with ants on response of birds to myrmecomorphic species, we tested hand-reared juvenile birds, lacking previous experience with prey from the wild. The birds were divided into several experimental groups and tested with ant-mimicking species either directly (naive birds) or following the avoidance training with putative ant models (*Lasius fuliginosus* and *L. emarginatus*); control group was tested with non-mimetic spiders (*Pardosa lugubris*). Naive birds mostly attacked all three ant-mimicking species, frequently killed, and consumed them. Ants were also initially attacked and killed, but the birds quickly learned to avoid them. Following this experience, the birds mostly left accurate ant-mimicking spiders (*L. berolinensis*) and damsel bugs untouched, but inaccurate ant-mimics and non-mimetic spiders were frequently attacked, killed, and eaten. The results suggest that selection by passerine birds drives higher mimetic accuracy in myrmecomorphic species.

Abstract ID: 1805
Poster board number:
P266

I remember you! Multicomponent warning signals and predator memory

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Visual antipredator warning signals are often multicomponent, i.e. they consist of colour, pattern, contrast, shape and size, and predators may use one or more signal components to discriminate between profitable and unprofitable prey. Although the role of particular components of visual warning signals in predator discrimination learning has been intensively studied, the importance of different components for predator long-term memory is considerably less understood. We tested 37 wild-caught great tits (*Parus major*) to find out which components of prey visual warning signals play an important role in prey memorability over a longer time period. We used artificial prey items – cyan and magenta paper 'bugs' with a contrasting black pattern – baited with a piece of mealworm (unpalatable baits soaked in quinine). Birds were first trained to discriminate between palatable and unpalatable prey differing in both colour and pattern. After four weeks, birds were divided into three groups and retested: first group was tested with prey that differed in both colour and pattern (training stimulus), second group with prey that differed only in colour, and third group with prey differing only in pattern. The birds remembered their experience with unpalatable prey even after four weeks without any reinforcement. Although the colour alone seemed to be a more salient cue than the pattern, the combination of both cues was more effective for prey recognition after four weeks than either colour or pattern alone.

Abstract ID: 2059

Poster board number:
P267

Are ladybird spiders (*Eresus* spp.) Batesian mimics of aposematic insects?

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Conspicuously coloured ladybird spiders (*Eresus* spp.) were considered to be undefended against predators and rather protected by their resemblance to similar, better defended species of the red-and-black mimicry ring. However, experimental support for this hypothesis is lacking. We tested the effectiveness of spiders' defences against their two potential predators, praying mantises (*Mantis religiosa*) and great tits (*Parus major*). We found that the ladybird spiders were completely undefended against the mantises. Surprisingly, the same was true for seven-spotted ladybirds (*Coccinella septempunctata*), which are probably the most ecologically relevant model of the spiders. Therefore, neither direct defence nor mimetic relationships provide ladybird spiders with sufficient protection against the mantises. Juvenile great tits always initially attacked both the spiders and ladybirds, but killed and consumed ladybirds considerably less frequently. When the prey was presented in a sequence, experience with spiders did not change the birds' responses to ladybirds and vice versa, indicating no effect of potential mimetic resemblance. By contrast, almost all wild-caught great tits killed and consumed the spiders, but avoided the ladybirds on sight. The experience with spiders highly increased the willingness of the birds to attack (but not to kill and consume) the ladybirds. However, the experience with ladybirds provided the spiders with no protection against the birds. This seemingly paradoxical outcome (mimic harms its model but receives no protection) could be partly explained by the simplified experimental environment. Furthermore, the actual cost for the model was relatively low due to negligible mortality risk.

Abstract ID: 2364
Poster board number:
P268

Do spiders ride on the fear of scorpions? A cross-cultural eye tracking study

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A hypothesis based on recent studies suggests that fear of spiders might stem from a generalized fear of chelicerates or fear of scorpions. We conducted an eye tracking experiment using a spontaneous gaze preference paradigm, with spiders and scorpions as threatening stimuli and grasshoppers as control stimuli. 67 participants from Somaliland and 67 participants from the Czech Republic (mainly university students in

both countries) were recruited and presented with a sequence of paired stimuli. Both Somalis and Czech people looked longer (duration of the gaze) and more often (number of fixations) on the threatening stimuli (spiders and scorpions) when presented with a control (grasshopper). When both threatening stimuli were presented together, Somalis participants focused significantly more on the scorpion, whereas we found no significant difference in Czech participants. Our results corroborate the hypothesis that fear of spiders originated as a generalized fear of chelicerates or fear of scorpions.

Abstract ID: 2381
Poster board number:
P269

Fear of snakes in the cradle of human kind

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When threatened, many well-protected animal species signal their dangerousness in a specific manner to repel a possible predator's attack. Therefore, on the receiver's side, a mechanism of early detection particularly sensitive to such threat display may be required by adaptive evolution. In the case of snakes, the warning is often signaled by a threatening posture. In this study, we aimed to explore whether human mind is fine-tuned for snake's intentional threat signalling rather than just unintentional cues of its presence. We investigated whether people pay greater attention to a snake in threatening posture as opposed to a snake in a relaxed posture and we compared the fear elicited by snakes in threatening and relaxed posture. We recruited participants from Somaliland in the Eastern Africa where modern humans probably evolved, and the Czech Republic. Ancestors of Somali people have never left the savanna environment while the people of the Czech Republic are a derived population that left both the geographic region and the environment of human origin. We found that both populations distinguished between the postures as snakes in threatening posture attracted more attention and elicited greater fear. This effect was especially pronounced in cobras but also in vipers. The mechanism of early snake detection mediated by increased fear could have already evolved in the common ancestor of modern humans.

Abstract ID: 2472
Poster board number:
P270

Predator response to two components of the putative deimatic display of the Colombian four-eyed frog

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Deimatic displays, where sudden changes in prey appearance elicit aversive predator reactions, have been suggested to occur in many taxa. These (often only putative) displays frequently involve different components that may also serve antipredator functions via other mechanisms (e.g. mimicry, warning signalling and body inflation). The Colombian four-eyed frog, *Pleurodema* brachyops, has been suggested to gain protection against predation through putative deimatic displays where they inflate and elevate the posterior part of their body revealing eye-like colour markings. We exposed stationary artificial frogs to wild predators to test whether the two components (eyespot/colour markings, posture) of their putative deimatic display, and their combination, provide protection from predation without the sudden change in appearance. We found that frogs with colour markings on their normal (non-defensive) posture were best protected from predation, whereas frogs without these markings in the same posture were attacked the most. Interestingly, elevated posture increased predation on frogs with colour markings, but frogs without them suffered lower predation when in the defensive posture. We did not detect any obvious additive effect of defensive posture and colour markings, but our findings suggest that the different components of P. brachyops' coloration may serve different functions during a deimatic display. The increased predation risk on frog models in defensive posture with colour markings may be a consequence of increased detectability caused by conspicuous eye spots being clearly displayed in a static position. Further research is needed to elucidate the role of each component when accompanied by sudden prey movement.

Symposium: S17. Brain, behaviour and cognitive evolution (id: 932)

Abstract ID: 1368
Poster board number:
P271

Sensory, neural, and life history predictors of anti-parasitic egg rejection as a cognitive trait

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Obligate brood parasitic birds lay their eggs in the nests of other species, reducing the host's own reproductive output. To circumvent these fitness costs, many – but not all – host species have evolved the ability to recognize and reject brood parasitic eggs. What sensory, neural, and life history factors predict egg rejection behaviors and why do individuals within and hosts across species vary in their likelihood of rejection? Previous focal and comparative studies have found that egg rejection rates covary with several biotic factors (including larger eye sizes, smaller relative brain sizes, and more northerly breeding latitudes), but much behavioral variation in the occurrence of egg rejection remains unexplained. Recently, tests of a corollary of the maternal investment hypothesis have been conducted by assessing whether individual and species with greater clutch sizes are more likely to eliminate parasitic eggs. Contrary to the prediction,

there was no evidence for a positive relationship between clutch size and egg rejection rate. Rather, the analyses suggest a consistent negative relationship between clutch size versus egg rejection rate within and across species. These results are instead consistent with two previously proposed alternative hypotheses: that egg rejection is constrained by a trade-off between maternal investment and anti-parasitic defenses, possibly mediated by endocrine mechanisms linked to parental care, and/or that cognitive decision rules facilitate the detection of dissimilar (parasitic) eggs in smaller clutches.

Abstract ID: 1453
Poster board number:
P273

Chromosomal rearrangements are responsible for altered neuroinflammatory regulation in parrots

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Parrots (Psittaciformes) are birds with advanced cognitive abilities outperforming mammals of similar size. In their evolution they came through massive chromosomal rearrangements, which caused several gene losses. Here we provide genomic evidence of cannabinoid receptor 2 (CNR2) gene loss shared in parrots. Our results based on interspecific comparison of immune response regulation in parrots (*CNR2* loss) and passerine birds (functional *CNR2*) suggests susceptibility of parrots to neurinflammation. In budgerigar (*Melopsittacus undulatus*), we detected a significant upregulation of interleukin 1 beta (*IL1B*) expression in the brain after experimentally induced sterile peripheral inflammation. In contrast with the parrots, no such upregulation was detected in zebra finch (*Taeniopygia guttata*). Further we analysed effects of neural inflammation on neuropeptides expression in parrots (*NPY*, *VIP*, *TAC1*, *PDYN*, *POMC*). We propose that *CNR2* loss, which acts as an immune regulator expressed mainly in immune cells including microglias in brain, might have contributed to parrot susceptibility to neurological disorders like depression-related behaviours. For this purpose parrots may serve as suitable models in future neurological studies.

Abstract ID: 1461
Poster board number:
P274

Reconstructing the ancestral vertebrate brain using a lamprey neural cell type atlas

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The vertebrate brain is a morphologically complex organ whose patterning is conserved across all present-day vertebrates and likely emerged more than ~500 MYA in common ancestors. To trace its cellular composition and diversification during evolution, we established a spatially resolved cell type atlas of the brain of the sea lamprey – a jawless species whose phylogenetic position affords the reconstruction of ancestral vertebrate traits – based on single-cell RNA-seq and *in situ* sequencing data. Comparisons of this atlas to neural data from the mouse and other jawed vertebrates unveiled various shared features that enabled the reconstruction of the core cell type composition, tissue structures, and gene expression programs of the ancestral vertebrate brain. However, our analyses also revealed key tissues and cell types that arose later in evolution. For example, the ancestral vertebrate brain was likely devoid of oligodendrocytes; our data suggest that these emerged from astrocyte-like precursors on the jawed vertebrate lineage. Further analyses suggest that the developmental structures giving rise to (sub-)pallial inhibitory neurons in lamprey are similar to those of gnathostomes and hence are likely to be ancestral. However, homologous neurons partly end up in different adult brain regions in the two main vertebrate lineages. To further investigate conserved brain developmental programs across vertebrates, we are generating and analyzing single-nucleus multiomics data for embryonic stages of the sea lamprey. Altogether, our work illuminates the cellular and molecular nature of the ancestral vertebrate brain, and provides a foundation for exploring the diversification of the brain during vertebrate evolution.

Abstract ID: 1714
Poster board number:
P275

The genetic basis of personality in long-tailed macaques

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Diversity in life is prevalent, from a species to an individual level. Like humans, animals, too, have “personalities”, i.e. consistent inter-individual differences, which make them unique entities encompassing specific behavioural and cognitive constructs. While personality traits are known to influence the survival and fitness of an individual, mechanisms underlying varying personalities are poorly understood, especially from an interdisciplinary point of view. We studied the personality traits of twenty-seven captive long-tailed macaques (*Macaca fascicularis*), focusing on a specific genetic predisposition that may explain said inter-individual differences. Functional polymorphisms located in

the catechol-o-methyltransferase (*COMT*, a hypothalamic-pituitary axis gene) are well known to modify stress reactions and cognitive abilities in humans. We ask whether similar *COMT* polymorphisms are present in long-tailed macaques and whether they can predict the personality traits of these macaques. We extracted DNA samples of all the individuals and sequenced them. Personality was assessed using a comprehensive multi-method and "bottom-up" approach of behavioural observations and experiments. We collected 280 minutes of focal data per individual and subjected them to various tasks and stimuli - novel objects and food items, puzzles, and predator models, in their naturalistic group settings, rendering ecological relevance. All the observations and experiments were repeated to look for consistency across time and context. We discuss how the *COMT* polymorphisms could considerably influence personalities in long-tailed macaques. This study illustrates the importance of studying highly conserved genes across humans and non-human primates to better understand the evolutionary basis of behavioural variations.

Abstract ID: 2395
Poster board number:
P276

Within and between species variation in cognitive and behavioural determinants of innovativeness

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Innovation ability is a key factor in the capacity to solve novel problems. Theory predicts that species with higher level of innovation ability are better able to adapt to unpredictable environmental changes. Innovation ability, however, varies not only between species, but also between populations of the same species, and even individuals within populations. Although studies on innovativeness have indicated its importance for adaptation and fitness, it is largely unclear why some animals are better capable of coming up with solutions to novel problems compared to others. We tested the hypothesis that a combination of correlated cognitive and behavioural specialisations that have evolved for specific functions other than innovation ability per se, act together to allow animals to innovate. We investigated this using three members of the Paridae family: the great tit(Parus major), blue tit (Cyanistes caeruleus), and marsh tit (Poecile palustris) at the between and within-species level. These species are closely related but show fundamental differences in foraging behaviour and cognitive specilisations. We expect that the cognitive and behavioural traits co-vary with performance in innovative problem-solving tasks and variation between these species is due to their niche specilisation. Comparing these species with distinct behavioural characters and specilisations allows us to explore what factors cause the evolution of cognitive differences at species level. The within-species approach allows us to study to what degree each of these cognitive and behavioural determinents would influence innovation ability. This study will shed more light on the evolution of innovative ability in natural bird populations.

Abstract ID: 2432
Poster board number:
P277

Faster transport through slower runs: ant relocation dynamics in nature

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Insect societies are often populous and decentralised decisions need to be made by individuals with limited local information when time is of the essence. Recruitment of colony members to food, defence or to a new nest fall under this category. Colony relocation in tandem running ants is a particularly important case where only a small number of leaders possess information about the new nest and time is crucial, as longer exposure is detrimental to the colony's survival and reproduction. We investigated the programmes and positional effects of individual members during relocation of the Indian tropical ant Diacamma indicum in their natural habitat. Analysis of more than 1000 transports across eight relocating colonies reveals that they have a path efficiency of 85%. We found that transporters reoriented towards the target nest within seconds of initiation and tandem running in this species is so well organised that over 97% of transports reached their target nest without facing any interruption indicating that the communication between leaders and followers was exceptional. With an average speed of 3.8 cm per second these are the fastest tandem running ants recorded. We used mixed-effects model to understand the effect of patch heterogeneity and transport type on the speed and path efficiency of these ants and found that tandem leaders reduced their speed when traversing grassy patches and relied upon the slower coupled adult-brood transport. This investigation of ants performing tandem runs through heterogeneous terrains showcases the exceptionally efficient recruitment dynamics during colony relocation.

Symposium: S18. The evolution of behavioural adaptations: Genes, neurons and ecology (id: 31)

Abstract ID: 978
Poster board number:
P278

The effects of neurogenetic architecture and signal information on behavioral evolution

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Trait evolution depends on factors that influence selection pressures and on factors that influence selection responses. Here, I will compare across taxa to illustrate how these factors affect evolutionary dynamics of sexual communication behaviors. In sexual communication, selection responses are dependent on neurogenetic architectures, i.e. the mapping of genes to neurons to signal/response. For example, cricket song rhythm and song rhythm preference are both dependent on rhythmicity in the nervous system. This rhythmicity is determined by rhythmic neural circuits, which are associated with many possible genetic factors and thus highly polygenic. In contrast, sex pheromone signals, such as those common to most moth species, are characterized by a one(few)-to-one mapping of genes to enzymes (in the female signal) or of genes to olfactory

receptors (in the male response). Variation in neurogenetic organization of traits thus may influence the distribution of changes in the genome and the extent of coupling among sex-specific traits associated with behavioral evolution. Sexual selection pressures depend on the information in the signal, e.g. stabilizing selection for signal components that inform about mate compatibility and directional selection for mate quality indicators. Different components of a signal that convey different types of information are evaluated separated in space, e.g. mate compatibility traits in the periphery by sensory receptors and mate quality traits subsequently in the central nervous system. This modular organization may not only affect the extent of variation in signal components, but also the relevance for a component in signal divergence and speciation.

Abstract ID: 1040
Poster board number:
P279

A multi-dimensional quantitative approach to study the evolution of social complexity

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The diversity and richness of social insects make them an excellent model for comparative studies on the evolution of complex societies. The current approach for research on the evolution of insect sociality is based on a qualitative and crude classification and suffers from several limitations: (i) It assumes that social traits always evolve together and in synchrony, which may falsely imply that social evolution always progresses along a single linear stepwise trajectory; (ii) It limits our ability to test the association between the level of sociality and quantitative "omics" molecular, physiological, and behavioral parameters. We are developing a novel approach that is based on quantitative indices for social complexity using bees as a model. As a first step, we compiled a comprehensive database of social traits for 70 species. Next, we performed data-driven statistical analyzes, which account for phylogenetic relations between species. Our approach enables quantification and mapping of sociality in species based on multiple types of data. Our results indicate a spectrum of sociality types in bees, which is wider than appreciated with the classical approach. We identified multiple axes that characterize regions of interest in the multidimensional trait space, suggesting non-trivial relations between different social complexity traits. Moreover, we discovered potential trajectories for sociality by calculating the molecular evolutionary rate of focal genes. Our approach is not taxon-specific, and can be used for comparative studies on other taxa – from ants to primates.

Abstract ID: 1103
Poster board number:
P280

The ecology of UV-vision in female *Heliconius erato & H. himera*

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Animal vision is important for mediating a multitude of complex behaviours. In neotropical *Heliconius* butterflies, vision guides fundamental behaviours such as oviposition, foraging and communication. Colour vision in *Heliconius* involves UV, blue and long-wavelength sensitive opsins. Additionally, *Heliconius* possess a duplicated UV opsin, and expression varies between species. In *Heliconius erato* opsin expression is sexually dimorphic, and only females express both UV-sensitive opsins, enabling UV wavelength discrimination. However, the ecological pressures that have driven these sex-specific differences in visual perception remain unresolved. In contrast to males, *Heliconius* females must lay eggs and invest heavily in finding hostplants, which mostly rely on visual cues. Therefore, improved UV wavelength discrimination in *H. erato* females could be an adaptation for hostplant recognition and may play a role in oviposition behaviour. Here, we tested whether UV vision is used for oviposition in *H. erato* females and*Heliconius himera* by manipulating the availability of UV in behavioural experiments. We found that UV did not influence the number of oviposition attempts or the number of eggs laid. The absence of UV reflectance in thehostplant, *Passiflora punctata,* and the minimal stimulation of the UV opsins using models of *H. erato* female vision, suggest that the presence of UV does not directly affect the ability of *Heliconius* females to find suitable oviposition sites. Overall, these findings suggest that UV perception female *Heliconius* are not used for oviposition. Alternatively, it could be used in the context of foraging or mate choice, but this remains to be tested.

Abstract ID: 1126
Poster board number:
P281

Modelling the evolution of learning

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The ability to learn from past experience is an important adaptation, but how natural selection shapes learning is not well understood. Here, we present a novel way of modeling learning using small neural networks and a simple, biology-inspired learning algorithm. We used this model to study the evolution of learning under various environmental conditions and different scenarios for the trade-off between exploration (learning) and exploitation (foraging). Efficient learning regularly evolved in our individual-based simulations. However, the evolution of learning was less likely in relatively constant environments (where learning is less important) or in case of short-lived agents (that cannot afford to spend much of their lifetime on exploration). Once learning did evolve, the characteristics of the learning strategy and the average performance after learning were surprisingly little affected by the frequency and/or magnitude of environmental change. In contrast, agent lifespan had a strong effect on the evolved learning strategy. Interestingly, a longer learning period did not always lead to a better performance, indicating that the evolved neural networks differ in the effectiveness of learning. Overall, however, our study shows that even a relatively simple learning mechanism can lead to efficient adaptation.

Abstract ID: 1146
Poster board number:

P282

Is bat predation risk driving the evolution of multimodal duetting in katydids?

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Predation is a strong selection force that acts on both the prey and the predator, results in an arms race between the two and plays an important role in shaping their lifestyles at the evolutionary time scale. The selection pressure is stronger on the prey which is at higher risk than the predator (Life-Dinner Principle). In orthopteran insects, acoustic mate-attraction signals are typically produced by males. Females perform phonotaxis and move towards the calling males. *Onomarchus uninotatus*, a pseudophylline bushcricket, has evolved an unusual mate-finding strategy wherein females respond to a male's acoustic call with tremulations, producing vibratory signals, which are then used by males to locate females. We proposed that bat predation risk might be the driving selection pressure for evolution of multimodal duetting. Using enclosure experiments with *O. uninotatus* and its predator bat *Megaderma spasma* we compared sex-specific predation risk of signaling and searching. We hypothesized that (1) tremulation evolved as a less risky strategy than acoustic signalling in terms of bat predation, (2) females reply with tremulations to avoid risky phonotaxis during mate search, and (3) for males, acoustic signaling has a higher predation risk than searching. Estimation of predation risk as an ecological cost acting on both sexes for their different mate-finding behaviours helped us to gain insight into the potential cause and consequences of their behavioural adaptation for mate-finding.

Abstract ID: 1250
Poster board number:
P283

The gut microbiota affects the social network of honeybees

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The gut microbiota influences animal neurodevelopment and behavior but has not previously been documented to affect group-level properties of social organisms. We used honeybees to probe the effect of the gut microbiota on host social behavior. We found that the microbiota increased the rate and specialization of head-to-head interactions between bees. Microbiota colonization was associated with higher abundances of one third of the metabolites detected in the brain, including amino acids with roles in synaptic transmission and brain energetic function. Some of these metabolites were significant predictors of the number of social interactions of bees. Microbiota colonization also affected brain transcriptional processes related to amino acid metabolism and epigenetic modifications in a brain region involved in sensory perception. These results demonstrate that the gut microbiota modulates the emergent colony social network of honeybees, and suggest changes in chromatin accessibility and amino acid biosynthesis as underlying processes.

Abstract ID: 1366

Poster board number:
P284

Social parasitism leads to transcriptomic shifts in the nervous system of captured ant workers

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The widespread lifestyle of social or brood parasites is characterised by the exploitation of the social behaviour of their hosts. Studies on how these parasites infiltrate host nests or circumvent host defences have yielded fascinating insights into parasite-host coevolution. Less studied, however, is how social parasites succeed in eliciting the altruistic behaviour of captured workers towards them and their offspring. We investigated this in the ant *Leptothorax acervorum*, host of the dulotic, obligate social parasite *Harpagoxenus sublaevis*. We shed light on molecular mechanisms underlying worker exploitation by contrasting the gene expression in the brain and the antenna of young host workers that we experimentally (re-)introduced as pupae into parasitic colonies, their natal, or another conspecific colony. The transcriptome from each tissue revealed that ant workers were affected by their adult social environment. Furthermore, gene expression in the antennae, but not in the brain was strongly linked to worker behaviour. Antennal gene expression changed in host workers living in parasitic colonies in a similar manner to those in colonies of alien conspecifics, suggesting that the altered chemical environment is the cause of these changes. Yet, transcriptomic alterations in the brain were more pronounced in workers within parasitic nests, indicating that social parasites or their environment influence host brain activity and then their behaviour. Our study demonstrated that the exploitation of social behaviours by brood parasites is linked to transcriptomic alterations in the central and peripheral nervous system. Whether and how exactly social parasites manipulate host behaviour remains to be investigated.

Abstract ID: 1585
Poster board number:
P285

Interaction between territoriality and traits of males in Neotropical Poison Frogs

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The territory is part of the extended phenotype of males and the ability of individuals to defend it may be an honest indicator of male quality or social status; therefore, territories can be targets of sexual selection. Other male traits including morphology, behavior, coloration, and ornaments may also be under sexual selection, being used by males to evaluate their conspecific competitors or by females to choose males. A frequent question is whether male traits and characteristics of their territory are correlated and what are the mechanisms that may mediate such associations when they exist. Because hormones are phenotypic integrators, by studying the role of testosterone in territoriality one may come closer to understanding the mechanisms mediating correlations or lack thereof between characteristics of territories and of males. We evaluated whether

variation in characteristics of territories, defined as defended areas which we measured using intrusion experiments, are correlated with variation in morphology, coloration, androgen levels, heterozygosity, and call activity. We used two species of poison frogs (Dendrobatoidea), *Oophaga lehmanni* and *Allobates* aff. *trilineatus*, which exhibit contrasting reproductive and acoustic communication strategies. We found that morphological traits (body length, weight, and thigh size), vocal activity, and androgen levels correlated with size and ecological attributes of the territory, but which traits covaried and whether correlations were positive or negative depended on the species. We were able to identify some male traits related to territory attributes, but whether females choose males based on territory traits, male traits, or both requires further research.

Abstract ID: 1593
Poster board number:
P286

Single cell sequencing of a parental brain

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A challenge to understanding the brain's control of behavior is its incredible cellular and spatial heterogeneity. This complexity can make find meaningful changes of gene expression linked to phenotypes of interest difficult if the tissue is sampled at a gross level; e.g., a whole brain, or forebrain, etc. This is because gene expression that is causally linked to behavior can be restricted to a few neurons and/or can be transiently expressed. Therefore, detected differential gene expression is biased to discover genes that had huge changes of expression or were broadly expressed across gross tissue samples. While genetic manipulations to influence the gene expression within only a few neurons is an excellent way to understand gene function, it is not a widely available tool outside of genetic model organisms. Single cell RNA-sequencing helps address the above issues by allowing investigators sample the transcriptomes of single cells. Single cell RNA-seq has allowed us to gain cell level resolution of a brain of a beetle, *Nicrophorus orbicollis*, while they provide parental care, including regurgitating food to offspring. This has also allowed cell type identification and gene co-expression networks of individual cells; something not possible with previous techniques. We have also found this technique to be particularly sensitive to genome/transcriptome assembly and annotation quality.

Abstract ID: 1755
Poster board number:
P287

To call or not to call: persistence of flexible alternative reproductive tactics in a tree cricket

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The persistence of polymorphisms is an important theme in evolutionary biology. Alternative reproductive tactics (ARTs) are discrete polymorphisms adopted by

individuals of some sexually reproducing taxa to maximise fertilisation success. ARTs can be fixed or flexible during an organism's lifetime. While proposed ultimate causes such as equal fitness of ARTs and frequency-dependent selection have been empirically demonstrated to explain the persistence of fixed ARTs, such evidence is lacking for flexibly expressed ARTs. Furthermore, since organisms commonly inhabit dynamic environments, it is important to assess the role of relevant ecological factors on the fitness effects of ARTs. Using mesocosm experiments, we examined the effect of predation risk on the expression and mating success of two reversibly expressed ARTs: acoustic signalling and silent, expressed by adult males of the tree cricket Oecanthus henryi. We exposed wild-caught populations of O. henryi in large outdoor enclosures to treatments comprising three different abundances of their predator, the green lynx spider Peucetia viridans. Behavioural observations across successive nights revealed that the abundance of predators did not alter the expression levels of both the ARTs relative to each other. Males demonstrated an equal likelihood of calling or remaining silent on a night. Both ARTs also resulted in similar mating success. The results support the hypothesis that the equal fitness of ARTs may explain the persistence of flexibly expressed ARTs under relevant ecological conditions.

Abstract ID: 1809
Poster board number:
P288

Assortative mate preferences in *Heliconius* and the role of genes, brains and environment

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The evolution of assortative mating is an important driver of reproductive isolation, but we still know relatively little about the neural and genetic mechanisms that contribute to divergent mating preferences, or how these interact with ecology. *Heliconius* butterflies are well known for their bright warning patterns, which are also involved in mate choice. However, differences in warning pattern are just one axis of ecological divergence that may contribute to speciation. *Heliconius erato* and *H. himera* are two recently diverged species adapted to different environments: Whereas *H. erato* is found in humid, low-land forest, *H. himera* is adapted to high elevation dry forests. In at least one comparison to *H. erato* populations, this shift in habitat-use has been accompanied by changes in neuroanatomy, flight behaviour and life history. To better understand how these differences relate to the evolution of mate choice, we have been conducting mate choice trials across low-land *H. erato* populations (*H. erato cyrbia* and *H. erato lativitta*, from the west and east of the Andes respectively) and high elevation *H. himera* populations. We will test if ecological shifts and adaptation to different sensory environments contribute to divergent mating preferences, focussing not only on male mating behaviours but also on female responses to male courtship. Moving forward these experiments will be linked to expression data of the sensory tissues and brain from these populations, and their hybrids, as well as QTL experiments to map the behavioural traits that differ across this environmental divide.

Abstract ID: 1814
Poster board number:

P289

Origin of a new olfactory sensory neuron population

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The olfactory sensory neurons (OSNs) that scan the environment for volatile cues are evolutionary dynamic. The diversification of OSNs presumably requires the coordination between the birth of new Odorant receptor (*Or*) encoding genes and the development of pathways that will give rise to neurons expressing these novel *Ors*. The molecular and cellular bases underlying this process remain mysterious, in part because of challenges to detecting the emergence new OSN and the intermediate steps in their formation. To investigate these questions, we are studying an *Or* subfamily named *Or67a*, which has been repeatedly duplicated/deleted within the *D. melanogaster* species group. Our microsyntenic analyses of *Or67a* subfamily members in 15 species revealed a remarkable number of *Or67a* gains/losses, often associated with unstable chromosomal regions enriched in transposable elements. Molecular evolutionary analyses identified multiple instances of adaptive changes among Or67a paralogs, which we are currently functionally characterizing with *in vivo* electrophysiological recordings. Using transgenic and fluorescent *in situ* hybridization approaches, we have found that most of the young intact *Or67a* duplicates are co-expressed with their paralogous receptors in the same neuron population. Intriguingly, however, we have identified one *Or67a* paralog that originated in the common ancestor of the *D. takahashii* and *D. suzukii* clade and was subsequently lost from all species except *D. suzukii* and its sister species, *D. subpuchrella*. In these two species, this Or67a paralog has evolved novel cell-specific expression, thus identifying the evolutionary origin of a unique olfactory channel.

Abstract ID: 1823
Poster board number:
P290

Using juvenile songbirds to study the genetic basis of the migratory syndrome

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Seasonal migration is a behavioral syndrome that requires the coordinated action of many traits (e.g., orientation, timing, fattening, wing length). Qualitative evidence suggests these traits are genetically determined but concrete knowledge of this topic is lacking. We used natural hybrids between two subspecies of the songbird the Swainson's thrush to study the genetic basis of the migratory syndrome. We (1) calculate heritability for multiple migratory traits and (2) tested for genetic correlations between these traits. We also (3) explored local patterns along the genome that were associated with these migratory traits. We used tracking data of over 230 birds including phenotypes from experienced adults as well as naïve juveniles to address these objectives. We find moderate to high values of heritability for several traits (e.g., orientation on fall migration and wing shape) and that many of these traits are genetically correlated (e.g., migratory distance and wings shape). These results are important for the evolution of these behavioural traits because selection on one trait will influence another. In addition, genetic mapping of these birds helped narrow down a previously identified region of the

genome that was associated with migratory orientation and uncover additional regions associated with wing morphology and timing of migration. Some of these regions lie in inversions but are not shared across traits. This is one of the most detailed genetic studies of the migratory syndrome to date, taking research on the genetics of migration – a trait important for ecology, evolution and conservation – further than ever before.

Abstract ID: 1881
Poster board number:
P291

Antimicrobial activity of the mud used to build the nests in birds

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Selective pressures exerted by parasites have led to evolve many behavioural adaptations in animals that allow them or their progeny to avoid, or diminish, the risk of infections. This is the case of self- and kin-medication, i.e., the use of antiparasitic substances synthetized by other organisms. For instance, in birds, it has been shown that different species may use several nest lining materials that regulate bacterial communities of nests, thus decreasing the probability of eggs and nestlings becoming infected. In the present work, we hypothesized that the structural material used by several bird species to build their nests, the mud, may have antibiotic properties that could be mediated by microorganisms living on this kind of material. To test this hypothesis, we collected mud from nests of different bird species and by means of antagonistic tests, we characterized the antimicrobial capacity of the material both, soon after collecting from active nests, and some months afterwards. We detected an interspecific variation in antimicrobial capacity and that it decreased after keeping the samples in the fridge for some months. These results may suggest that the antibiotic capacity of the collected mud could be mediated by the microbiota growing in the material. Our results also add to broadly accepted antibiotic properties of the material used to build the nests, which may have great importance for avoiding bacterial infections of adults and offspring during their stay in the nests.

Abstract ID: 1961
Poster board number:
P292

Evolutionary dynamics of olfactory receptor genes in ray-finned fish

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The olfactory system is involved in multiple behaviours in diverse fish species such as reproduction, feeding or kin recognition, among others. At the molecular level, the first step in odour perception is driven by cell surface receptors expressed in the olfactory epithelium. These olfactory receptors bind to environmental odorant molecules, inducing a cascade that convert a primary chemical signal into an electrical impulse that is decoded in the brain. Remarkably, each olfactory neuron expresses only one receptor gene from a usually extensive repertoire. This intricate regulation is key for the

processing of smell due to the axonal convergence in a singular olfactory glomerulus of those sensory neurons expressing the same receptor. To understand how olfaction responds to a plethora of distinct environments and behavioural adaptations, we study the evolution of olfactory genes in approximately two hundred species across ray-finned fish phylogeny. We also analyse the impact of observed genomic changes at the transcriptome level in a reduced subset of the studied organisms. Furthermore, we identify particular morphological and ecological traits associated to changes in the olfactory molecular substrate in ray-finned fish.

Abstract ID: 2027
Poster board number:
P293

Inclusive fitness and the evolution of nuptial gifts

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Two major theories dominate contemporary evolutionary biology: sexual selection, concerning how natural selection works through differences in reproductive success caused by competition over mates, and kin selection, concerning how natural selection works through the reproductive success of an individual's genetic relatives. Recent years have seen a renewed interest in the interaction between these two selective forces. Both theoretically and empirically, the focus has been on how kin selection shapes the evolution of harmful male phenotypes. However, the focus on male harmful phenotypes means that the current literature cannot make predictions about other classes of sexually-selected traits. One example of such traits are nuptial gifts. Nuptial gifts are gifts that typically male animals transfer to females during courtship and mating. Ranging from food and salivary gland secretions to spermatophores and proteins present in the semen, nuptial gifts have been described has enhancing, being neutral, or even detrimental to female fitness. Nuptial gifts' effect on male fitness are clearer. Such sexual strategies can only be maintained if they confer net fitness benefit to their carriers. However, such perspective does not consider the potential role of kin selection in shaping sexual selection. Specifically, by aligning the evolutionary interests of different individuals through inclusive fitness, kin selection might facilitate the evolution of traits that are costly to their carriers. Here, through the use of new inclusive-fitness mathematical models, we consider the potential role of kin selection in shaping the evolution of nuptial gifts under a wide range of demographic and ecological factors.

Abstract ID: 2035
Poster board number:
P294

Molecular basis of the social control of reproduction and behavior in ants

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Major transitions in evolution are central to the diversity and complexity of life. They correspond to transitions from solitary life forms to complex social structures that relies on the cooperation of specialized units. One classical example is the transition from

solitary to social insects. Division of labor in social insect colonies has received a lot of attention, especially via comparisons of the fertile queen caste and the sterile worker caste. While this approach has proven powerful, the interpretation of such comparisons is limited due to the many intrinsic differences between queens and workers. We use alternative study systems to investigate the molecular mechanisms underlying division of labor. Specifically, we are interested in the impact of the social context on physiological and behavioral transitions within the life cycle of social insect colonies. One system is the clonal raider ant *Ooceraea biroi*, where larvae control the reproduction and behavior of the workers in a biphasic life cycle. The other system is the process of colony foundation in the black garden ant *Lasius niger*, during which workers induce behavioral changes in queens. Therefore, both systems involve strong effects of the social environment on typical components of division of labor, allowing us to experimentally manipulate the transitions in the colony life cycles. I will present some of our ongoing work on how transcriptomic and epigenetic modifications correlate with reproductive and behavioral variation in response to the social context. I will also discuss how our results may shed light on the evolution of eusociality.

Abstract ID: 2075
Poster board number:
P295

Evolution of gene expression in the chemosensory tissues of ecologically diverse fly species

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Insect chemosensory organs display incredible morphological and functional diversity, and sex-specific functions. Despite their many striking features, our understanding of gene expression evolution in these tissues remains incomplete. We have generated transcriptomes for five sensory tissues (antenna, proboscis + maxillary palp, forelegs, ovipositor, and larval head) for males and females of six ecologically diverse Drosophila species. Species comparisons revealed pervasive gene expression changes associated with both morphological and chemosensory functions. In antenna for instance, ~ 30% of 1:1 orthologs have changed in expression at least once over the past 15 million years. When examining expression breadth according to gene ages. We found that young genes and highly duplicated gene families were disproportionately tissue specific, suggesting a role in chemosensory organ specialization. Given the role that these organs play in sex-specific behavior, we examined the patterns of sex-biased gene expression. Patterns of sex-biased expression vary remarkably among sensory tissues and do not reflect the phylogenetic relationship of the species. To relate these expression changes to the evolution of organ composition by generating cross-species single cell atlases for the same chemosensory tissues. Analyses of these data are revealing species-specific elevated gene expression associated to the expansion of single neuron populations. Together, our work demonstrates the power of combining cross-species bulk RNA-sequencing with matched single cell RNA transcriptome data for elucidating the origins of sensory diversification.

Abstract ID: 2082
Poster board number:
P296

Evolutionary genetics of visual adaptation in *Heliconius* butterflies

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By influencing key behaviors, such as foraging and mating success, the match between an animal's sensory systems and the local sensory environment will have important implications for individual fitness. Adaption will depend on genetic architecture, but we still know relatively little about the genetic basis of sensory structures in wild populations. The Neotropical *Heliconius* butterflies, which are well known for their aposematic signals, rely heavily on visual cues for mating and foraging. Diversification in *Heliconius* is characterized by shifts in habitat use and exploitation of different sensory habitats, and we expect their visual systems should be tuned to their local sensory environment. In particular, the closely related sympatric species *H. cydno* and *H. melpomene* differ in their visual habitat: at our study site in Panama, whereas *H. cydno* is found in darker closed-canopy forests, *H. Melpomene* is found in forest edge habitats. First, we confirm that the eyes of *H. cydno* are larger than *H. melpomene* (and that males have larger eyes than females in both species), both in terms of absolute size and facet count. Taking quantitative genetics approach we tested whether these shifts in eye size is a result of selection, rather than drift. Finally, by measuring the eyes of hundreds of interspecific hybrids we performed a QTL analysis to begin to undercover the genetic architecture of this key adaptation.

Abstract ID: 2168
Poster board number:
P297

Mitonuclear interactions modulate nutritional preference

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In nature, organisms are faced with constant nutritional options which fuel key life-history traits. Studies have shown that species can actively make nutritional decisions based on internal and external cues. Metabolism itself is underpinned by complex genomic interactions involving components from both nuclear and mitochondrial genomes. Products from these two genomes must coordinate how nutrients are extracted, used, and recycled. Given the complicated nature of metabolism, it is not well understood how nutritional choices are affected by mitonuclear interactions. This is under the rationale that changes in genomic interactions will affect metabolic flux and change physiological requirements. To this end we used a large Drosophila mitonuclear genetic panel, comprising 9 isogenic nuclear genomes coupled to 9 mitochondrial haplotypes, giving a total of 81 different mitonuclear genotypes. We use a capillary-based feeding assay to screen this panel for dietary preference between carbohydrate or protein. We find strong levels of sexual dimorphism for this trait, with females consuming a lot more protein than males. Furthermore, we find significant mitonuclear interactions modulating nutritional choices. This work gives us deeper insights on how key metabolic interactions can have large implications on behaviour.

Abstract ID: 2233
Poster board number:

P298

Does trophic environment affect behavior and gene expression in the facultative parasitic blowfly?

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One of the greatest challenges in biology is to understand complex phenotypes, and how they evolve and interact with the environment. Feeding habits are complex phenotypes that might be influenced by environmental changes. Some blowfly species have a flexible feeding habit alternating between parasitism and necrophagy. Here, we investigated the effect of developmental substrate on phenotypes in a facultative parasitic blowfly, *Lucilia cuprina*. We reared blowflies for 13 generations on fresh or rotten substrates. We tested how these substrates affect behavior (female oviposition site and larval feeding preferences) and gene expression over generations. Larvae and females were able to choose between four options: fresh or rotten meat at 25C or 33C. We hypothesize that initially there will be no differences in the phenotypes. In the last generation, behavior and gene expression will become distinct and this will be specific to the substrate where blowflies were reared. We show that larvae feeding and female oviposition site preferences differ. Regardless of the developmental environment, larvae have a fixed preference for rotten substrate at 25C, and females' oviposition displays a more diverse set of substrates (fresh or rotten), while also preferring to lay eggs at 25C. After selection, larvae presented 1875 and females 100 differentially expressed genes between rearing substrates. These results suggest that the developmental environment does not affect behavioral phenotypes, however greatly affects gene expressions, especially during development. Finally, different environments partially affect feeding habits, probably changing expression of genes related to substrate use and metabolism necessary for survival.

Abstract ID: 2359
Poster board number:
P299

Parental care and paradox decisions: does relatedness play a role in nursery choice?

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One strategy to survive times of low nutritional availability is cannibalism, which increases survival chances of the aggressor. Cannibalism entails various costs, such as the possibility of injury during opponent subjugation and the reduction of inclusive fitness by consuming close relatives. Cannibals consistently minimise costs by being both larger and distantly related to their opponent. In species with elaborate parental care, bringing offspring close to a potential cannibal would be counter-intuitive, unless the cannibal and

its potential prey are related. Male dyeing poison frogs transport their freshly-hatched tadpoles to small water pools which are often occupied by larger, potentially cannibalistic conspecifics.This work aims to better disentangle the apparently counter-intuitive deposition decisions by fathers: are selected pools minimising the threat of cannibalism? We investigated how the average body size of tadpoles in a pool changes in function of the density therein and their degree of relatedness. We would expect that individuals within a pool with multiple tadpoles are more similar in size and closer in relatedness. Our findings support our hypothesis, suggesting that a homogenisation in body sizes with higher numbers of tadpoles per pool could be a mechanism by which the risk of cannibalism is reduced. Ongoing relatedness analysis will reveal whether this is due to the degree of relatedness or a consequence of tadpole density and therefore limited resources. However, our findings will shed light on the evolution of the seemingly paradoxical deposition behaviour of caring parents that put their offspring at risk of cannibalism.

Symposium: S19. Eco-evolutionary dynamics and feedbacks in invasive species (id: 39)

Abstract ID: 1673
Poster board number:
P300

Evolution of Na+/K+-ATPase, a candidate gene under selection during invasions in a common copepod

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With climate change and biological invasions, many taxa are experiencing changes in habitat salinity globally. The copepod *Eurytemora affinis* complex has shown a repeated ability to cross major salinity boundaries in both wild populations and laboratory selection experiments. While previous work has found paralogs of the ion transporter gene family *Na^+/K^+-ATPase* (NKA) under selection during these freshwater invasions, little is known about the broader evolutionary history of NKA across major arthropod subphyla. In addition, whether the same single nucleotide polymorphisms (SNPs) under selection during rapid invasions also show signatures selection on a macroevolutionary scale is unknown. Furthermore, the protein structural changes conferred by selectively beneficial SNPs in NKA have not been identified. Therefore, the goals of this study are to: (1) conduct a phylogenetic analysis of the alpha and beta subunits of NKA across 35 arthropod taxa, (2) infer branches and sites under selection among paralogs of NKA in *E. affinis* and in other arthropod taxa, and (3) map candidate SNPs under selection onto the protein model of NKA. Preliminary phylogenetic results indicate largely monophyletic and significantly elevated paralog counts of both the alpha and beta subunits of NKA in *E. affinis* complex. These recent gene duplications suggest that both subunits of NKA have played a vital role in the evolution of *Eurytemora* on a macroevolutionary scale. Comparing SNPs under selection between this phylogeny and previous studies on rapid invasions will elucidate the role that NKA plays in the wide osmoregulatory range of the species complex.

Abstract ID: 1791
Poster board number:

P301

Molecular analysis of lately introduced populations of lizard supports invasiveness at species level

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In recent years, development of molecular genetics and phylogeographic tools has greatly improved our inference of invasion dynamics and the demography of biological invasions, allowing a more objective determination of alien status. The Italian wall lizard, *Podarcis siculus*, native to the Italian Peninsula, Sicily and the Adriatic coast, has been introduced in Corsica, Sardinia, Menorca since historical times. Besides these regions, scattered populations were later reported from the Iberian Peninsula, France, Switzerland, Turkey, Greece, UK and North America. Here, we provide molecular evidence regarding the origin of *P. siculus* in seven new introduced populations: Romania (Bucharest, Alba Iulia), Croatia (Zagreb, Karlovac), Italy (Lampedusa Island), Azerbaijan (Baku) and Canada (Vancouver). Taking advantage of the high genetic substructuring, we used mtDNA gene (cyt-b) of individuals from introduced populations and across the native range to identify the putative origins of these populations. Our phylogenetic analysis suggests that the Alba Iulia (Romania) population originated from Tuscany, while the population from Azerbaijan is admixed including two distinct clades (Sicily, Tuscany). Samples from Bucharest also have admixed origins in Tuscany and the Adriatic. Less surprisingly, samples from Zagreb and Karlovac are included within the Adriatic clade while those from Lampedusa originated from Sicily. The Canadian individual is derived from the Tuscany clade (together with published samples from Kansas, New York). Overall, our results, uncovering multiple origins and clade admixture in alien populations, demonstrate that genetic data are essential for inferring the invasion pathways of alien species, particularly in systems with a long history of human influence.

Abstract ID: 1801
Poster board number:
P302

Using invasions to understand adaptation: genomic reconstruction of the house sparrow global spread

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The well-known house sparrow (*Passer domesticus*) is a small bird renowned for its charismatic nature and close association to humans. House sparrows can be found living and breeding on almost every continent in the world, almost exclusively in near proximity to human habitation. The house sparrow is thought to have spread across Eurasia from the Middle and Near East alongside the spread of agriculture and the establishment of

fixed settlements during the Neolithic era. However, due to multiple intentional and accidental introductions from the mid-19th century onwards, the species is also invasive in Australasia, Southern Africa, and the Americas. In modern North America, the house sparrow now exists from Southern Panama all the way to the Northwest territories of Canada, attesting to the species' ability to survive in a diverse range of environments. This research aims to understand evolutionary success in biological invasion by reconstructing the history of the house sparrow invasive spread. Using whole genome resequencing, we generate further understanding of the genomic structure within the invasive range. Our results reconstruct the house sparrow invasion history to identify demographic changes between populations. We also studied parallel latitudinal clines within the United States and Australia to demonstrate the parallel evolution of new traits from bottlenecked founder populations, suggesting that certain genome regions and traits may be more beneficial for evolutionary success. Invasive species are an excellent model for understanding complex evolutionary processes, and this research will inform future work on understanding the genomics of successful adaptation to new environments.

Abstract ID: 1887
Poster board number:
P303

Multi-year monitoring of *Asclepias syriaca* spread in protected reserve of Deliblato Sand in Serbia

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Asclepias syriaca, (common milkweed), is an invasive species that has already been naturalized in 23 countries worldwide. Anticipated climate changes are predicted to help further its future spread beyond its current distribution. The common milkweed occurs in various habitats, most often those modified by humans, such as roadsides, railway areas, wastelands, abandoned orchards, vineyards, and abandoned arable land. Its massive occurrence threatens native species diversity, penetrating into natural and semi-natural habitats. Deliblato Sands, special Serbian nature reserve, the largest European continental sandy terrain located in the south-east part of the Pannonia Plain, is also subject to invasion by *A.syriaca*. In 2015 we analyzed the presence of *A.syriaca* on borders of natural protected reserve along the roads leading to reserve, as well as on approx. 200 km of roads and paths in the natural reserve itselve. Those inner roads and paths were subsequently monitored in 2017, 2019, and 2021. for persistence and spread of already detected locations of *A.syriaca* and the occurrence of the new ones. Influence of proximity of reserve borders with different levels of infestation, type of use (commercial roads, tourist tracking paths), and levels of protection (three levels of protection exist on D. Sand), were analyzed. The largest increase in numbers was detected in the areas with the most intensive human activity. This study of dispersal and range extension can serve as a basis for further analysis of eco-evolutionary dynamics on *A.syriaca* populations and localities in the Deliblato Sand natural reserve.

Abstract ID: 1958
Poster board number:
P304

Cuticular hydrocarbon diversification drives aggression in the invasive ant *Cardiocondyla obscurior*

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Cuticular hydrocarbons (CHCs) are important cues for nestmate recognition and aggression behavior in social insects. In invasive ants, CHC profile similarity among colonies has been hypothesized to contribute to the ecological success of populations by diminishing intraspecific aggression. The ant *Cardiocondyla obscurior* has successfully colonized habitats around the world, reaching high local population densities. However, despite being invasive, antagonistic interactions between non-nestmates commonly occur in this species. Using behavioral experiments and gas-chromatography coupled with mass spectrometry (GC-MS), we show that (1) individuals of invasive Brazilian populations with depleted CHC profiles receive virtually no aggression from non-nestmates and (2) in untreated individuals, aggression levels are significantly correlated with CHC profile differences between colonies. These findings provide first empirical evidence for a role of CHCs and chemical diversity in antagonistic interactions in *C. obscurior*, with important implications for evolutionary and population dynamics as well as the invasive potential of this ant.

Abstract ID: 2151
Poster board number:
P305

Spider mites do not modify their interaction with plant defences when evolving with a competitor

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Plant infestation by herbivores is known to induce the production of plant defences. However, some herbivores, such as the spider mite *Tetranychus evansi,* can suppress such defences. This is to their benefit, as their performance increases in suppressed plants. However, such suppression should be displayed only when benefits exceed costs. Here, we hypothesize that evolving in presence of an interspecific competitor entails an ecological cost that selects against defence suppression. We tested this by performing experimental evolution of *T.evansi* on tomato plants in presence or absence of its congeneric competitor, *T.urticae*. After 53 generations, we measured the expression of PI-IIc and PPO-D, genes involved in the Jasmonic acid pathway, known to be involved in plant response to spider mites. Our results show that evolving with a competitor does not lead to changes in the ability to suppress plant defences. Possibly, *T. evansi* benefits more from its own suppression than its competitor. Alternatively, *T. evansi* may have a lower ability to detoxify plant defences than *T. urticae*, suffering more from lower suppression than its competitor. In any case, these findings suggest that the costs of suppression are lower than the benefits even in the presence of a competitor, which has important implications for the (co)evolution of *T. evansi* and its competitors.

Abstract ID: 2207

Poster board number:
P306

Conservation genomics in Italian pike: contrasting hybridization with non-native European pike

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Centuries before it was described as a distinct species in 2011, **Italian pike** (*Esox flaviae*) faced the challenge of habitat loss and degradation due to wetland reclamation. Today, climate change is not the only threat to its survival: being a prized game fish, **non-native European pike** (*Esox lucius*) has been used in stocking practices for decades, resulting in **displacement and hybridization** and placing the genetic identity of the Italian pike at risk. Supportive breeding programmes have so far contrasted the damage by identifying hybrids with traditional conservation genetics tools such as microsatellite markers. However, current approaches may lack resolution to detect **complex patterns of introgression** and to distinguish between native and hybrid individuals. To address this issue, millions of high-quality Single Nucleotide Polymorphisms (SNPs) were generated from Whole Genome Sequencing data for both species and for the first time in Italian pike, and were implemented to analyse population structure, fine-scale introgression and genome-wide signals of molecular adaptation using both allelic frequency- and haplotype-based selection scans. Key findings include i) the extent of **genomic divergence** across the two pike species, ii) the **discordance**, in some cases, between microsatellites and SNPs with regard to detection of hybrids, and iii) **gene functions putatively under selection** in either species, including olfactory perception, immune response, metabolism and pigmentation. This project provides valuable insight into the genomics of a non-model species and warns of the potential loss of genomic adaptation due to hybridization that may hinder its resilience to a changing environment.

Abstract ID: 2245
Poster board number:
P307

Inheritance mechanisms in knotweeds – are they driven by population genetics or the environment?

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Plant invasions impose ecological and economic problems and it is crucial to understand the evolutionary processes that underly invasion success in order to successfully manage existing invaders, and to prevent future invasions. Alien knotweeds (*Fallopia* ssp., *Reynoutria* ssp. complex) are one of the most invasive species in Europe and cause serious problems in nature protection. Once established, they enable both generative and vegetative reproduction. Vegetative reproduction prevails in all knotweed

taxa and the overwhelming majority of localities. However, localities with high cytological and genetic variability, suggest ongoing generative reproduction. Based on cytological and genotype variability (SSRs) of clones collected across Europe, we studied the seed production of particular clone variants, seedling cytotype variability and vitality. The seed production and germination of particular genotypes differ and only specific cyto and genotypes combination allows the offspring establishment. In some populations, only octoploid cytotypes of the hybrid *F. ×bohemica* (2n = 88) and high genotype variability of octoploids were found. In others, genotype variability was mainly found in hexaploid hybrids (2n = 66). Moreover, in some extremely invasive populations, almost no diversity was detected and the knotweeds have adapted to different habitats through epigenetic or other nongenetic means. The study describes processes that have been implicated as adaptive in invasion success, focusing on various forms of hybridisation, backcrossing, and polyploidization during offspring production leading to novel traits, and may thus help to understand the huge successes of some plant invaders, especially those that are genetically impoverished.

Abstract ID: 2319
Poster board number:
P308

The hidden signature of biological invasions with hybridization

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The accumulation of genome-wide molecular data has emphasized the important role of hybridization in the evolutionary history of many organisms. Despite a number of examples of hybridization occurring during biological invasions, the resulting spatial patterns at the level of genomes remain poorly understood. By using spatially explicit simulations, we explored the spatial distribution of introgression across the area of colonization of an invasive taxon hybridizing with a local one. The general resulting pattern for neutral loci is an increasing introgression of local genes into the invasive gene pool with the increase in the distance from the source of the invasion, and a decreasing introgression of invasive genes into the local taxon. While there is some variation in this general trend depending on the scenario investigated, we confirm this pattern is consistent with published empirical observations. Spatial heterogeneity of introgression within taxon is thus an expected neutral pattern in structured populations after a biological invasion with a low to moderate amount of hybridization. By using additional simulations, we argue that the spatial pattern of Neanderthal introgression in modern humans, which has been documented to be higher in Asia than in Europe, can be explained by a model of hybridization with Neanderthals in Eurasia during the range expansion of modern humans from Africa. Our results support the view that hybridization during range expansion may explain spatially heterogeneous introgression patterns without the need to invoke selection.

Symposium: S20. Unravelling the interplay between plasticity and evolution during rapid global change (id: 941)

Abstract ID: 1010
Poster board number:
P309

Weak thermal limit plasticity exposes insects to extreme temperature events

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Extreme temperature events are increasing in frequency and intensity due to climate change. Such events threaten insect species, including those with roles as pollinators, pests and disease vectors. Animals can enhance their critical thermal limits through acclimation, yet whether such plasticity is widespread and sufficient to aid insect populations under climate change is unknown. Here, we use meta-analyses across 1,374 effect sizes from experimental studies to show that thermal limit plasticity is pervasive but generally weak: for every 1°C rise in acclimation temperature, critical thermal maximum increased by 0.09°C and for a 1°C decline, critical thermal minimum decreased by 0.15°C. Moreover, publication bias suggests that the magnitude of plasticity is overestimated. Development was an important predictor of variation in plasticity: juvenile insects were more plastic than adults and, in some contexts, hemimetabolous (non-metamorphosising) insects had greater plasticity than holometabolous (metamorphosising) insects. Overall, current experimental studies show that plasticity of thermal limits is unlikely to aid most insect species during extreme climatic events, yet there is urgent need for more studies in under-represented taxa and geographic regions.

Abstract ID: 1021
Poster board number:
P310

Developmental plasticity in heat tolerance: ontogenetic variation, persistence and future directions

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Ectothermic animals represent most of the animal diversity on the planet and yet, are the most challenged by rising temperatures. As such, understanding the factors affecting thermal tolerance is crucial for predicting the impact climate change will have on ectotherms. However, the role developmental plasticity plays in allowing populations to cope with thermal extremes is poorly understood. Neglecting how early environmental experiences shape thermal tolerance (i.e., developmental plasticity) may be an important oversight given that early life experiences have major and often persistent effects on phenotypes. To quantify the acute and persistent influence of early thermal environments on thermal tolerance, we systematically reviewed 6000 studies and meta-analysed data from 150 studies. In this talk, I will address the following questions: How much do early thermal environments impact heat tolerance, and is that enough to compensate for rising temperatures? Are embryos more plastic than juveniles? Do early thermal environments have persistent influence on heat tolerance? What is the current state of knowledge and what are pressing future directions in the field?

Abstract ID: 1080

Poster board number:
P311

Individual reversible plasticity as a genotype-level bet-hedging strategy

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Reversible plasticity in phenotypic traits allows organisms to cope with environmental variation within lifetimes, but costs of plasticity may limit just how well the phenotype matches the environmental optimum. An additional adaptive advantage of plasticity might be to reduce fitness variance, in other words: bet-hedging to maximize geometric (rather than simply arithmetic) mean fitness. Here we model the evolution of plasticity in the form of reaction norm slopes, with increasing costs as the slope or degree of plasticity increases. We find that greater investment in plasticity (i.e. a steeper reaction norm slope) is favoured in scenarios promoting bet-hedging as a response to multiplicative fitness accumulation (i.e. coarser environmental grains and fewer time steps prior to reproduction), because plasticity lowers fitness variance across environmental conditions. In contrast, in scenarios with finer environmental grain and many time steps prior to reproduction, bet-hedging plays less of a role and individual-level optimization favours evolution of shallower reaction norm slopes. However, the opposite pattern holds if plasticity costs themselves result in increased fitness variation, as might be the case for production costs of plasticity that depend on how much change is made to the phenotype each time step. We discuss these contrasting predictions from this partitioning of adaptive plasticity into short-term individual benefits versus long-term genotypic (bet-hedging) benefits, and how this approach can inform partitioning the roles of microevolution versus thermal plasticity in recent observed advances in avian egg laying dates.

Abstract ID: 1109
Poster board number:
P312

Evolutionary demise of a social interaction: partners differ in the rate of interacting trait loss

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Social interactions between animals are suggested to be increasingly vulnerable to breakdown in this changing world. Phenotypic plasticity enables animals to flexibly adjust their behaviour to their social environment – sometimes through the expression of adaptive traits that have not been exhibited for several generations. We investigated how long social adaptations can usefully persist when they are not routinely expressed by using experimental evolution to document the loss of social traits associated with the

supply and demand of parental care. Populations of burying beetles Nicrophorus vespilloides were evolved over 48 generations - in 'Full Care' populations traits associated with the supply and demand of care were expressed, whereas in 'No Care' populations we prevented expression of these traits experimentally. We then revived trait expression in the No Care populations at generations 24, 43 and 48 by allowing parents to supply post-hatching care, and compared these social traits with those expressed by the Full Care populations. We found that offspring demands for care decayed in the No Care populations more rapidly than a parent's capacity to supply care. Furthermore, male care decayed faster than female care. We suggest that this reflects differences in the strength of selection on offspring, males and females, for the expression of alternative traits which are more likely to enhance fitness when post-hatching care is disrupted.

Abstract ID: 1190
Poster board number:
P313

In a changing world, farmed-wild hybridisation alters a key life-history trait in Atlantic salmon

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Hundreds of thousands of farmed Atlantic salmon escape into the wild every year where they can interbreed with natural populations. It is crucial to understand how farm-wild hybridization can affect important life history traits, and consequently demography and fitness of wild fish under future climates. Using multiple common garden experiments carried out under natural freshwater conditions over several years allowed us to test the role of ultimate (e.g. genetic) and proximate (e.g. environmental cues) factors shaping seaward migration variation. During this critical phase of the salmon life cycle fish first abandon freshwater territories and move subsequently towards the sea. We found differences between farmed, captive-bred and wild progeny in the timing, morphology and behaviour during this critical period of transition from pre-smolt to smolt. Farm progeny initiated and completed seaward migration earlier than wild progeny. Larger domesticated smolts could survive better at sea but initiating and completing seaward migration earlier could lead to a phenological mismatch on feeding grounds. Farm-wild hybrids as well as progeny of local captive-bred fish were found to be intermediate in timing and morphology suggesting additive genetic variation and decoupling of genetic background and domestication. We show that life history decisions (and associated life history traits) of wild fish can be greatly affected by the dual threat of introgression and environmental change.

Abstract ID: 1290

Poster board number:
P314

How is phenological plasticity constrained by habitat artificialization? Empirical evidence in tits.

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Phenotypic plasticity is the capacity of organisms to express traits differently under different environmental conditions. We know that the degree of plasticity varies between populations, but we still understand poorly the drivers of this variability. In particular, multidimensional plasticity has received little attention despite the fact that in the wild, organisms are submitted to the simultaneous variation of several environmental factors. Identifying which interactions constrain the expression of plasticity shapes our understanding of the adaptive nature of plasticity and is a crucial step to evaluate the limits of plasticity as a mechanism through which organisms can adapt to global change. Bird phenological plasticity is a text book example of responses to climate change, but we know little about how other components of global change are constraining the expression of this plasticity. To investigate local environment effects, such as the degree of human disturbance, we will use a comparative approach relying on data from constant ringing effort sites, based on a protocol for collecting data from free flying birds (incl. species and age). The temporal variation of the proportion of first year birds among all captured birds, can be used as an index of phenology. This large-scale design allows to study phenological plasticity of reproduction in resident populations along a gradient of habitat degradation. More specifically, we will test whether the level of ground waterproofing, a measure of the degree of urbanization, impact on blue tits plasticity. We expect that urbanization, by increasing stress levels or confusing phenological cues, limits plasticity.

Abstract ID: 1382
Poster board number:
P315

Maladaptive reproductive responses to developmental temperature in the European corn borer moth

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Recent work suggests maladaptive plasticity may contribute substantially to population response to rapid global change. Fertility and fecundity are often influenced by elevated temperatures but how this plasticity in reproduction may promote or hinder genetic evolution remains unclear, in part because estimates of reproductive plasticity and its sensitivity to the developmental timing of disturbance are often lacking. We quantified reproductive plasticity in response to temperature at different life stages in the European corn borer moth, *Ostrinia nubilalis*. Lepidoptera undergo metamorphosis with distinct life stages having different heat tolerances, and we measured stage-specific, additive, and carry-over effects of exposure to elevated temperature (+5^{o}C). We found that when elevated temperatures were experienced through pupal development and into early adulthood, corn borers produced significantly fewer eggs. However, exposure for shorter time periods (only the larval or only the pupal stage) had few effects on reproductive

output. Our results suggest that the developmental timing of environmental changes matter to reproductive outcomes. We predict that this decrease in egg laying is maladaptive and may be selected against under warming climates.

Abstract ID: 1405
Poster board number:
P316

Phenotypic plasticity enhances adaptation potential to fluctuating warm environments

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Increasing temperatures are a stressful abiotic factor negatively impacting species viability and reproduction. When approaching fertility limits, species are known to become sterile, although they can recover fertility when encountering milder temperatures. Despite the current interest in thermal reproductive stress, few studies explore the long-term evolutionary implications. Experimental evolution is a powerful tool to understand how species will adapt to new environmental challenges and hence, investigate evolutionary dynamics. Using this tool on the model *Drosophila melanogaster,* we ask how adaptation to constant or fluctuating warm environments affects reproduction and thermotolerance. After 32 generations we conducted assays at different developmental temperatures to disentangle the effects of genetic and environmental variation on the phenotype. We also aimed to understand the role of phenotypic plasticity in thermal adaptation by combining both common garden and non-common garden experiments. For that, we measured different reproductive and fitness traits such as viability, body size, egg size, fertility recovery curves and survival after several cold and heat shocks, with an emphasis on male traits, as males are more vulnerable to thermal stress. We found major differences in reproductive trait expression across regimes after thermal adaptation. Notably, populations experiencing a fluctuating environment showed higher fitness than those held at constant temperatures. In addition, when maintained under warm conditions, individuals showed increased thermotolerance compared with those from the control regime. Finally, our results support that phenotypic plasticity could be important for thermal adaptation while relaxing selection is not enough to compensate fitness loss in a changing environment.

Abstract ID: 1503
Poster board number:
P317

Poison frog social behaviour under global change: potential impacts and future challenges

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The current and cascading effects of global change challenge the interactions both between animals and between them and the environment they inhabit. Amphibians are an ecologically diverse class with a wide range of social and sexual behaviours, making

them a compelling model through which to understand the potential adaptations of animals faced with the effects of human-induced rapid environmental changes (HIREC). Poison frogs are a particularly interesting system as they display diverse social behaviours, thus offering a tractable system to investigate how diverse, closely-related species may respond to the impacts of HIREC. Here, we discuss the potential impacts of HIREC on poison frog behaviour, and the future challenges this group may face in response to such change. We pay special attention to parental care and territoriality, which are emblematic of this clade, and consider how different species may flexibly respond and adapt to increasingly frequent and diverse anthropogenic stress. More specifically, we hypothesise that some parents may increase care (i.e. clutch attendance, distance travelled for tadpole transport) in HIREC scenarios, and that species with more generalist oviposition and tadpole deposition behaviours may fare more positively than their less flexible counterparts; we predict that the latter may either face increased competition for resources limited by HIREC or will be forced to adapt and expand their natural preferences. Likewise, we hypothesise that human-driven habitat alteration will disrupt the acoustic and visual communication systems due to increased noise pollution and/or changes in the surrounding light environment.

Abstract ID: 1568
Poster board number:
P318

Heat-induced plant plasticity influences herbivore and pollinator preferences and plant reproduction

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Plants respond developmentally to increases in temperature, in a process known as thermomorphogenesis. However, little is known about how this heat-mediated plastic changes affect the behaviour of insect pollinators and herbivores, and the resulting consequences for plant fitness. To investigate this, we grew fast-cycling *Brassica rapa* plants at 23 °C (ambient) or at 24°C with 3 separate 30°C days (heat-treated). Heat-treated and ambient plants were phenotyped (floral traits, scent and color), then arranged in a matrix or in two-choice tests and exposed to both pollinators (*Bombus terrestris*) and pollinating herbivores (*Pieris rapae*). We measured flower visitation, oviposition of *P. rapae*, herbivore development and seed output. Heat-treated plants produced more but smaller flowers, with lower UV reflectance and emitted a different volatile blend with a lower total emission. This negatively impacted visitation by both the pollinator and pollinating herbivore: heat-treated plants received less first choice visits by bumblebees and butterflies, and less flower visits by butterflies. Oviposition first choice was also lower in heat-treated plants, although the final egg load did not differ. Seed output (fitness) was lower in heat-treated plants, and we show that this was i) because of a reduction in flower fertility due to temperature, and ii) more importantly because of the reduced visitation of pollinators. Thus, our study highlights an important mechanism by which global warming can alter plant-insect interactions and negatively impact plant fitness.

Abstract ID: 1778
Poster board number:
P319

Fish plastic and evolutionary metabolic response to freshwater hypoxia

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While hypoxia (i.e. low dissolved oxygen level in water) events occur naturally, global change and human activities have exacerbated their strength and temporal fluctuations. As populations may not be able to escape the hypoxic conditions, especially in freshwater ponds, it is crucial to understand how and through which mechanisms organisms can respond and adapt to these fluctuating environments. When directly exposed, individuals may be able to adjust their phenotypes through plasticity but continued exposure to hypoxia over generations may require adaptation and evolution. Using two populations of wild three-spined sticklebacks (*Gasterosteus aculeatus*) exposed to different levels of hypoxia conditions in their natural habitats and experimentally exposed to fluctuating hypoxia (20% air saturation during the night and 100% during the day to mimic the natural hypoxic conditions in freshwater ponds), we investigated the contribution of plastic and evolutionary response in the fish metabolism (growth, swimming capacity, aerobic and anaerobic metabolism). We showed adaptation in fish growth, swimming and aerobic metabolism, fish exposed to hypoxia in their natural habitats possessing higher capacities. However, only fish anaerobic metabolism was affected by the experimental hypoxic conditions. These results revealed a rapid plastic response to hypoxia in fish anaerobic metabolism, while continued exposure likely induced an evolutionary response in fish aerobic metabolism. By integrating the independent and interactive effects of plasticity and adaptation, this project provides new insights on the capacity of fish to respond to new environmental conditions.

Abstract ID: 1800
Poster board number:
P320

Fluctuating heat stress during development exposes reproductive costs and putative benefits

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Temperature and thermal variability are increasing worldwide, with well-known consequences. However, effects on other potentially more thermally-sensitive reproductive traits are less understood, especially when considering thermal variation. Our goals were to test how exposure to different average temperatures that either fluctuated or remained constant impacts different male reproductive performance traits and to assess adaptive potential to future heat stress.
We took advantage of a set of *Drosophila melanogaster* isogenic lines of different genotypes, exposing them to four different thermal conditions. These conditions represented a benign and a stressful mean temperature, applied either constantly or fluctuating around the mean, and experienced during development when heat stress avoidance is hindered because of restricted mobility.

Both costs and benefits to different thermal conditions on reproductive performance were found, with some responses varying between genotypes. Mating success improved under fluctuating benign temperature conditions and declined as temperature stress increased regardless of genotype. Fertility and productivity were severely reduced at fluctuating mean high temperature for all genotypes, but some genotypes were unaffected at constant high mean temperature. These more thermally robust genotypes showed a slight increase in productivity under the fluctuating benign condition compared to constant high temperature, despite both thermal conditions sharing the same temperature six hours daily. Increasing thermal stress resulted in higher heritability and evolvability.
While thermal stress increased genetic variation that could provide adaptive potential against climate warming, this is unlikely to compensate for the overall severe negative effect on reproductive performance as mean temperature and variance increase.

Abstract ID: 1845
Poster board number:
P321

Plasticity in a multivariate world: impact of density on phenological plasticity in Great Tits

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Phenotypic plasticity, the capacity of a genotype to modify its phenotypic expression in response to environmental variation, is a major adaptive mechanism. Plasticity has often been studied as a response to variation of a single factor, but in the natural world, animals experience a multitude of varying factors in their environment. If expressing plasticity is costly, and if the phenotypic optima differ depending on interactions between environmental factors, then impacts of simultaneous variation of factors could alter the expression of plasticity (multidimensional plasticity). Further, conditions experienced early in life might affect the organism's performance, but the extent to which they modify an individual's ability to express phenotypic plasticity in the future is poorly understood. One factor of particular interest is density of conspecifics as it drives competition for resources thereby influencing individual performances and may also influence the optimal phenotype. Breeding time plasticity in response to temperature in passerines, is an extensively studied example of adaptive plasticity in the wild. We will be utilising data obtained from a long-term monitoring project on Great Tits, including a density manipulation experiment to understand the limits of expression of plasticity. Our goal is to study the expression of lay-date plasticity in response to multivariate environmental conditions. Particularly, we investigate how density of conspecifics affects the expression of plasticity through (1) potential carry over effects arising from environmental conditions experienced during development of chicks (early-life) and (2) within year interactions with temperature and rainfall.

Abstract ID: 2141
Poster board number:
P322

Can parasites adapt to elevated temperature? Experimental evolution and a survey of heated lakes

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Global warming is predicted to impact the prevalence and severity of infectious diseases. However, empirical data supporting this statement usually stem from experiments in which parasite fitness and disease outcome are measured directly after temperature increase. This might exclude the possibility of parasite adaptation and does not allow to test whether observed changes in fitness result from thermal adaptation or phenotypic plasticity. To incorporate the adaptive response of parasites into predictions of disease severity in a warmer world, we used a two-fold approach. First, we undertook an experimental evolution assay in which a fungal parasite of phytoplankton was maintained at elevated or control temperatures for several months; the performance of each parasite population was then assessed under both temperature environments. Second, we tested "warmer hence sicker" prediction in more natural settings; by comparing the prevalence of plankton parasites between five artificially heated lakes and four nearby non-heated control lakes, using both microscopy and DNA-metabarcoding approaches. The heated lakes, which receive warm water from two power plants, have experienced an elevation in water temperature of ca. 3–4 °C for the last 60 years, and are therefore a very convenient models for addressing modifications of host-parasite interactions in a warming world. Neither approach confirmed the popular "warmer hence sicker world" scenario, instead they underlined the context-dependent impact of temperature increase on host-parasite interactions and disentangling the evolutionary and plastic components of species' responses to climate change.

Abstract ID: 2203
Poster board number:
P323

Male indirect genetic effects on lay date: the role of social plasticity in evolutionary rescue

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Changes in avian breeding phenology are among the most apparent responses to climate change in free-ranging populations. A key question is whether populations will be able to keep up with the expected rates of environmental change. There is a large body of research on the mechanisms by which lay dates track temperature change and the consequences of (mal)adaptation on population persistence. Often overlooked is the role of males, who can influence the lay date of their mate through their effect on the pre-laying environment. We explore how social plasticity causing male indirect genetic effects can help or hinder population persistence when female traits underpinning lay date and male traits influencing female's timing of reproduction have a shared genetic basis and both respond to climate-mediated selection. We extended quantitative genetic moving optimum models to predict the consequences of social plasticity on the maximum

sustainable rate of temperature change and evaluated the model using a combination of simulated data and empirical estimates from the literature. Our model suggests that predictions for population persistence may be biased if social plasticity and cross-sex genetic correlations are not considered, and the extent of this bias depends on the difference between sex-specific sensitivities to temperature change. Our model highlights that more empirical work is needed to understand sex-specific effects of environmental change on fitness and its consequences for population dynamics. While we discuss our model in the context of avian breeding phenology, the results can be generalized to different contexts and types of social interactions.

Abstract ID: 2238
Poster board number:
P324

A tit's quick wit: examining cognitive differences between urban and forest birds

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A fundamental question in evolutionary biology has been to understand how organisms adjust to novel ecological conditions and opportunities, including urbanisation, by altering their phenotypes. Specifically, we investigated inhibitory control, an executive cognitive function that is central to decision-making and allows animals to adapt to sudden changes in their environment. High inhibitory control is also shown to be associated with high foraging flexibility. Although this cognitive trait may facilitate adaptation to changing conditions, it has rarely been examined in the context of the evolutionarily novel environments presented by urbanisation. To investigate whether cognitive control varies along an urban-forest gradient, we used a motor detour-reaching task to examine inhibitory control in wild great tits (*Parus major*) over two years from ten study sites that differed in the degree of urbanisation. As urban organisms are thought to be more behaviourally and cognitively plastic and better at problem-solving, we predict that urban tits will make fewer errors and detour around the barrier more quickly during the task compared to non-urban tits. We present results on whether urbanisation correlates with cognitive control in our study system, and also discuss how cognition correlates with exploration behaviour in a novel environment, a trait closely linked to the fast-slow personality axis. We are also investigating if the phenotypic trends observed in the wild are maintained in a common garden experiment in spring 2022. This will help disentangle the genetic and plastic effects that act on potential differences in cognition between populations affected by varying levels of urbanisation.

Abstract ID: 2407
Poster board number:
P325

Cold shock resistance in easly developmental stages of Drosophila melnogaster

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Cold shock resistance is one the most important physiological and biological adaptation in insects to combat thermal stress. When exposed to cold shock of -5°C each generation for over 200 generation, adults fruit flies were found to be more resistant to cold shock in terms of increased survival, increased mating frequency and male mating ability under stress.In this study we hypothesized that if selected for cold shock resistance in adult stage, other developmental stages will also respond positively to it. We also checked if the ability to rapidly cold harden exists in all of the developmental stages.
The study was done on 6 hrs old eggs, 96 hrs old larvae, 166 hrs old pupae and 288 hrs old adults by exposing them to -2°C, -5°C,-8°C ,-10°C for one hour post a pre-treatment of 0°C for 2 hours.
We found out that larval stage is the least resistant to cold shock following pupae and eggs. We also found an impact of selection as pupae from selected population had higher survival than controls post cold shock. Unlike some the previous studies we did not find existence of Rapid cold hardening(RCH) in any of the stages besides adults at 0°C for 2 hours.

Abstract ID: 2454
Poster board number:
P326

Animal migration to higher latitudes: environmental changes and increasing threats

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Every year, many wild animals undertake long-distance migration to breed in the North, taking advantage of seasonally high pulses in food supply, fewer parasites and lower predation pressure in comparison with equatorial latitudes. Growing evidence suggests that climate change-induced phenological mismatches have reduced food availability. Furthermore, novel pathogens and parasites are spreading Northwards, and nest or offspring predation has increased at many Arctic and North temperate locations. Altered trophic interactions have decreased the reproductive success and survival of migratory animals. Reduced advantages for long-distance migration have serious consequences for community structure and ecosystem function. Changes in the benefits of migration need to be integrated into projections of population and ecosystem dynamics and targeted by innovative conservation actions. By using recently established migration profitability framework, we will discuss how various animal populations are able or not – to cope with changing benefits of migratory behaviour from ecological and evolutional temporal perspectives.

Symposium: S21. Epigenetics goes wild! Epigenetic diversity and the evolutionary potential of wild populations. (id: 942)

Abstract ID: 1046
Poster board number:
P327

Spontaneous epigenetic changes and natural epigenetic variation in a filamentous fungus

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Some epigenetic changes can be inherited from parents to offspring, this opens up the possibility that epigenetic variation can contribute to evolutionary change. So far strongest evidence for spontaneous epigenetic changes, in DNA methylation, comes from plants, but whether epigenetic inheritance is common in other taxa is poorly known. In the filamentous fungus *Neurospora crassa*, DNA methylation is dependent on an underlying histone modification: trimethylation of lysine 9 in histone 3 (H3K9me3). We created mutation accumulation lines and determined genome wide DNA methylation patterns in these lines. We observed that DNA methylation patterns change spontaneously in *N. crassa,* and that this signal is stronger at the level of differentially methylated regions. We estimated rates of spontaneous epigenetic changes and examine patterns of natural variation. We hypothesize that DNA methylation changes reflect changes in H3K9me3, raising the intriguing possibility that spontaneous changes in chromatin modifications are inherited in *N. crassa*. We also observed that genetic mutations interact with chromatin modifications as H3K9me3 domains differ in mutation rate and spectra. We see these patterns reflected in natural genetic variation.

Abstract ID: 1069
Poster board number:
P328

Parasite infection mediates intergenerational DNA methylation in the three-spined stickleback

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Parasites are arguably among the strongest drivers of evolution. While the genetics and genomics of parasite resistance of hosts are growingly well understood, major gaps remain about the role and mechanisms of phenotypic plasticity within and across generations. Previous studies on the three-spined stickleback (*Gasterosteus aculeatus*) have shown that paternal infection with a nematode parasite is associated with increased selection in the offspring generation but also increased tolerance upon infection. The genome-wide DNA methylation pattern differed between infected and control fathers, demonstrating the link between infection and DNA methylation. In the present work, we used reduced representation bisulfite sequencing on 135 fish and asked (1) whether some parental DNA methylation induced by the infection can be transmitted to the next generation, and (2) which genes and gene networks are affected. We investigated

overall fractional DNA methylation, as well as differential methylation between infected and control offspring, depending on the paternal infection status. We show that an improved body condition of offspring correlates with a lower global DNA methylation count, possibly indicating a link between tolerance and methylation. Strikingly, the infectious status of fathers strongly correlated with change in the methylome of the offspring, regularly beyond the offspring infection status itself. This project advances our understanding of the mechanisms of phenotypic plasticity in aquatic organisms and their consequences on adaptive evolution.

Abstract ID: 1131
Poster board number:
P329

Epigenetic and gene expression differences are associated with reproductive sucess in aphid morphs

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Polyphenism occurs when multiple discrete phenotypes are produced from a single genotype. Polyphenisms are hypothesised to contribute to the evolutionary success of aphids (*Acyrthosiphon pisum*), which show multiple polyphenisms, including reproductive and wing polyphenism. Several studies have investigated the role of wing development genes in aphid wing polyphenism. However, the underlying mechanism, role of epigenetic regulation and trans-generational trade-offs of wing polyphenism remain poorly studied. We used two polymorphic aphid genotypes and found that the N127 genotype showed higher alternative morph production in comparison to N116 genotype. We further found higher reproductive success in the wild-type, which may suggest a trade-off between reproduction and the ability to disperss .These effects are maintained for at least one generation after the exposure to the inducing crowding conditions. To start establishing the molecular pathways underpinning polyphenisms, we investigated gene expression, using RNAseq and qPCR, as well as DNA methylation levels of 13 candidate genes with different roles in aphid development, such as wing formation and development, carotene production and metabolite regulation. Eleven genes were significantly differentially expressed between dispersal and non-dispersals morphs; of these, four (DMAP1, rpd3, Hsp83, Mad) further showed significant differences in methylation. Our results demonstrate that aphid genotypes respond differently to stressful conditions, and the trade-offs between reproductive success and dispersal ability might persist for more than one generation. We further found methylation and gene expression levels differed between morphs and between genotypes, providing insight into key genes that may play an important role in aphid polyphenism.

Abstract ID: 1135
Poster board number:
P330

Assimilation of an acquired character by plasticity guided genetic and epigenetic inheritance

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Since Waddington's demonstration of the inheritance of an acquired trait by genetic assimilation that there is an intense debate about the role of phenotypic plasticity in evolution. It is proposed that plasticity could induce the establishment of heritable epigenetic alleles that contribute to the evolution by genetic assimilation. We recapitulate Waddington's pupal heat-shock experiment to address the role of plasticity and epigenetic inheritance using a set of inbred and outbred flies. These flies exhibit ectopic veins spontaneously at low penetrance levels, giving us a unique chance to test the effect of plasticity in the assimilation by selection with or without the heat-shock induction ("assimilated" and "non-assimilated" flies respectively). Strikingly, the ectopic veins were assimilated at high penetrance levels after a few generations of selection for both the assimilated and non-assimilated in inbred and outbred flies. We combine transcriptome, epigenome, and genotyping analysis to uncover the underlying genetic and epigenetic changes responsible for the evolution of the ectopic veins in these flies. The assimilated and non-assimilated inbred flies share the deregulation of putative wing vein genes by the fixation of the same genetic alleles, but interestingly, the assimilated flies exclusively showed Hsp90 deregulation putatively driven by an epigenetic allele. The outbred assimilated and non-assimilated flies have evolved by the fixation of population's specific regulatory changes in wing developmental genes. We propose that plasticity plays a crucial role in evolution by genetic assimilation, which may induce the establishment of heritable epialleles but also expose otherwise cryptic alleles.

Abstract ID: 1148
Poster board number:
P331

The role of DNA methylation in transgenerational adaptation of (a)sexual offspring of Fragaria vesca

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Environmentally induced epigenetic variation (DNA methylation in particular) that is passed to the offspring might enable transgenerational adaptation of plants to changing environment. Nevertheless, solid evidence is still scarce. Moreover, meiosis resets most of the environmentally induced DNA methylation across sexual generations, thus acting as a barrier reducing the role of DNA methylation in transgenerational adaptation. However, plants can also reproduce by means of vegetative propagation, i.e. by clonal reproduction that lacks meiosis. We test the ability of a clonal herb *Fragaria vesca* to adapt to climatic conditions predicted to be prevalent at the end of this century (increased mean temperature for 4 ^{o}C, CO_2 level for 800ppm, drought periods) via transgenerational effects. By using an isogenic inbred line of *F. vesca*, we compare transgenerational adaptation at the level of phenotypic variation to future climatic conditions between sexual and clonal (asexual) offspring. Moreover, we compare the role of DNA methylation variation in the observed transgenerational adaptation between clonal and sexual offspring by whole genome bisulfite sequencing. Our study is the first study directly evaluating the role of heritable epigenetic variation among clonal and sexual offspring in transgenerational adaptation of plants to novel climatic conditions.

Abstract ID: 1191
Poster board number:

P332

Epigenetic markers of chronological age and survival in a wild passerine

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Within-populations there can be considerable individual variation in the onset and rate of senescence; individuals may have biological ages (BA) that differ from their chronological age (CA). Measuring CA and BA in wild populations is difficult but vital if we are to understand the complex social, environmental and genetic factors affecting senescence. DNA-methylation clocks, which generate age-predictions based on age-correlated methylation levels at cytosine-guanine pairs, offer a promising solution; accurately reflecting both CA and BA in humans. However, DNA-methylation clocks in wild populations remain taxonomically bias (towards mammals) and rarely incorporate BA-components, such as condition or survival. In this study, we developed ribosomal DNA-methylation clocks to estimate both CA and survival (a component of BA) in a population of Seychelles warblers (*Acrocephalus sechellensis*). Clock-estimates of CA (derived from methylation at 67 CpG sites) were strongly correlated with known CA, with a mean difference of 2.2 years (based on leave-one-out cross-validation). Importantly, we show that rDNA-methylation and clock-estimated CA (while controlling for known CA) are also associated with individual differences in survival prospects, suggesting rDNA-methylation captures components of BA. In this talk, I will discuss the consequences of these findings for the development of future DNA-methylation clocks and the potential utility of DNA-methylation as a marker of BA/survival for the study of wild population senescence.

Abstract ID: 1390
Poster board number:
P333

Differential methylation, epigenetic clocks, and island-mainland divergence in a small mammal

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Geographically isolated populations, including island-mainland populations, tend to exhibit phenotypic variation in many species. The so-called island syndrome occurs when different environmental pressures lead to insular divergence from mainland populations. This phenomenon can be seen in an island population of Nova Scotia masked shrews (*Sorex cinereus*), which have developed a specialized feeding habit and digestive enzyme compared to their mainland counterparts. Epigenetic modifications, such as DNA methylation (DNAm), can impact phenotypes by altering gene expression

without changing the DNA sequence. Here, we used a *de novo* masked shrew genome assembly and epigenome-wide assay to investigate morphological and DNA methylation patterns between island and mainland populations. Island shrews were morphologically and epigenetically different than their mainland counterparts, exhibiting a smaller body size; remarkably, the gene ontology analyses mirrored these phenotypes including genes for the digestive enzyme phenotypes. Moreover, island shrews appeared to age faster than their mainland counterparts. This study provides an example counter to the prevailing island syndrome morphological patterns, along with novel epigenomic insight into the drivers of island-mainland divergence in mammals.

Abstract ID: 2162
Poster board number:
P334

The role for epigenetics in the evolution of plasticity of avian phenotypic traits

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Epigenetic mechanisms such as DNA methylation, are affecting gene expression during early development. At the same time, they provide a plausible mechanism that translates environmental changes to phenotypic changes. If these induced environmental changes are maintained throughout the lifetime of an organism or are inherited transgenerationally, they have the potential to influence the expected evolutionary outcome of rapid environmental changes such as climate change and urbanization. Evidence for this hypothesis is largely lacking in vertebrates. Using the great tit (*Parus major*) as an ecological model organism, we here show that the roles of epigenetic variation are diverse. Where DNA methylation seems to play a major role in shaping a preprogrammed early life development, between-individual variation in methylation is largely explained by genetic variation. We repeatedly find low correlations of between-individual variation in methylation with environmentally induced phenotypic changes, providing limited scope for adaptive phenotypic changes via environmentally induced DNA methylation. Within-individual fluctuations in DNA methylation nonetheless rely on environmental input, suggesting that genetic variation related to this epigenetic variation is a strong candidate explaining the genetic underpinning We conclude that DNA methylation mostly represents a series of processes that orchestrate a dynamic change in gene expression under the control of genetic variation. of phenotypic plasticity. We here present results supporting this idea and discuss the implications.

Abstract ID: 2197
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P335

Adaptive potential of epigenetic switching during adaptation to fluctuating environments

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Epigenetic regulation of gene expression allows for the emergence of distinct phenotypic states within the clonal population. Due to the instability of epigenetic inheritance, these phenotypes can inter-generationally switch between states in a stochastic manner. Theoretical studies of evolutionary dynamics predict that the phenotypic heterogeneity enabled by this rapid epigenetic switching between gene expression states would be favored under fluctuating environmental conditions, whereas genetic mutations, as a form of stable inheritance system, would be favored under a stable environment. To test this prediction, we engineered switcher and non-switcher yeast strains, in which the uracil biosynthesis gene *URA3* is either continually expressed or switched on and off at two different rates (slow and fast switchers). Competitions between clones with an epigenetically controlled *URA3* and clones without switching ability (*SIR3* knock-out) show that the switchers are favored in fluctuating environments. This occurs in conditions where the environments fluctuate at similar rates to the rate of switching. However, in stable environments, but also in environments with fluctuation frequency higher than the rate of switching, we observed that genetic changes dominated. Remarkably, epigenetic clones with a high, but not with a low, rate of switching can co-exist with non-switchers even in a constant environment. Our study offers an experimental proof-of-concept that helps defining conditions of environmental fluctuation under which epigenetic switching provides an advantage.

Abstract ID: 2221
Poster board number:
P336

Do chromatin-TE interactions contribute towards transgenerational plasticity in wild fruit flies?

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Two factors predicted to influence acclimation and adaptation under environmental change are epigenome regulation and transposable element (TE) activity under stress. Lab studies suggest that interactions between these factors affects genome evolution in the fruit fly Drosophila melanogaster, generating transgenerational phenotypic change. However, little is known about how these processes operate in natural populations. To shed light on this, we combine genomic, epigenomic and transcriptomic experiments with multigenerational phenotypic assays using wild D. melanogaster from Spain and Finland.

Lab populations were set up using equal numbers of F1 offspring from wild-caught females. In the F2 generation, genomic and epigenomic variation in three Spanish populations and one Finnish population were measured. In the F3, the effects of a short heat stress on the epigenome and transcriptome were assessed for one Spanish and one Finnish population. Several life history traits were measured in a separate cohort of F3 flies. Three generations later (F6), transgenerational effects on the epigenome, transcriptome, and life history traits were measured.

Heat stress in the F3 reduced egg-to-adult viability among eggs laid in the 1-2 days, but no significant effects were detected at later time points (eggs laid after 3-4, 5-6, and 13-14 days). However, F6 descendants of heat-stressed flies had increased egg-to-adult viability, and for the Spanish population, reduced time-to-pupation. Ongoing analysis of 'omic data is assessing: a) natural variation in TE landscapes and chromatin profiles, and

their relation to gene-expression under stress, and b) whether chromatin and gene expression changes could contribute towards transgenerational phenotypic effects.

Abstract ID: 2223
Poster board number:
P337

Genotyping of the seagrass cymodocea nodosa identifies candidate genes for environmental adaptation

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Plant populations distributed along broad latitudinal gradients often show patterns of clinal variation in genotype and phenotype. Differences in photoperiod and temperature cues across latitudes influence major phenological events. Here, we used an array of 4,941 SNPs derived from 2b-RAD genotyping to characterize population differentiation and levels of genetic and genotypic diversity of three populations of the seagrass *Cymodocea nodosa* along a latitudinal gradient extending across the Atlantic-Mediterranean boundary (i.e., Gran Canaria - Canary Islands, Faro - Portugal and Ebro Delta - Spain). Our main goal was to search for potential outlier loci that could underlie adaptive differentiation of populations across the latitudinal distribution of the species. We hypothesized that such polymorphisms could be related to variation in photoperiod-temperature regimes occurring across latitudes. The three populations were clearly differentiated and exhibited diverse levels of clonality and genetic diversity. Nine SNPs were reliably identified as outliers across the three sites by two different methods and three SNPs could be associated with specific protein-coding genes by screening available C. nodosa transcriptomes. Two SNPs-carrying contigs encoded for transcription factors, while the other one encoded for an enzyme specifically involved in photoperiodism/regulation of flowering time, namely Lysine-specific histone demethylase 1 homolog 2. When analyzing biological processes enriched within the whole dataset of outlier SNPs identified “regulation of transcription” and “signalling” were among the most represented. Our results highlight the fundamental importance signal integration, gene-regulatory networks and epigenetic regulation via DNA (de)methylation, could have for enabling the adaptation of seagrass populations along environmental gradients.

Abstract ID: 2326
Poster board number:
P338

The role of DNA methylation in gene expression and phenotypic plasticity in a social spider

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Epigenetic variation, such as variation in DNA methylation patterns, appears to be highly variable among taxa, and our understanding of the functional significance of this variation is incomplete. We performed whole genome bisulfite sequencing of the social spider *Stegodyphus dumicola*, and show that DNA methylation occurs mainly in CpG context and is concentrated in genes. We used RNA sequencing to investigate the role of DNA methylation in gene regulation, and found higher expression of methylated genes compared with genes that are not methylated, and that methylated genes are more stably expressed across individuals than unmethylated genes. This lends support for the implication of DNA CpG methylation in regulating gene expression in invertebrates. Differential DNA methylation among populations is consistent with a possible role of DNA methylation in local adaptive responses. Species with low genetic diversity, such as *S. dumicola*, are restricted in their ability to adapt genetically, and may therefore additionally rely on phenotypic plasticity in responding to local environmental conditions. Using a common garden set-up, we assessed temperature tolerance in spiders collected along a climate gradient. Reaction norms in high and low temperature tolerance varied among populations, indicating population-specific phenotypic plasticity in temperature tolerance. RNA sequence data suggests a role of gene expression in these plastic responses. DNA methylations were population-specific, but were not inducible in response to temperature acclimation, and we found no unequivocal relationships between gene-body methylation and gene expression. The study suggests different contributions of gene expression and DNA methylation to population-specific plasticity in temperature tolerance.

Abstract ID: 2338
Poster board number:
P339

DNA methylation in wild barn swallow populations: effects of age and genetic variation

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DNA methylation, as a proxy for epigenetic variation, has been implicated in several evolutionary and ecological processes, such as rapid adaptation to novel environments. However, DNA methylation remains an indirect proxy for putatively heritable, non-genetic variation and the degree of methylome variation among individuals is dependent on a multitude of factors. Cell type, age and sex are notable examples, as well as the added complication that DNA methylation variation can arise from spontaneous mutation, environmental or genetic induction. Therefore, to reliably assess the contribution of DNA methylation to evolutionary processes, we first need to examine the impacts of these covariates. Here, we use data from several natural populations of the barn swallow (*Hirundo rustica*) to explore the impact of age and genetic variation on DNA methylation variation. We jointly investigated genome-wide patterns of 5-methyl-cytosine DNA methylation and genetic variation (WGS data) in the barn swallow. A global sampling design across all six described subspecies as well as individuals of known age from the German population have helped untangle the contribution of age and genetic variation on observed patterns of methylome variation. We screened for CpG loci that are significantly associated with age, as well as used population genetic techniques to decompose the evolutionary signal contained in both methylome and genetic variation

and quantify the degree of covariation. Exploring these covariates and determining the extent to which they influence 5mC patterns in the barn swallow allows us to further explore the potential role of epigenetic marks in evolutionary processes.

Symposium: S22. Phenotypic plasticity's importance in evolution: Same old dog or new tricks? (id: 971)

Abstract ID: 1122
Poster board number:
P340

Non-heritable mutations as a source of foresight for adaptative phenotypes

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The genetic variability in the soma of organisms is abundant and some of it may lead to the development of adaptive phenotypes. However, beacause most of that variation is not heritable and it is typically associated to deleterious effects, the study of its adaptive importance has been limited. We hypothesized that non-heritable somatic mutations can offer foresight of adaptive genotypes in a non-heritable way, and that by doing so, it can guide the evolutionary trajectories of populations towards adaptation. When somatic mutations produce beneficial phenotypes, selection can act on the possibility of acquiring those mutations. As a result, the frequency of alleles within a population that are mutationally close to the adaptive genotype will increase and, eventually, because of a higher abundance of alleles mutationally close to it, the adaptive genotype will be more likely to arise in the germline of individuals in the population. Using simulations of populations exploring an adaptive landscape, we showed how non-heritable somatic mutations can indeed promote adaptation, bias evolutionary trajectories and help traverse fitness valleys whenever they can influence the development of phenotypes. The somatic exploration of the space of genotypes allows populations to sample evolutionary trajectories leading to adaptive phenotypes ahead of their heritability and it offers a mechanism to understand the genetic assimilation of non-heritable traits.

Abstract ID: 1203
Poster board number:
P341

Individual variation in social plasticity affects predictions of evolutionary change

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Individuals can affect the phenotype and reproductive success of their conspecifics as a result of social interactions, such as competition, cooperation or mating. These effects arising from social interactions are of major importance because they can change the

rate of evolution if they have a genetic basis or alter the intensity of selection. However, their magnitude, and thus their evolutionary impact, should depend on the ability of social partners to respond and plastically change their phenotype during social interactions. We used an analytical model and computer simulations to identify the conditions under which phenotypic plasticity in social traits acts as a constraint limiting the rate of evolution and when it acts as a driver accelerating evolutionary change. Our preliminary results show that the rate of evolution of social traits depends on the sign and magnitude of the genetic correlations linking the level of plasticity to the average expression of these traits. These results highlight the importance of individual differences and potential average-plasticity correlations in the evolution of both plasticity and the average value of a social trait. More generally, our study provides a mathematical framework to explore the mechanisms through which phenotypic plasticity can alter the rate of evolution in the context of social interactions.

Abstract ID: 1318
Poster board number:
P342

Multifaceted insect cuticle: different stages-different patterns

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Striking colour patterns in insects perceived through an eco-evo-devo perspective have been crucial in understanding the adaptive and genetic basis of pigmentation. The pigmentation trait also exhibits phenotypic plasticity wherein a single genotype can induce alternate phenotypes in response to environmental changes. Phenotypic plasticity could therefore enhance organismal fitness if the expressed phenotype is an optimal match for the environment. Surprisingly, phenotypic plasticity at the pupal stage remains under-explored compared to larval and adult stage in holometabolous insects. It should be emphasized that in the fruit fly model system extensively used to dissect the molecular pathways of pigmentation, pupal pigmentation plasticity has not been hitherto reported. Here, we quantify pupal pigmentation in response to temperature for a tropical *Drosophila melanogaster* population. *D. melanogaster* adults exhibit abdominal pigmentation plasticity in response to temperature. Flies reared at low/ high temperatures exhibit contrasting (darker/ lighter) abdominal pigmentation respectively. Darker/ lighter abdomen has been associated with attainment of faster thermal stability in colder/ hotter environments respectively. Interestingly, experiments on pupal temperature exposure contradict this speculation. Accordingly, an exposure to 30°C from the late third instar to 24 hr post pupation yield darker pupae compared to 18°C. We are currently investigating putative selection pressures involved in shaping the positive correlation between temperature and pupal pigmentation. Additionally, we aim to address the overlap if any in the molecular pathways underlying pupal and adult pigmentation. Our study thus connects selection pressures and molecular pathways for a common trait but across distinct developmental stages.

Abstract ID: 1331
Poster board number:
P343

Plant phenotypic plasticity affects pollinator-mediated selectio

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Environmentally-induced changes in the phenotype (i.e. phenotypic plasticity) are often observed in all kinds of organisms. Up to now, the role of plasticity in affecting biotic interactions and the resulting phenotypic selection has rarely been studied. Here we investigated the link between plasticity and selection in a greenhouse experiment. We studied fast cycling *Brassica rapa* plants, which grew on two different natural soil types (limestone and tuff), with or without aphid herbivory, and with either bumblebees or hand pollination. Plants showed strong plastic responses in nectar, morphology and floral scent to different soil types and herbivory. We found positive selection on plant morphology; this selection was stronger for bee-pollinated plants and differed for plants with and without aphids. In absence of herbivores, selection was stronger for plants growing on richer soil (tuff) than in plants growing on poorer soil (limestone). On the poorer soil, we found that plants were under different selection depending on herbivory: a principle component representing plant height, flower number, and flowering time was under significantly stronger selection in plants with herbivory than in those without herbivory. This pattern reflects bumblebees' tendency to over-proportionally visit tall plants with many flowers when those phenotypes were rare (i.e. in plants on poor soil with herbivory), thus causing stronger positive selection on this trait-combination. We therefore suggest that in stressful environments, a shift in pollinator behavior due to plant plasticity may speed up adaptation to local environmental factors.

Abstract ID: 1515
Poster board number:
P344

Gene expression plasticity role in adaptation : confrontation of empirical and simulation data

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The evolution of plasticity can be studied by observing the response of organisms to changing environments, and predicted from theoretical models, but those approaches are rarely confronted. We designed a simulation protocol to model the evolution of gene expression plasticity *in silico*, and compared it with the empirical evolution of transcriptomes during experimental evolution. Our empirical data has been obtained in *Zymoseptoria tritici* (Ascomycota) submitted to constant ("cold" and warm") and fluctuating (regular change between "warm" and "cold") thermal environments for one year. Transcriptomes have been sequenced in evolved lineages and ancestors at both temperatures, giving access to temperature-sensitive gene expressions before and after evolution. In parallel, we simulated the evolution of gene regulatory networks in a Wright-Fisher population genetics model, accounting for complex gene regulation and plasticity – i.e., gene networks were able to sense the environment and respond accordingly. Both approaches were used to address the same set of questions, dealing with how (i) the phenotype (gene expression), (ii) the gene expression plasticity, and (iii) the co-expression networks evolve in stable vs. fluctuating environmental conditions.

Abstract ID: 1558

Poster board number:
P345

Evolution of robustness and plasticity in gene regulatory networks

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Biological systems are robust to different kinds of perturbations, including environmental factors and genetic mutations. Robustness emerges from the complexity of physiological and developmental mechanisms, which evolution can be studied theoretically with numerical models. In order to understand how robustness emerges from complex systems, we simulated the response of gene regulatory network models to various selection scenarios. Simulations confirm that robustness (and its opposite, sensitivity) are evolvable, and that systems evolve towards robustness under stabilizing (canalizing) selection, and towards sensitivity under fluctuating selection (favoring plasticity). Robustness is a general property of gene networks, as networks robust to environmental disturbance also tend to be robust to mutations. Yet, the correlation between robustness to different sources of perturbation is not perfect, and there exists heritable variation in directions favoring e.g. robustness to mutations and sensitivity to the environment. Theoretical results suggest that robustness to various factors evolve as correlated quantitative traits, which response to direct or indirect selection can be predicted based on their covariance patterns.

Abstract ID: 1596
Poster board number:
P346

Maternally-transferred thyroid hormones in birds are evolutionary constrained

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Maternal effects have been recognized as a potent source of transgenerational developmental plasticity. In oviparous animals such as birds, various substances of maternal origin in the egg yolk collectively act as a mediator of maternal effects. This includes maternally-transferred hormones, some of which are metabolic products of other hormones. These hormones are, therefore, unlikely to be deposited independently of one another. One class of such substances are thyroid hormones (THs), whose two main forms – triiodothyronine (T3) and thyroxine (T4) – have been reported to be able to influence offspring in wild and captive birds. Since T4 is the precursor of T3, yolk T3 may be constrained by the availability of T4 either before or after the transfer process. Nevertheless, there is evidence that yolk T4 has a labile pattern over the laying sequence within individuals, suggesting a larger potential for adjusting offspring phenotype to the environment, while T3 appears to be subject to stricter physiological

and/or genetic control. However, because of T3's higher affinity to bind to the nuclear receptors, selection should act on T3 rather than T4. This begs the question whether T3 still has ample capacity to respond to selection, or if it is constrained by T4. We approach this question by examining variation in T3 and T4, and covariation between them, at the individual, population, and species levels. Our results will generate specific and testable hypotheses for further experimental work to understand the selective potential of hormone-mediated transgenerational plasticity.

Abstract ID: 1837
Poster board number:
P347

Does the definition of a novel environment affect the ability to detect cryptic genetic variation?

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Anthropogenic change is exposing populations to novel environments which are hypothesised to release cryptic genetic variation, a hidden store of variance that can fuel evolution. However, support for this hypothesis is mixed. One reason could be a lack of clarity in what we mean by ‘novel environment’, an umbrella term encompassing environments that were previously infrequent or entirely absent from a population’s evolutionary history. These different types of novelty could have contrasting implications for whether phenotypic plasticity hides, or exposes, cryptic genetic variation. Here we use a meta-analytic approach to investigate changes in the total genetic variance of multivariate traits in ancestral versus novel environments. We compared absolute novel environments, those not represented in a population’s evolutionary past, to extreme novel environments, involving frequency or magnitude changes to conditions present in a population’s ancestry. Overall, we identified no broadscale pattern of increased genetic variance in novel environments and found the type of novel environment did not explain any significant variation in effect sizes. When effect sizes were partitioned by experimental design, we found increased genetic variation in studies based on broad-sense measures of variance, and decreased variation in narrow-sense studies. Therefore, study design, not the definition of novelty, is important in understanding environment-dependant variation, revealing non-additive sources as a key component of cryptic variation.

Abstract ID: 1914
Poster board number:
P348

Phenotypic plasticity of *Iris pumila* leaf functional traits in response to experimental warming

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Plant physiology, fitness and distribution largely depend on temperature, hence it is expected that global warming will extensively alter their biodiversity as well as the ecosystem functioning. Variations in plant functional traits are widely used to predict the

impact of global warming on vegetation, as they usually reflect the plant's adaptive strategies to essential environmental resources, including temperature. To assess how plants respond to climate warming, we investigated the phenotypic expression of two major leaf functional traits, specific leaf area (SLA) and stomatal density (SD), to a temperature rise of 1°C. A total of 40 *Iris pumila* genotypes, which were consistently cultivated in a growth room at baseline temperature (23/19°C day/night), were exposed to elevated temperature (24/20°C day/night). Within each temperature treatment, the last fully developed leaf was harvested from every genotype and analyzed for the SLA and SD. The mean value of both investigated traits increased significantly with temperature. Leaves developed under elevated temperature exhibited 7% greater SLA and 22% higher SD compared to those developed under ambient temperature. These results suggest that *I. pumila* plants are able to counteract rising temperatures by the plastic response of SLA and SD. Such a capacity to acclimate its major leaf functional traits to altered temperature conditions may provide *I. pumila* a resilience to climate warming that will be occurring within its natural habitats.

Abstract ID: 1929
Poster board number:
P349

The role of juvenile hormone in developmental polyphenism of an ant with obligately sterile workers

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Ants express extreme forms of polyphenism in which the same genome generates discrete castes that fulfill distinct functions in colonies. The degree of polyphenism varies among species, from colonies composed of morphologically undifferentiated individuals to colonies with queens specialized for reproduction and obligately sterile workers responsible for all other colony tasks. This makes ants excellent models to study proximate mechanisms underlying caste polyphenism, which ultimately allowed the major evolutionary transition to superorganismality. Juvenile hormone (JH) is known to play a key role in caste development in honeybees, and can mediate differential growth of ant worker castes. However, understanding the role of JH in ant caste polyphenism has remained challenging because of the diversity of factors associated with caste determination in ants, and the lack of adequate model species for such studies. The latter problem has been partly resolved by the recent discovery that caste is determined and can be identified visually in the egg stage of the tramp ant *Cardiocondyla obscurior*. This model system gives us the opportunity to manipulate the JH content of eggs and larvae of known caste trajectory. In my project, I characterize the growth of queens and workers over the course of development. I then use experimental manipulation of JH levels in eggs and larvae to quantify how the hormone affects caste-specific growth and development. Finally, I assess caste-specific expression of JH-responsive genes. This project will provide insight into the general mechanisms underlying polyphenism in ants, improving our understanding of this fundamental aspect of superorganismality.

Abstract ID: 1938
Poster board number:
P350

Trait-dependent mechanisms influence lifespan and behavioural plasticity in *Drosophila melanogaster*

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For plasticity to evolve requires sensory systems that can track environmental change over the appropriate timescale. However, organisms may have multiple responses to the same environmental variable, raising the question of whether a common sensory pathway underlies the responses across traits. We investigated this using responses to social environments, which have a myriad of effects on individuals, altering reproduction, immune function, cognition and ageing. Specifically, *Drosophila melanogaster* males are highly plastic in response to rival males, modifying their behaviour to mate for longer. However, exposure to rivals is stressful, significantly reducing lifespan. *D. melanogaster* perceive their rivals by using a suite of sensory cues; interfering with at least two of olfactory, auditory or tactile cues eliminates the behavioural response. We tested to see if the removal of sensory cues, linked to behavioural changes, also influenced lifespan. Wings were removed from rival males to eliminate song and olfaction was interrupted through either removal of the focal fly's antennae or through the use of an *Orco* olfactory mutant. Whilst these combinations of auditory and olfactory cue influences behavioural responses to a rival, we found that they did not alter the reduction in lifespan of males exposed to rivals. These findings indicate that plasticity in different traits used to respond to social cues does not occur through common sensory pathways. Hence, the mechanisms underlying plasticity driven by the same environmental conditions are trait-dependent.

Abstract ID: 1973
Poster board number:
P351

The mutational origins of phenotypic plasticity

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The evolution of phenotypic plasticity is usually investigated by analyzing standing genetic variation. That variation must originate via spontaneous mutation, and once established, mutation may increase or decrease plasticity. We report a novel analysis of multigenerational mutation accumulation experiments in the crustacean *Daphnia pulex* where we quantify mutational effects on life history plasticity. In four parallel experiments initiated with ancestors that differ in their degree of plasticity, we quantify plasticity of juvenile specific growth rate with respect to food level. In addition, we reanalyze data from Davenport, et al. (2021, *Evolution* 75: 1513-1524) to quantify mutational effects on temperature-driven life history plasticity. Our results show that both mutational increases and decreases of life history plasticity occur at scales relevant to short-term adaptation. After ~40 generations, 3/21 and 2/21 mutation accumulation lines respectively showed increases and decreases of life history plasticity with respect to temperature. Our juvenile growth assays showed similar rates of mutational plasticity, and, although the details depended on ancestral clone, increases in plasticity tended to be more common than decreases. Plasticity shifts usually occurred because mutation had greater effects in a single environment, rather than influencing phenotypic expression in different environments in opposite directions. Because trait plasticity likely represents a larger mutational target than an environment-specific trait, we tested the

hypothesis that the rate of mutational input for trait plasticity exceeds that of environment-specific traits. Our data did not support this hypothesis, perhaps because estimates of trait plasticity are noisier than estimates of environment-specific traits.

Abstract ID: 2039
Poster board number:
P352

The role of the gut microbiome in *Drosophila* socially-driven plasticity

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Many animals exhibit phenotypic plasticity in response to their social environment. The social environment can influence the microbiome, not just through the transfer of microbiota, but intrinsically, via the gut-brain axis. This therefore raises the question of whether the microbiome mediates social effects on hosts. Male *Drosophila melanogaster* exhibit an increase in mating duration in response to the presence of rival males. This signal of future mating competition also reduces their lifespan, improves their cognitive ability and alters their microbiome composition. The gut microbiome is able to influence ageing and cognition, so it is possible that it plays a role in the socially-driven phenotypic plasticity seen in in *Drosophila*. We kept male *D. melanogaster* alone or in groups, and interfered with the microbiome using oral antibiotics. The difference in lifespan between single and grouped flies was significantly reduced in the flies fed antibiotics, compared to those which were not. Antibiotics did not alter the extension of mating duration shown by grouped flies compared to single, but had a small effect on behaviour and cognition. Therefore, it seems that the microbiome has a role in some *Drosophila* social responses, but other factors are also involved. These results shed light on the importance of considering the gut microbiome when investigating mechanisms underlying phenotypic plasticity.

Abstract ID: 2244
Poster board number:
P353

From environmental to genetic control - and back? Transitions in sex determination in amniotes

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Extensive variability ranging from environmental sex determination (ESD), where sexes do not differ in genotype, to genotypic sex determination (GSD) can be observed in amniotes, the group comprising mammals and sauropsids (avian and non-avian reptiles). Transitions (or a lack of transitions) among particular reproductive modes represent a fascinating evolutionary and developmental problem. Transitions between ESD and GSD can be viewed as a shift between a polyphenism, the environmentally-controlled development of alternative morphs, here males and females, and genetically-driven

polymorphism. ESD has traditionally been considered common and evolved many times in reptiles, with nearly haphazardly distributed transitions between ESD and GSD in both directions. However, we present current data showing that many of the independent "origins" of ESD within GSD lineages were based on misassignment of GSD species. In fact, ESD is relatively rare, although we at the same time present new evidence for ESD in five species from two lizard families. The phylogenetic distribution across amniotes shows a quite robust resistance of GSD to a transition to ESD, which is concentrated in a few lineages. ESD may be ancestral in amniotes and evolutionary very stable. Next to the phylogenetic distribution of ESD and GSD, we review the evolutionary and developmental mechanisms, which could explain the evolutionary stability of ESD and GSD (sex chromosomes) in amniote lineages and obstacles to transitions between them. The evolution of sex determination in amniotes represents an interesting system for understanding limits for a shift between environmental and genetic control of a crucial polymorphic trait.

Abstract ID: 2297
Poster board number:
P354

Phenotypic plasticity is decoupled from genomic specialization in domesticated fungi

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Humans have made fermented food and beverages for millennia, the populations of microorganisms used for fermentation are expected to be structured as a result of strong selection on phenotypes. The diversity of fermented food microorganisms provide a unique opportunity to assess whether similar or different specialization mechanisms have shaped their genomes. Here, based on population genomics and phenotypic assays, we reconstructed the domestication history of four *Penicillium* lineages used for cheese or dry-cured meat maturation. We leveraged on whole genome sequencing of con-specific strains from food and other environments, wild sister species, century-old type specimens and ancient samples. In all cases we found clear phenotypic differences between strains isolated from food environments and con-specific wild strains or sister species. These differences were not mirrored by consistent genotypic differentiation, with cheese maturation lineages showing strong reduction of genetic diversity while we detected no differences between dry-cured meat strains and their wild relatives. We found evidence of multiple horizontal gene transfers that were particularly abundant between species used for the same type of fermented food product. The phenotypic space of strains used for cheese and dry-cured meat maturation was consistently larger than that of their wild relatives when comparing food fermentation related traits. Our study showcases the complex interplay between phenotypic plasticity and genomic diversity and has important implications for our understanding of domestication.

Symposium: S23. The evolution and consequences of non-mendelian inheritance (id: 40)

Abstract ID: 1044
Poster board number:
P355

Rapid evolution of *cid* variants shift *Wolbachia*-induced cytoplasmic incompatibility patterns

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Wolbachia are maternally-inherited endosymbiotic bacteria that cause reproductive parasitism in their arthropod hosts. In the mosquito *Culex pipiens*, they cause cytoplasmic incompatibility (CI), a conditional sterility by which crosses between an infected male and an uninfected female, or between mosquitoes infected by incompatible *Wolbachia* are sterile. CI is most probably based on toxin-antidote interactions in which *Wolbachia* in males produce toxins, inducing embryonic defects, unless *Wolbachia* in females produce compatible antidotes. In *Culex pipiens*, *Wolbachia*-induced CI results in a total sterility: hosts' reproduction is fully conditioned by its maternally-inherited endosymbiont and host nuclear genes have no influence on CI. The *cidA* and *cidB* *Wolbachia* genes have recently been found to encode key CI effectors, *cidB* being the toxin, and *cidA* being the antidote. The newly obtained structure of the CidA-CidB co-crystal highlighted that toxin and antidote interact through 3 interaction zones. In *Culex pipiens*, the highly complex crossing patterns between different lines correlate with amplification and diversification of *cid* genes, with up to 6 different copies detected within a single *Wolbachia* genome. Compatibility between mosquito lines have been shown to correlate with the repertoires (sets of *cid* genes copies) present in their *Wolbachia*. Here, we show that rapid changes in crossing phenotypes can emerge through microevolution of *Wolbachia*'s *cid* repertoire within an isofemale line. We found that distinct *Wolbachia* repertoires emerged by loss of variants, and that recombination, shifting the aminoacids exposed at the CidA-CidB interaction zones, can lead to compatibility changes, giving insights on crossing patterns evolution.

Abstract ID: 1076
Poster board number:
P356

Genome-wide characterization of genetic variation for pollen expression in *Rumex hastatulus*

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Selection acts on both gametophytic and sporophytic phases of the plant life cycle. The differences in ploidy, morphology and development between the two phases while sharing a common genome can cause differential or even opposing selection, creating genomic conflicts. Theoretical studies suggest the conflict between the two phases may generate balancing selection and maintain genetic variation. Additionally, purifying selection purges deleterious mutations in haploid pollen and affects patterns of genetic diversity. Despite the potential of selection on the gametophytes, the genomic

prevalence of pleiotropic effects that gametophytic selection has on the sporophytes remains unknown. Here we examined the population genomic signals of pleiotropy between the gametophytic and sporophytic phases of *Rumex hastatulus*, a dioecious, outcrossing and wind-pollinated plant. We used expression data across tissues and phases (pollen, pollen tube, flower bud and leaf), combined with neutral diversity statistics and distribution of fitness effect analysis, and tested the genomic prevalence of genes under balancing selection due to antagonistic pleiotropy or purifying selection through haploid purging. This research furthers our understanding of the genome-wide characteristics and consequences of plant gametophytic selection.

Abstract ID: 1180
Poster board number:
P357

Transcriptonal patterns on the germ-line-restricted chromosome in blue tits

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Transcriptonal patterns on the germ-line-restricted chromosome in blue tits
Jakob C. Mueller, Yifan Pei, Alexander Suh, Bart Kempenaers
The germline-restricted chromosome (GRC) is an extra chromosome of variable size and sequence widespread among the germlines of songbirds. There is some evidence for non-Mendelian inheritance of the GRC (mostly maternal transmission) with expected consequences on gene content, sex-specific expression and sex-biased selection. The first few genomic characterizations of songbird GRCs suggest a high turnover in gene content leaving each species' GRC quite idiosyncratic. Here, we assemble and functionally annotate the blue tit GRC sequence for the first time. By comparing the male and female transcriptome we search for evolutionary signals of sexual conflict or resolution thereof. Our results reveal expressed GRC-linked paralogs of the autosomal and sex chromosomes with different isoform structures and potentially modified functions. These are thus key candidate genes for elucidating the evolutionary significance of the songbird GRC.

Abstract ID: 1388
Poster board number:
P358

Potential for recent selfish spread of the germline-restricted chromosome in zebra finches

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Germline-Restricted Chromosomes (GRCs) are fascinating chromosomes characterized by their elimination from somatic tissues during development and non-Mendelian inheritance. In songbirds, the GRC is mostly inherited from the mother. But occasional paternal inheritance of the GRC was observed in the zebra finch and multiple lines of evidence pointed towards a scenario where one GRC haplotype has recently spread through the zebra finch population via paternal spillover. However, due to difficulties in assembling the GRC, some of these results were only based on the inspection of <1% of the GRC estimated size. Here, we took advantage of a newly assembled 90.39 Mb long-read GRC reference assembly containing ~54 % of the expected GRC length and implemented a bespoke pipeline that called 1133–11735 SNPs over 56.32 to 85.75 scorable Mb representing 33.67– 51.25 % of the GRC size (values varying depending on the filtering parameters). Using our pipeline, we found that nucleotide diversity is indeed very low in most of the assembled GRC and that a well-resolved phylogenetic tree derived from our GRC-linked SNPs is in strong discordance with the mitochondrial tree. By extending previous findings to a much larger portion of the GRC, our results further support the suggestion of a recent selfish sweep of the zebra finch GRC, potentially via repeated paternal spillover. Additionally, our work serves as proof of concept that high-throughput population genetics of the GRC is possible. Our pipeline will be useful for population genetics analyses of the GRCs in other songbird species.

Abstract ID: 1429
Poster board number:
P359

Gross physical damage to testes is associated with the suppression of sperm-killing meiotic drive

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Sperm-killing X-chromosome meiotic drive enhances its own transmission into subsequent generations, often at a cost to the rest of the genome. As a result, there is selection pressure for suppression of drive to evolve, and this can result in ongoing co-evolution between drive and suppressors. Here we study the X-chromosome drive system in *Drosophila subobscura* called “SR”. In males, SR chromosomes kill Y-bearing sperm, resulting in the production of only daughters and the enhanced transmission of SR. We recently discovered suppressors that can restore Y-chromosome transmission and prevent the transmission bias of SR. We expect SR to rapidly spread to fixation in the absence of suppression, or alternately for suppressors to spread and completely suppress drive. However, SR has remained at an intermediate and stable frequency in North Africa for at least 50 years and suppression of drive remains rare. Thus, we hypothesised that the suppressors may be associated with substantial costs. We examined the testes of unsuppressed SR males and suppressed SR males and found startling evidence of gross physical damage to suppressed SR males’ testes in comparison to unsuppressed SR males. This is the first evidence of high costs of suppression of meiotic drive. Our findings imply that even if suppressors evolve to counter meiotic drive, they can have such high costs that their spread is limited and allows drive to persist.

Abstract ID: 1430
Poster board number:

P360

Evolution of alternative reproductive systems in *Bacillus* stick insects

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Stick insects of the genus *Bacillus* feature a variety of reproductive strategies including canonical sex, female-producing parthenogenesis and hybridogenesis (elimination of the paternal genome and clonal transmission of the maternal genome). The different parthenogenetic and hybridogenetic lineages were suggested to be of interspecific hybrid origin between the same two sexual species, but it remains unknown whether they derive from independent hybridization events or whether a single event was followed by a secondary diversification of reproductive modes. Here we revisit the different species and hybrid lineages within the genus *Bacillus* using a *de novo* chromosome-level reference genome and RADseq data of > 500 wild-caught individuals. We confirm that two hybridogenetic lineages and one parthenogenetic lineage show the genomic signatures of a diploid F1 hybrid species with the maternal genome from the sexual species *B. rossius* and the paternal genome from the sexual species *B. grandii*. A second parthenogenetic lineage shows the genomic signature of an allo-triploid, derived from three parental species, *B. rossius*, *B. grandii* and *B. atticus*. We then phased the parental haplotypes in each hybrid lineage to infer their phylogenetic relationships and study the origin of different reproductive modes. Preliminary phylogenomic analyses suggest one or two independent hybridization events with at least one secondary reproductive mode diversification, most likely a transition from hybridogenesis to parthenogenesis and triploidy. These findings indicate transitions between unorthodox modes of reproduction that were previously not known to occur, suggesting that the loss of sex *per se* can be a driver of reproductive mode diversification.

Abstract ID: 1513
Poster board number:
P361

Sperm, what are they good for? -- Reproductive anomalies in the flea beetle *Altica lythri*

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Sexual reproduction should involve the formation of a zygote consisting of equal parts of paternal and maternal genes. However, not every species produces offspring that are actually genetically related to both of their parents.
The flea beetle *Altica lythri* exhibits a complex population genetic structure with conspicuous reproductive anomalies. One of its three mitochondrial haplotypes (HT1) is known to produce only female offspring. However, copulation with a male of a different haplotype (HT2 and HT3) is necessary to produce fertile eggs. We hypothesise that the production of fertile eggs occurs through gynogenesis, a form of parthenogenetic reproduction, in which the sperm is merely needed to trigger embryogenesis. In this case, even with successful mating, males would not pass their genes to the next generation.

To establish whether paternal genomes are completely excluded or whether some paternal gene leakage is happening, we use ddRAD markers to analyse paternity. This technique allows us to monitor several thousand markers throughout the genome simultaneously, and ultimately reveal whether parts of the male genome appear in the offspring. We also use histological analyses to investigate whether normal meiosis takes place in the ovaria of HT1 females. Finally, by using fluorescent antibodies that bind to the centromere of chromosomes as well as a fluorescent DNA stain, we validate the chromosome numbers at different stages of egg development. Our preliminary results indicate that gynogenesis is actually happening, however, small fractions of the paternal genome do leak into the otherwise gynogenetic, and mostly clonal, female offspring.

Abstract ID: 1570
Poster board number:
P362

Meiotic drive causes adaptive testis enlargement during early development in the stalk-eyed fly

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Meiotic drive subverts Mendel's law of equal segregation through the biased transmission of a selfish gene in conflict with the rest of the genome. The sex-ratio 'SR' X-linked meiotic drive system in the stalk-eyed fly destroys all Y-bearing sperm, producing female-only broods. Unlike other SR systems, drive males do not suffer fertility loss. Instead, they have greatly enlarged testes that compensate for gamete destruction. We predicted that enlarged testes arise from extended development with resources re-allocated from the accessory glands, which tend to be reduced in size in drive males. To test this, we tracked testis and accessory gland growth over 5-6 weeks post-eclosion before males attain sexual maturity. Against our prediction, we found that drive testes were already enlarged at eclosion. In addition, the greater allocation of resources to testes during development did not retard accessory gland growth, whose size did not differ between drive and wildtype males during development, contrary to previous reports. There was evidence of a general trade-off with eyespan, as males with larger relative eyespan had larger accessory glands but smaller testes. These results point to adaptive changes in the allocation of resources to traits that affect male reproductive success that is likely to benefit both drive and wildtype males.

Abstract ID: 1743
Poster board number:
P363

Meiotic drive and sperm competition: can sperm loss be mitigated?

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The X-linked 'Sex Ratio' (SR) meiotic drive system in *Teleopsis dalmanni* stalk-eyed flies causes degeneration of all non-carrier Y-sperm, leading to the production of female-only offspring broods. We tested whether the killing of sperm reduces drive-male fertility during sperm competition. Previous studies suggest that drive-males sire fewer offspring,

either because they produce less or lower quality sperm. However, our recent findings appear to contradict this view, as drive-males transfer the same numbers of viable sperm during mating. We investigate this further by performing reciprocal mating trials to measure the success of drive-male sperm in competition with standard male sperm (two males per female, one mating per male). Although the success of individual males varied greatly, there was no difference in the number of offspring sired by drive and standard males, regardless of their mating position. We performed a further experiment to test the success of drive-males under higher competition — i.e., when a female is multiply mated (two males per female, multiple matings for standard males only) — and report our preliminary findings. Overall, we find drive-males are not at a disadvantage during sperm competition. This suggests that the evolution of larger testes in drive-males entirely mitigates the costs of sperm loss caused by meiotic drive. This situation is unlike that observed with other species, such as *Drosophila*, and helps explain the high ~20% SR frequency in wild populations of *T. dalmanni.*

Abstract ID: 1774
Poster board number:
P364

Extremely rapid genetic content evolution on the germline-restricted chromosome in passerine birds

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The germline-restricted chromosome (GRC) of passerine birds represents an extraordinary chromosome with a peculiar mode of non-Mendelian inheritance and tissue-specific elimination. The GRC was first discovered more than two decades ago in zebra finch, but recent studies suggest that it is likely present in all passerines, the most species rich avian order, encompassing more than half of all modern bird species. Despite its wide taxonomic distribution, studies on this chromosome are still scarce and limited to a few species. Here, we analysed the GRC size and genetic content in several closely related estrildid finch species of the genus *Lonchura* using cytogenetic approaches as well as whole genome assemblies. We show that the GRC varies enormously in the genetic content as well as size, ranging from a tiny micro-chromosome to one of the largest macro-chromosomes in the cell. Such variation can be seen not only among recently diverged species but also within species and sometimes even between germ cells of a single individual. In one species, we also observed variation in GRC copy number among male germ cells of a single individual. Our results reveal the extraordinarily dynamic nature of the GRC likely caused by its unstable mitotic and meiotic inheritance and frequent gains and losses of sequences on this chromosome leading to substantial differences in genetic composition of the GRC between and even within species. Such differences might theoretically contribute to reproductive isolation between species and thus accelerate the speciation rate of passerine birds compared to other bird lineages.

Abstract ID: 1878
Poster board number:
P365

Genome fractionation in asexuals: mechanisms, consequences for selection and link to gene function

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Hybridization and genome duplication have played crucial roles in the evolution of many animal and plant taxa. The subgenomes of parental species undergo considerable changes in hybrids and polyploids, which often selectively eliminate segments of one subgenome. However, the mechanisms underlying these changes are not well understood, particularly when the hybridization is linked with asexual reproduction that opens up unexpected evolutionary pathways. To elucidate this problem, we compared published cytogenetic and RNAseq data with exome sequences of asexual diploid and polyploid hybrids between three fish species; Cobitis elongatoides, C. taenia, and C. tanaitica. Clonal genomes remained generally static at chromosome-scale levels but their heterozygosity gradually deteriorated at the level of individual genes owing to allelic deletions and conversions. Interestingly, the impact of both processes varies among animals and genomic regions depending on ploidy level and the properties of affected genes. Namely, polyploids were more tolerant to deletions than diploid asexuals where conversions prevailed, and genomic restructuring events accumulated preferentially in genes characterized by high transcription levels and GC-content, strong purifying selection and specific functions like interacting with intracellular membranes. Although hybrids were phenotypically more similar to C. taenia, we found that they preferentially retained C. elongatoides alleles. This demonstrates that favored subgenome is not necessarily the transcriptionally dominant one. This study demonstrated that subgenomes in asexual hybrids and polyploids evolve under a complex interplay of selection and several molecular mechanisms whose efficiency depends on the organism's ploidy level, as well as functional properties and parental ancestry of the genomic region.

Abstract ID: 2099
Poster board number:
P366

Premeiotic genome endoreplication is an unexpectedly rare phenomenon in gynogenetic hybrid fishes.

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Sexual reproduction, predominant in the majority of eukaryotes, can be disrupted by hybridization which may alter the canonical gametogenic pathways thus leading to the emergence of asexuality. In asexual vertebrates, premeiotic genome duplication is the most widespread gametogenic alteration, which accelerates ploidy of germ cells, thus allowing chromosomal pairing in meiosis and formation of unreduced eggs. To investigate the frequency of this alteration among germ cells, we selected gynogenetic

hybrids from European spined loaches (*Cobitis*). This genus includes several sexual species among which *C. taenia* and *C. elongatoides* create diploid and triploid hybrids. Hybrid males are sterile but females produce unreduced gametes via premeiotic genome endoreplication. To check whether genome endoreplication occurs in all germ cells, we analyzed pachytene oocytes of hybrid females. We found two populations of cells that differed in ploidy levels. Only a minor portion of pachytene oocytes have their genome duplicated, while the vast majority of pachytene oocytes had unduplicated genomes forming a mixture of bivalents and univalents. However, in diplotene, we detected only oocytes with duplicated genomes suggesting that only oocytes with duplicated genomes proceed beyond pachytene. In juveniles and adult hybrids, individual duplicated cells locate among clusters of nonduplicated cells, suggesting that genome endoreplication occurs prior onset of meiosis but not in the early developmental stages. Thus, in asexually reproducing hybrid fish from the *Cobitis* genus, genome duplication occurs only in some germ cells contributing to gamete formation, while the vast majority of oocytes with nonduplicated genomes are unable to proceed beyond pachytene.

Abstract ID: 2140
Poster board number:
P367

Repetitive DNA dynamics in asexually reproducing killifishes

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Metazoan genomes are composed of a substantial proportion of repetitive DNA such as transposable elements and satellite DNA. Sequence and copy number variation of these repetitive sequences is known to be greatly influenced by homologous and non-homologous recombination. In addition, the rapid evolution of these selfish genetic elements has been linked to reproductive isolation between species.

The Mummichog *Fundulus heteroclitus* and the Banded Killifish *F. diaphanus* are primarily saltwater and freshwater species, respectively. While these species have diverged ~15 million years ago, they are known to hybridize in multiple locations with intermediate salinities, where they sometimes produce asexually reproducing all-female clonal lineages. As such, it is predicted that meiotic recombination is effectively disrupted in these clonal lineages, with unclear consequences for the evolution of transposable elements and satellite DNA. The *Fundulus* system thus offers unique opportunities to investigate repetitive DNA dynamics.

We have performed low-coverage whole genome sequencing of females from both parental lineages as well as several asexually reproducing hybrids from three clonal lineages. I will present our preliminary characterization of repetitive DNA content in this system.

Abstract ID: 2291
Poster board number:
P368

Cytological map of the zebra finch GRC at the lampbrush stage

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In 1998, in a detailed study of chromosome sets in germline cells of zebra finch *Taeniopygia guttata* (Estrildidae, Passeriformes) an additional chromosome was discovered. While somatic cells have the diploid chromosome number 2n=80, the growing oocytes and spermatocytes contain germline-restricted chromosome (GRC). In zebra finch, GRC is the largest chromosome, spanning about 150 Mbp. It is eliminated from the somatic cells and differentiating spermatocytes, but always presents in oocytes, thus transmitting via female meiosis. The function of GRC is unknown, it may contain sequences important for germ cell differentiation and mature oocyte functioning. While GRC genomic and transcriptomic studies are in progress, cytogenetic analysis can be improved strongly by exploring the chromosome in its lampbrush phase, isolated directly from the oocyte nucleus. Here, we describe in detail the lampbrush GRC morphology, construct a cytological map of its chromomere pattern. We traced the change in the morphology of the GRC to the postlampbrush stage. We performed FISH on GRC at the lampbrush stage to localize telomere and centromere tandem repeats, as well dph6 fragment, known to be highly amplified in zebrafinch GRC. A characteristic feature of the GRC-bivalent at the lampbrush stage is heterochromatic loopless DAPI-positive regions. They do not contain the phosphorylated form of RNA polymerase II but can be associated with coilin-positive bodies of unknown function. We speculate that the large heterochromatic blocks may play a role in GRC transmitting during meiotic divisions, acting as neocentromere.

Abstract ID: 2304
Poster board number:
P369

GRC behavior during meiosis and embryogenesis in songbirds

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Germline-restricted chromosome (GRC) has been described in all examined songbird species. GRC is present in germ cells, absent in somatic cells, eliminated during spermatogenesis and transmitted generally via oogenesis. However, little is known about how GRC is eliminated from somatic cells and how GRC meiotic behavior differs in the distant songbird lineages. We prepared a series of slides from embryo cell suspension of zebra finch (*Taeniopygia guttata*). We showed that in a freshly laid egg the proportion of cells with GRC is around 20.3%. After two hours of incubation it decreases to 10.6%. Our findings indicate that GRC elimination process is initiated at an early developmental stage during the egg movement through the oviduct and being completed over gastrulation. We showed that GRC meiotic behavior of great tit (*Parus major*) is similar to that of zebra finch, Bengalese finch (*Lonchura striata domesctica*), sand (*Riparia riparia*) and pale (*Riparia diluta*) martins. These species exhibit sexual dimorphism in GRC copy number. Most females contain two GRC copies while most males – one GRC copy. We observed mosaicism for GRC copy number in female great tits. Four out of seven

females contain cells with either one or two GRC copies. We assume that the features of GRC meiotic behavior common between different species were formed under selection pressure and contribute to the effective transmission of GRC through generations. This research was funded by RSF, project number 20-64-46021 and the Ministry of Science and Higher Education of the Russian Federation, project number 2019-0546 (FSUS-2020-0040).

Abstract ID: 2330
Poster board number:
P370

Evolutionary innovation in the long-term absence of sex in the oribatid mite *Platynothrus peltifer*

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Asexuality is considered an evolutionary dead-end, but some 'ancient asexual organisms', like oribatid mites, have persisted and diversified over time. Very little is known about the processes that could generate evolutionary novelty and adaptability in the absence of sex. We analysed potential genomic footprints of innovation in the haplotype-resolved, chromosome-scale genome of the ancient asexual oribatid mite *Platynothrus peltifer*. Large-scale structural variants might not play a major role, as there are few rearrangements within and between chromosomes as well as between haplotypes. However, heterozygosity is maintained and divergent haplotypes, as well as horizontally acquired genes, feature allele-specific expression with an functional enrichment in e.g. metabolic pathways, resource uptake and immune system. We further analyzed the evolutionary trajectories of these alleles, as these processes might contribute to adaptation and evolutionary novelty in the absence of sex. Moreover, TE activity could supply the substrate for novelty via modulating gene regulation of these mites. Overall, identifying such signatures of evolutionary innovation will help to understand why some asexuals can escape the dead-end fate and to identify the benefits of sex vice-versa.

Abstract ID: 2361
Poster board number:
P371

Non-genetic inheritance: is it time for the genotype-phenotype framework to evolve?

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The genotype-phenotype distinction is essential for our understanding of living systems. These two concepts are the core of genetics and heredity, and they are also deeply interconnected with our current notion of development - and of evolution of development –, which could be regarded as the process by which phenotypes are generated from genotypes. However, this distinction, and in particular the genotype concept, have not

been fully developed as a testable theory that incorporates what we have learned since these concepts were originally defined during the first years of Mendelian genetics. We argue that this lack of further theoretical development is the source of multiple long-standing problems, from conceptual paradoxes such as the so-called extragenetic inheritance to lamarckian controversies. Here, we reframed the genotype-phenotype theory by providing four experimentally verifiable criteria - self-templating, phenotypic expression, plastic identity and inheritance - to define and identify genotypes, accounting for all potential sources of biological inheritance, from molecular structures to learned behaviours. By providing a definition of the genotype concept that is independent from its identification with genome sequence, we propose a framework of nested genotypical systems that progressively increased the evolvability and complexity of living systems. Finally, we consider the implications of this new genotype-phenotype framework for our understanding of development and evolution of life.

Abstract ID: 2421
Poster board number:
P372

Integration of endogenous circular DNAs is a frequent source of chromosomal structural variation

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When an eukaryotic cell divides, the chromosomes are segregated evenly to the daughter cells in a process orchestrated by their centromeres. Accordingly, genes and alleles are distributed equally, preventing sudden gene loss or copy number changes. DNA circularization, however, frees the DNA from the centromere control, which opens new possibilities for genes to spread, replicate or get transcribed. Circular DNAs are a common feature of eukaryotic genomes and have been shown to drive adaptive processes in yeast and in human tumors. However, what it means for a gene to be on a circle has largely been unexplored, mainly due to lack of model systems. Here, we generate endogenous circular DNAs that can be selected and be maintained in a population of cells. We study the effects of circularization on cell growth, segregation, gene expression and gene mobility. We show how circularization is able to change the segregation rate of genes and increase their copy number heterogeneity. We also find that circles can reintegrate back into the linear genome and generate structural mutations more frequently than translocations. Finally, we observe that circularization is able to free genes from transcriptionally inactive areas and allow their expression. Collectively, our results show a new way in which genes can bypass the restrictions imposed by chromosomes on segregation and copy number, resulting in substantial phenotypic changes after very few generations.

Abstract ID: 2424
Poster board number:
P373

Searching for toxin-antidote elements in an ant social supergene

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Supergenes are tightly linked sets of co-adapted loci controlling complex phenotypes. However, the suppression of recombination also favours the evolution of selfish genetic elements, which tend to destabilize the polymorphism. In the Alpine silver ant, *Formica selysi*, colony social organization is determined by a supergene. The supergene haplotype associated with multi-queen colonies acts as a post-segregation distorter, by causing a lethal maternal effect. Specifically, when queens bear the selfish haplotype, only eggs having inherited this haplotype hatch into larvae. Here, we investigate the hypothesis that the selfish haplotype contains a toxin-antidote element, a genetic dyad composed of a maternally-deposited toxin and a zygotically-expressed antidote. By combining transcriptomic and proteomic analyses, we identify sets of candidate genes for both toxin and antidote. Further investigations will be needed to confirm the identity and function of the toxin-antidote elements. Identifying genetic elements involved in supergene transmission distortion will be an important step towards a better understanding of the role of selfish genetic elements in supergene evolution.

Symposium: S24. Progress and prospects in adaptation genomics (id: 935)

Abstract ID: 994
Poster board number:
P374

A two-step adaptive walk rewires nutrient transport in a challenging edaphic environment

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In some cases, adaptation to new environments may occur through single steps, but for complex traits, adaptation is likely to involve multi-step adaptive walks that include a mix of variant types and selective mechanisms. However, we lack concrete examples of multi-step adaptive walks in nature. We examine the evolutionary dynamics in a native *Arabidopsis thaliana* population as it colonized the base of an active stratovolcano characterized by low soil manganese (Mn). We show that a two-step adaptive walk rewired nutrient homeostasis in this population. In the first step, a loss of function variant that disrupted IRT1, the primary iron (Fe) uptake transporter, rapidly fixed in a hard selective sweep, increasing Mn but limiting Fe in the leaves. In the second step, as substructure began to develop on the island, multiple independent tandem duplications occurred at *NRAMP1* and rose to near-fixation in a soft selective sweep, compensating *IRT1* loss by improving Fe homeostasis. This study provides a clear example of multi-locus adaptive walk and reveals how the successive sweeps reshaped the phenotype and spread over space and time.

Abstract ID: 1201
Poster board number:

P375

Dissecting the molecular mechanisms of adaptive life history variation in Atlantic salmon

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The evolution of life histories is a central topic in evolutionary biology, yet mechanisms that encode for adaptive life history variation remain poorly understood at the molecular level. We have investigated the molecular machinery that is associated with variation in a key adaptive life history trait, age at maturity, using Atlantic salmon reproductive organ development as a model. Atlantic salmon is among the most variable vertebrates on Earth in terms of age at maturity. Salmon maturity age is associated with genetic variation in a single genome region containing the transcription co-factor gene *vestigial-like 3* (*vgll3*). The *vgll3* locus shows striking contemporary evolution towards encoding for earlier maturation age. The molecular mechanisms that translate genetic variation into maturity differences, however, remain largely unknown. By using transcriptomics, epigenomics, ex-vivo organ culture, and a common-garden experiment with Atlantic salmon males raised up to sexual maturity, we investigated the molecular mechanisms by which *vgll3* allelic variation controls maturation onset of the salmon testes. We show here that *vgll3* genotype has broad impacts on the transcriptomic trajectory of the differentiating testis from early spring up till breeding time. By using chromatin immunoprecipitation-sequencing to map gene regulatory regions associated with VGLL3 protein, we further show that VGLL3 plays a role in regulating many key developmental processes in the testis. The results shed light on the molecular machinery behind adaptive variation in age at maturity and identify new players in the genotype-phenotype map controlling this central life history trait.

Abstract ID: 1226
Poster board number:
P376

Untangling the role of sexual selection on genomic divergence

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Sexual selection is believed to be an important facet of genomic divergence between sexes, populations, and species. However, it is difficult to untangle the effects of sexual selection from other evolutionary forces such as natural selection and drift. Here we manipulate sexual selection, using experimental evolution with *D. pseudoobscura* populations for around 200 generations to isolate the role of sexual selection. We sequenced individual males from multiple replicates within each treatment at different timepoints and examined which regions of the genome are undergoing positive or balancing selection. We identified selective sweeps and the degree of linkage disequilibrium across the genome. Recent evidence shows that rapid adaptation can result in parallel adaptation within only a few generations. We took advantage of the resolution that our multi-timepoint approach gives us to examine how sexual selection causes adaptation across replicated populations and whether these changes are steady

over time, or prone to fluctuation. Initial results point to considerable differences between replicates, indicative of possible non-parallel adaptation. However, overall consistent signatures of sexually selected divergence are localised to distinct regions of the genome.

Abstract ID: 1230
Poster board number:
P377

The dynamics of adaptation to stress from standing genetic variation and *de novo* mutations

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Adaptation from standing genetic variation is an important process underlying evolution in natural populations but we rarely get the opportunity to observe the dynamics of fitness changes in real time. Here, we used the power of microbial experimental evolution and whole population sequencing to track the phenotypic and genomic changes of genetically diverse yeast populations in environments with different stress levels. We found that populations rapidly and in parallel increased in fitness in stressful environments. The founder's genetic diversity was quickly depleted, however, not to the same degree in all populations and environments. Some populations fixed all ancestral variation in < 30 generations while others maintained diversity across hundreds of generations. We also observed parallelism at the gene and pathway level. Specifically, we detected up to five genes harbouring multiple independent mutations in different populations, and a general enrichment for mutations affecting downstream effectors of the high-osmolarity-glycerol pathway in three out of four environments. Adaptation to the most stressful environment was characterised by the fast evolution of functional haploidy, likely driven by standing genetic variation. Around 35% of all populations contained aneuploidies at least once during experimental evolution, one of which was maintained for hundreds of generations in different replicates independently. This work shows that experimental evolution is a great tool to address the interplay between standing variation and the influx of *de novo* mutations, leading to a better understanding of the demographic and environmental drivers and constraints of a population's capacity to adapt to environmental change.

Abstract ID: 1231
Poster board number:
P378

Genetic responses of local populations in response to the establishment of novel invasive species

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Native biodiversity is threatened by introduction of novel invasive species which currently occurs at increasing pace. Evidence for adaptive responses in local populations to invasion have been reported but the debate on role of evolutionary and plastic changes in this adaptation to invasion is ongoing. To understand the evolutionary consequences of invasions on local populations, investigating the genetic diversity in response to the changed selection pressures in the environment of the local populations at different stages of invasion is urgently needed.
Isopod *Idotea balthica*, a key herbivore of the Finnish Archipelago Sea, provides a unique model system to investigate the adaptive responses of local populations in face of invasion. Since 2009 a novel predatory invader, the mud crab *Rhithropanopeus harrisii* has been establishing in the Archipelago Sea. Field observations suggest that herbivorous crustaceans and molluscs have declined since the mud crab invasion started leaving open the question of adapting to presence of mud crab and retaining genetic diversity to adapt to changing salinity and temperature. The genetic effects of invasion in *I balthica* are examined with a recently obtained low coverage whole genome sequencing dataset consisting of 185 individuals across 9 *I. balthica* populations facing different stages of the mud crab invasion. This dataset is used to address whether mud crab experienced populations differ from mud crab naïve populations and whether the differences suggest potential for adaptive evolution in local *I. balthica* populations or mirror demographic effects resulting from mud crab predation.

Abstract ID: 1289
Poster board number:
P379

Estimating the distribution of fitness effects from single spontaneous mutations in Escherichia coli

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The distribution of fitness effects (DFE) of new mutations is important for many concepts in evolutionary biology, such as the rate of genomic decay, the maintenance of genetic variation and the potential benefits of sex and recombination. Previous work has attempted to measure the DFE in a variety of organisms by allowing multiple mutations to accumulate within the organism. However, extrapolating the effect of single mutations by measuring the aggregate effect of many mutations on an individual's fitness is not precise. Additionally, these mutations have often been artificially introduced and may have fitness effects that are not representative of the 'real' DFE. I will attempt to produce an unbiased estimate of the DFE of new mutations in E.coli by allowing single mutations to accumulate naturally and subsequently measuring their fitness in isolation and in competition. I have grown 200 E.coli lines for 1000 generations, the average time it takes for one mutation to accumulate per line. Subsequent sequencing will allow me to identify E. coli harbouring single mutations. Growth curve measures and flow-cytometry cell counts from mutant-reference strain competition assays will allow me to infer the fitness effects of individual spontaneous mutations (the real DFE). This research sets the groundwork for later analysis of the single mutant individuals' transcriptome, which will allow me to quantify the joint DFE and effects on phenotype. The form of this distribution is dictated by the degree of pleiotropy and plays a critical role in determining the amount of genetic variation maintained for quantitative traits.

Abstract ID: 1315
Poster board number:
P380

Fitness landscape analysis reveals that the wild type allele is sub-optimal and mutationally robust

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Fitness landscape mapping and the prediction of evolutionary trajectories on these landscapes are major tasks in evolutionary biology research. Evolutionary dynamics is tightly linked to the landscape topography, but this relation is not straightforward. Here, we analyze a fitness landscape of a yeast tRNA gene, previously measured under four different conditions. We find that the wild type allele is sub-optimal, and 8%-10% of its mutants are fitter. We rule out the possibilities that the wild type is fittest on average on multiple conditions or located on a local fitness maximum. Instead, we find that the wild type is mutationally robust ('flat'). Similar observations of flatness or mutational robustness have been so far made in very few cases, predominantly in viral genomes.

Abstract ID: 1326
Poster board number:
P381

Demographic history, hybridisation and genomic variation of two Atlantic puffin subspecies

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The Atlantic puffin (*Fratercula arctica*) is one of the world's most iconic seabirds. The morphologically largest subspecies (*F. a. naumanni*) is limited to the High Arctic, yet genomic data has recently revealed a hybrid population on the island of Bjørnøya, where it interbreeds with the smaller *F. a. arctica*. Here, we use whole genome sequencing approaches to investigate signals of local adaptation, introgression and demographic history of these two subspecies and their hybrid population. We assembled and annotated a chromosome-resolved reference genome and sequenced six individuals from each population to 20X coverage. Using a range of methods with varying temporal resolution, we reveal the demographic history of the three populations within the last 1M years and show when the two subspecies split from their common ancestral population. We further assess whether SNPs, structural variants and short tandem repeats are associated with specific genomic regions, potentially playing a role in the phenotypic and ecological differentiation between the two subspecies. Additionally, we evaluate evolutionary patterns and dynamics within the hybrid population by analyzing introgressed genomic regions in the hybrid individuals. Our observations provide a detailed understanding of the patterns of genomic differentiation that are crucial for evaluating the extent of local adaptation and interbreeding in these vagile seabirds.

Abstract ID: 1362

Poster board number:
P382

Comparative genomics evidence striking convergence in adaptive duplications in mosquito species

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Evolutionary convergence is defined as the acquisition of similar traits in divergent species in response to similar selective pressures. Apart from the canonical fish/cetacean, or flight examples, striking, yet more discreet, examples can be found. This is the case of resistance to insecticide of mosquitoes from two genera that diverged over 145 millions years ago. Due to the large-scale use of insecticides, a similar single point mutation in the *ace-1* gene (R allele) independently spread in populations of both *Anopheles* and *Culex* mosquito species, resulting in resistance. In that case, the phenotypic convergence is supported by a convergence at the molecular level. The R allele is however highly deleterious compared to the susceptible allele (S) in absence of insecticides. This evolutionary trade-off governs the allele dynamics. This already significant convergence goes further, as similar structural variants were subsequently selected for in both genera. They associate several R copies (homogeneous duplications RX), or pair R and S copies (heterogeneous duplications D) of the *ace-1* gene. Far from being limited to *ace-1*, the amplicons have complex genomic structures of hundreds of kilobases encompassing *ace-1*.
I will first present the convergent adaptive response in *Anopheles* and *Culex* genera, then I'll discuss their respective singularities by uncovering the key differences in the fine-scale genomic structures (whole genome sequencing, over 450 samples analyzed). Finally, I will discuss these results in regard to the fitness impacts of those duplications, and the wide range of phenotypes, exhibiting different trade-offs, they create.

Abstract ID: 1369
Poster board number:
P383

Genes under selection in two inverted chromosomal regions of the western honey bee (Apis mellifera)

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The western honey bee (*Apis mellifera)* is characterized by its large native range, living from high mountains to low tropics, thus being well adapted to various climatic conditions. East African mountain regions are of particular interest as high mountains are populated by *monticola* subspecies, denoted as mountain bee that differs in phenotype when compared to bees of surrounding savannahs (*scutellata* subspecies). Morphologically and behaviorally, they can be distinguished, with *monticola* being less aggressive, darker and larger. However, the distinction between the two subspecies is still debated since genetically, only a little differentiation exists, except for two regions on chromosome 7 (r7) and chromosome 9 (r9). Both regions were identified as inversions, which are frequently associated with adaptation. Inversions suppress recombination, leading to selection of favorable variants. r7 and r9 include genes involved in memory

formation, learning and metabolism , which are good candidates for high altitudes adaptation. This study focuses on the detection of sites under positive selection in genes located in r7 and r9 to narrow down potential adaptations signs. Data was made of 52 East African honey bee samples from four different whole-genome projects (PRJNA357367, PRJNA294105, PRJNA237819, PRJNA481428). We first clustered samples according to each gene (IqTree) and then studied selection patterns across genes inside r7 and r9 (PAML). Preliminary results show genes, involved in metabolism and learning, exhibiting sites under selection. Further analysis will include genomic and transcriptomic data from additional samples to elucidate the regulatory network underlying *A. mellifera* adaptation to high elevation habitats.

Abstract ID: 1396
Poster board number:
P384

A single nucleotide variant in Eip75B affects the evolution of fecundity in Drosophila

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Genomics approaches have provided powerful tools to identify natural variants associated with the evolutionary adaptation of quantitative traits, but functional validation of these variants is rare. The nuclear hormone receptor and PPARg-homolog *Ecdysone-induced protein 75B* (*Eip75B*) has been associated with the evolution of ageing and life history in the fruit fly, *Drosophila melanogaster*. Using RNAi knockdown, we have demonstrated that reduced expression of this gene indeed affects lifespan, egg laying rate and egg volume, but it is unknown how representative these tests are for the functional effects of natural allelic variants. We, therefore, aimed to functionally validate a naturally-occurring SNP variant located within a cis-regulatory domain of *Eip75B* that has been associated with the experimental evolution of longevity and fecundity. For this, we screened wildtype lines with alternative SNP alleles and we conducted genomic editing with the precision of a single nucleotide using CRISPR/Cas9. These experiments revealed that this SNP has a significant effect on fecundity and egg-to-adult viability, but not on longevity or other life-history traits. These results demonstrate a causal, pleiotropic effect of a single nucleotide polymorphism on two complex fitness-related traits.

Abstract ID: 1432
Poster board number:
P385

Population genomics of the waterbuck (*Kobus ellipsiprymnus*)

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The waterbuck (*Kobus ellipsiprymnus*) is a species of antelope found throughout central and southern Africa. Two subspecies are currently recognised, the common (*K.*

ellipsiprymnus ellipsiprymnus) and Defassa (*K. ellipsiprymnus defassa*), with the latter listed as “Near Threatened” by the IUCN Red List. Karyotypes are variable within and between the subspecies, ranging from 2*n* = 50 to 2*n* = 54. These have been caused by Robertsonian fusions between chromosomes 6 and 18 (the common waterbuck) and chromosome 7 and 11 (both the common and Defassa waterbuck). Chromosome polymorphisms have not been shown to cause reproduction isolation between the different karyotypes, as introgression has been seen within the hybrid zone where the two subspecies distributions overlap. Previous studies have used mitochondrial DNA and microsatellites to determine the population structure of the species but lack resolution due to limited genetic markers and sampling. In this study we present the first long-read genome assembly of the waterbuck using PacBio HiFi sequencing from a captive sample of the Defassa subspecies with a standard karyotype of 2*n* = 54. Furthermore, we utilise 24 skin samples from museum specimens dating back over 100 years and carry out low-coverage resequencing to determine the historical phylogeography and genetic diversity of the species. These samples will be supplemented with modern samples, to compare temporal shifts in genetic diversity. Our newly sequenced genomes will provide a resource for studying the evolutionary history and speciation of the waterbuck, with implications for future conservation management of the subspecies and further understanding of speciation.

Abstract ID: 1520
Poster board number:
P386

Closer than they appear: Low divergence and no structure in pest beetle populations

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The red flour beetle is an invasive pest that lives in patchy isolated habitats often treated with insecticides and pesticides. This harsh environment causes frequent population size fluctuations and adaptation to local conditions. To investigate whether these conditions impact population genetic structure, we collected eight populations of red flour beetle from geographically separated grain storehouses. We measured several fitness-related traits and found significant divergence in traits like external immune function and development rate. To understand the genomic basis of this phenotypic divergence, we sequenced 3 to 5 whole genomes from individuals from each of the eight populations and used single nucleotide polymorphism (SNP) markers to measure genomic diversity, pairwise divergence and identify signatures of selection in the genome. First, we find that overall genomic divergence between these populations separated by 10 to 2000 kilometres, is very low in comparison to previous estimates for similarly separated populations. Second, there is no discernible population structure and no correlation between genomic distance and geographic distance. These results suggest that there is significant intermixing between these populations possibly due to human-assisted migration. Interestingly, we find signatures of selection in genes involved in signalling activity and lipid metabolism but unexpectedly, not in or near any genes previously known to be involved in insecticide resistance suggesting that complex physiological modulation may be responsible for local adaptation. We emphasise that populations of a pest beetle can diverge phenotypically despite low genomic divergence and adapt to local conditions using complex traits.

Abstract ID: 1530
Poster board number:
P387

Genomic signatures of sexually antagonistic and sex-limited selection on body size

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While sexually dimorphic phenotypes constitute a glaring demonstration of sex-specific selection, characterizing its genomic signatures has proven demanding as the selection history is typically unknown. One of the most prevalent sexually dimorphic phenotypes is body size, reflecting divergent action of both natural and sexual selection on the sexes. Here we investigate the genomic footprints of sex-specific selection on body size and body size dimorphism using an experimentally tractable seed beetle, *Callosobruchus maculatus*. We combine 10 generations of replicated artificial selection with temporal genomic data (whole genome re-sequencing of pools of individuals at three time points). Our goal is to compare sexually antagonistic selection regime, which increased size dimorphism by 50%, to three sex-limited selection regimes (bi-directional on male size and towards increased female size), and to genetic drift controls. We will describe the number, genomic distribution and role (coding vs regulatory) of loci contributing to body size variation and body size dimorphism by characterizing allele frequency changes across generations. Since our quantitative genetic analysis has shown that sexually antagonistic selection preserved more genetic variation than sex-limited directional selection we will also test for the signatures of balancing selection. The characterization of loci with segregating sexually antagonistic polymorphisms will advance our understanding of how genetic variation is maintained and how genetic conflict may be resolved to achieve different adaptations in males and females.

Abstract ID: 1631
Poster board number:
P388

Role of evolutionary capacitance for adaptation in red flour beetles, *Tribolium castaneum*

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Evolutionary capacitance might explain how genomes maintain sufficient variation as the raw material for evolutionary change. It is the process by which populations 'store' genetic variants in the form of cryptic genetic variation (CGV) and then release them under stressful environmental conditions. Heat shock protein 90 (HSP90) is a molecular chaperone that is supposed to be an important evolutionary capacitor that enables such release of CGV, followed by subsequent assimilation of potentially adaptive phenotypes. In the model organism *Tribolium castaneum* (red flour beetle), we have previously found that experimental reduction of HSP90 repeatedly led to assimilation of a reduced eye phenotype, which has potential fitness benefits under continuous light stress. HSP90 is also known to be a potential capacitor of behavioral variation, in particular diurnal

rhythmicity, as indicated by a study in *Drosophila*. As flour beetles possess a functional molecular clock, we monitored locomotor activity, a standard readout of the circadian clock, upon inhibition of HSP90. We observed differences in the overall activity profiles in comparison to control beetles. Along with these results, we will present further data regarding the potential fitness benefits of the HSP90-regulated reduced eye phenotype under light stress. Our approaches provide urgently needed, but rare experimental tests of the potential role of evolutionary capacitance for adaptation.

Abstract ID: 1635
Poster board number:
P389

The genomics of adaptation to host plant using the comparative framework of the pea aphid complex

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A major goal in evolutionary biology is to understand the genetic basis of evolutionary change. Sympatric populations of insects adapted to different host plants, i.e., host races, are good models to investigate how adaptation to different habitats and resources may induce adaptive differentiation and lead to reproductive isolation. Here, we took advantage of the continuum of divergence across several pea aphid host races to investigate the patterns and determinants of genomic differentiation at different divergence stages and characterize the distribution and nature of barrier loci. Using genome-wide pool-seq data in 16 European populations adapted to different host plants, we first characterized the divergence continuum in terms of differentiation level, divergence time, and potential ongoing gene flow. We then analyzed the genomic landscape of differentiation and its determinants across the different pairs of populations and identified potential barrier loci by combining Fst, Dxy, and D-like statistics along the genome, while controlling for recombination. Comparing the genomic distribution and nature of barrier loci between pairs of populations adapted to different host-plants and at different divergence levels allowed us to test whether adaptation to different host plants involves the same genes and metabolic pathways and to assess if barrier loci underlying host-plant specialization evolve in the early stages of divergence (i.e., in the lowly differentiated pairs of populations along the continuum), while other classes of barrier loci (e.g. loci underlying sexual isolation) accumulate later on, possibly as a consequence of reinforcement.

Abstract ID: 1793
Poster board number:
P390

Genome evolution of the painted lady - a rising star of the insect migratory genomics

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Gene family expansions and crossing over are two main mechanisms for generating novel genetic variants that can be picked up by natural selection. Therefore, characterization of these processes is crucial for understanding how organisms adapt to the environment. We developed a high-density linkage map and detailed genome annotation based on information from a high-contiguity genome assembly to investigate lineage specific gene family expansions and characterize the recombination landscape in the painted lady butterfly - a non-diapausing, highly polyphagous species famous for its long-distance migratory behavior and almost cosmopolitan distribution range. Our results reveal a complex interplay between regional recombination rate variation, gene duplications and transposable element activity shaping the genome structure of the painted lady. A key result is that we identify several lineage specific gene family expansions, the functions of these gene families are associated with protein and fat metabolism, detoxification, and defense against infection - critical functions for the painted lady's unique life-history characteristics. Furthermore, the detailed recombination maps allow us to characterize the regional recombination landscape, data that reveal a strong effect of chromosome size on the recombination rate, a limited impact of GC-biased gene conversion and a positive association between recombination and short interspersed elements. Given the combination of traditional linkage mapping, detailed genome annotation and comparative genomics approaches, where we both characterize the genome structure and recombination landscape of a model species for migratory research and identify candidate genes for adaptations to a migratory life-style.

Abstract ID: 1825
Poster board number:
P391

The effect of hatchery-imposed selection on wild and farmed Australian blue mussels (*Mytilus sp.*)

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While aquaculture is important it may have adverse environmental and ecological impacts if not managed appropriately. This can include selection for traits that increase fitness in aquaculture settings, or are commercially important, but are maladaptive in the natural environment. Aquaculture often rears large numbers of highly related individuals that when released into the wild could cause genetic swamping and inbreeding as well as an increase in the frequency of maladapted traits in natural populations. Here we assess the impact of standard hatchery-imposed selection on the genetic diversity of farmed blue mussels. Specifically, we aimed to test: i) if there is a decline in genetic diversity through the early hatchery rearing processes, ii) if there is any evidence for

increasing relatedness among the larvae suggesting selection for certain familial lineages, and iii) testing if farmed and natural adult populations show any evidence of genetic declines, inbreeding or genetic swamping. Using mirosatellite markers, we investigated the genetic divcersity of larvae (three timepoints collected) and adult populations (wild and farmed). Results showed that the hatchery spawning rotocol appeasrs to capure high levels of genetic diversity in the larvae that do not appear to decline significantly as the larvae move through the rearing process. However, selection and/or genetic drift does appear to be operating during the process. Overall, our data suggest that the selection processes applied allowed the mainteneance of high geneti divesrity among hatchery produced larvae and does not lead to genetic swamping of natural blue missel populations in the surrounding area.

Abstract ID: 1835
Poster board number:
P392

Experimental evolution to uncover genome dynamics and effect of gene flow on adaptive divergence

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Adaptive divergence is a key evolutionary process generating biodiversity by means of natural selection. The outcome is expected to vary by the degree of migration between diverging populations. Yet, empirical evidence on the role of gene flow during adaptive divergence is still limited. This study investigates the adaptive evolutionary changes in 132 sexually reproducing populations of fission yeast that were propagated for 126 generations (incl. ~1,000 asexual cycles) under constant disruptive ecological selection and different levels of migration. Whole-genome pool sequencing of the evolving populations allowed insight into allele frequency dynamics of all mutations across time. As expected from Fisher's fundamental theory, we observed a gradually decreasing rate in both fitness gain and the build-up of genetic divergence. Parallel adaptation was pervasive for a number of novel mutations enriched for a subset of biological pathways, but not necessarily for the same genes. The effect of gene flow changed through time. Midway of the experiment in generation 53, adaptive divergence was most significant at the extreme ends of the gene flow gradient (allopatry and sympatry). By contrast, in generation 126 divergence was maintained in allopatry and emerged under low levels of gene flow (parapatry). Diverging ecotypes that coexisted in sympatric populations for generation 53, became fixed in generation 126 for either ecological strategy. This study sheds light on the speed and molecular basis of adaptive divergence under varying degrees of gene flow.

Abstract ID: 1919
Poster board number:
P393

The genomic patterns of divergence in the Oriental clade of the *D. melanogaster* species group

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The Oriental clade within the *Drosophila melanogaster* species group is ecologically diverse and has contributed to our understanding of morphological innovation (serrated ovipositors, wing spots), behavioural evolution (sexual selection, courtship), and contains one of this century's major global pests, *D. suzukii*. Our lab has also been interested in temperature-related physiological and behavioural changes among these species. We are especially intrigued by the putatively recent divergence between *D. lutescens* and *D. takahashii*, where we have identified shifts in temperature preference behaviours that are consistent with local adaptation. Intriguingly, this species-pair remains crossable in lab conditions, and they are suspected of having a hybrid zone in the southern region of the Japanese island Honshu. In this study we have revisited the "Oriental clade" using a comparative genomics approach. We draw on five existing genomes, and add a *D. lutescens* genome, in order to improve estimates of species relationships and split times within the clade. Among other results, we resolve branching order within the *D. takahashii* subclade. Surprisingly, despite their ability to cross, we infer a relatively deep divergence estimate of 4.52My for *D. lutescens* and *D. takahashii*. To test the hypothesis that the two species continue to hybridise in nature, we have generated a population genomic dataset for *D. lutescens* and *D. takahashii* samples that were recently collected from their overlapping ranges. Together, these studies provide important new insights into the evolutionary history of this important *Drosophila* clade, and will help identify cases of adaptive change, including those related to temperature.

Abstract ID: 1941
Poster board number:
P394

The genomics of avian adaptation and speciation: from oceanic to sky islands

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The isolation of populations through colonisation or habitat fragmentation may be a major evolutionary driver of diversification and speciation. Avian models of oceanic and sky island systems provide insight into how colonisation events and gene flow may interact with selection to shape genetic variation at different spatial scales. Using whole genome sequences, we assess incipient speciation in an island endemic passerine, Berthelot's pipit (*Anthus berthelotii*), and across a young radiation in the fastest evolving avian lineage, *Zosterops*, to understand which evolutionary processes may have driven divergence over the last 2 million years. Pairwise comparisons of species populations provide detail on: (1) Population history and divergence timeframes; (2) the strength of selection acting between populations; (3) the rate of accumulation of genomic divergence and (4) environmental drivers of divergence and speciation. Using pairwise F_{ST} across the genome, we identify strongly divergent 'genomic islands' among populations and species. We ask whether whole genome sequences suggest similar patterns of ecological adaptation across geographic and temporal scales in avian species evolving in different ecological contexts. Together these analyses provide better understanding of

how evolutionary mechanisms shape patterns of genetic diversity and divergence following the establishment of new populations, and how this may lead to speciation.

Abstract ID: 1953
Poster board number:
P395

Species divergence driven by ecology and mating system in taxonomically complex British Euphrasia

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Taxonomically complex groups (TCGs) are characterised by populations that are difficult to assign to discrete and unambiguously defined species. A good non-model plant system for investigating the evolutionary factors blurring species boundaries are eyebrights (*Euphrasia*), a genus that has remarkable diversity in ploidy, mating system and ecology. In Great Britain there are 21 species usually found in different ecological niches, which are exceptionally hard to identify on the basis of morphology or DNA barcoding. Here, we test the hypothesis that species boundaries are maintained by narrow regions of the genome likely to underlie adaptive divergence, while the rest of the genome experiences extensive gene flow. To understand geographic genetic structure and the nature of species differences, we applied genotyping-by-sequencing (GBS) and spatially-aware clustering methods to extensive population samples from all British eyebright species. We found: 1) a distinctive genetic cluster which mainly consists of the selfing heathland specialist *E. micrantha* in Northern Scotland, 2) other genetic clusters largely correspond to geographic regions rather than individual species, 3) closely related species showed low species-level differentiation with a few genomic outlier regions. Our results show eyebrights are characterised by extensive homogenising hybridisation, with species differences maintained by few genomic regions. Distinctive taxa, such as *E. micrantha*, might have experienced a different post-glacial colonization history or maintained their distinct identities due to selfing. Overall our results highlight how ecological factors and mating system may play a crucial role in shaping genomic divergence in this taxonomically complex group.

Abstract ID: 1990
Poster board number:
P396

Signals of Epistatic Interactions in Time Series Genomic Data

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The relationship between genotype and phenotype has been difficult to solve since the foundation of modern genetics. Only recently have advances in sequencing provided the

information needed to infer the genetic architecture of many complex traits. Genetic architecture of a trait includes the effects of individual genes, gene-gene interactions (epistasis), and gene by environment interactions that underlie the trait. Evolve and resequence studies have become a popular method to infer the genetic architecture of traits. However, existing methods for identifying alleles underlying a trait focus on individual alleles at a time, removing any information on how genes interact with one another. Thus, my project addresses the challenge of inferring epistasis underlying traits by characterizing how the genotype changes over the course of phenotypic adaptation. Using forward time population genetic simulations, I show that patterns in genomic adaptation contain several tell-tale "signals," which can be used to differentiate between certain types of epistasis acting among genes undergoing selection. Taken together, this method can be used to distinguish different types of epistasis, which can be used to understand the genetic architecture underlying complex diseases or traits. Furthermore, my method will provide fundamental insights into mechanisms of evolution. Different types of epistasis have been theorized to either constrain or promote adaptive evolution. However, epistasis has traditionally been regarded as unable to directly respond to selection. My novel approach will enable researchers to comprehensively explore the role of epistasis in response to stressors or environmental change.

Abstract ID: 2065
Poster board number:
P397

Genomic relatedness matrix-based heritability of immune function in an invertebrate

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Complex immune defences have evolved to counter the severe threat parasites and pathogens pose on organisms. Here, we asked how heritable are the non-specific immunological traits of the immune system? We used high-marker density genotyping to estimate the genetic relatedness of self-compatible hermaphroditic snails, *Lymnaea stagnalis,* from a natural population to assess quantitative genetic parameters for immune function under field conditions. We estimated additive genetic variance and covariance of three phenotypic immune traits: haemolymph phenoloxidase, laccase and antibacterial activity while controlling for variation in immune activity arising from the season and snail resource level. We also controlled for trematode infection status of the snails as *L. stagnalis* is a common host for these castrating parasites. We calculated genomic relatedness between 566 field-collected snails using around 19,000 independent Single Nucleotide Polymorphism markers. Heritability of immune traits ranged from 0.12 to 0.22. We found a positive genetic correlation between phenoloxidase and laccase activity and signs of negative genetic correlation between laccase and antibacterial activity. This is the first study estimating genomic relatedness matrix-based heritability and genetic correlations of immune function on a local

population of an invertebrate in the wild. Our results suggest evolutionary potential in snail immune function and that genetic trade-offs among immune traits may maintain within-population genetic variation in immune activity.

Abstract ID: 2115
Poster board number:
P398

Genomic investigation of potential adaptive introgression in two cryptic bat species

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Understanding the evolutionary consequences of introgressive hybridization is a major objective in Evolutionary Biology. The two bat species *Myotis davidii* and *Myotis mystacinus* are morphologically very similar but represent two highly divergent genetic lineages. Both species have wide distribution zones, both spanning major parts of Europe and Asia including a large potential hybrid zone in Eastern Europe and the Caucasus. Earlier studies found signs of mitochondrial introgression between the two species and observed a recent range expansion of *M. davidii* towards the West. In this study, we are analyzing whole genome shotgun sequencing of currently 66 bat individuals. Population genomic bioinformatic methods are used to investigate the role of adaptation during range expansion of *M. davidii* and to explore the role of introgression in this process. Within both species, we found genetic divergence among geographically distributed populations. We also found strong signs of introgression in *M. davidii,* but not in *M. mystacinus* populations. These findings raise questions about the connection between introgression and the range expansion of M. davidii, in which likely adaptation to changing environments plays a role.
In further analyses we will scan the genome of both species for signs of introgression and selection. We will also use demographic modeling to further unravel the evolutionary history of these two cryptic bat species.

Abstract ID: 2191
Poster board number:
P399

Deciphering the genetic architecture of polygenic adaptation in *Tribolium castaneum*

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Characterizing the dynamics of polygenic adaptation in populations undergoing environmental change is of primary importance for biologists. However, detecting the causal variants of polygenic traits under selection is challenging, as weak but meaningful

associations are often under the barrier of statistical detection, and are hidden by phenotypic plasticity, genetic redundancy or drift.
In this context, experimental evolution is a promising tool. Indeed, controlled environments in the laboratory and omic advances allow researchers to characterize the adaptive architecture at many levels of the genotype-to-phenotype map. Here, we used individual-level RNA-seq and fitness measurements to decipher the adaptive architecture in populations of *Tribolium castaneum* (red flour beetle) adapting to stressful conditions (heat and drought) for twenty generations. In these populations, phenotypic divergence at the level of transcript expression occurred through a mix of plastic and evolutionary changes.
By combining the detection of quantitative trait loci associated with variation in expression and plasticity and by quantifying the divergence of gene expression traits associated to fitness, we were able to characterize the genetic architecture of expression levels and their plastic responses under selection. Importantly, estimates of transcript-level selection gradients allowed us to better characterize changes in expression levels and allele frequencies after 20 generations of evolution. We were able to show that on average genes with expression levels under positive selection in a new environment increased their expression after 20 generations, and vice-versa for negatively selected genes. We found that genetic variants associated with those genes also changed in allele frequency over time.

Abstract ID: 2239
Poster board number:
P400

The role of inbreeding in genetic depletion: genomic diversity of tundra bluethroat populations

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Genetic variation is necessary to maintain population viability and future adaptive potential. Vertebrate populations reduced in size are prone to depletion of genetic diversity, inbreeding and accumulation of deleterious mutations. Reduced genetic diversity is considered as a major risk for population extinction. However, recent studies showed that even if with gene flow maintains genetic diversity, populations are at risk of local extinction if their size is small. We explored the impact of population demography on genetic diversity of the tundra Bluethroat subspecies (*Luscinia svecica svecica*) from Krkonoše Mountains (Czech Republic). The Krkonoše population was established just decades ago and experienced initial expansion followed by gradual decline leading to extinction. Using ddRADseq approach we analysed a series of samples collected between 2001 and 2007 from the Krkonoše population (89 individuals) and compared it with outbred populations of *L. s. svecica* from Scandinavia (23 individuals) and an outgroup *L. s. cyanecula* population (21 individuals) from Třeboň lakes (Czech Republic). Based on 24,000+ loci, SNP results showed a gradual decline in nucleotide diversity over five years in Krkonoše, followed by a sudden increase in the last two years. The increase can be related with the occurrence of several migrant individuals clustering with the outbred Scandinavian population. Our study demonstrates that temporal increase in local

diversity does not guarantee a population survival. Finally, a few cases of a possible hybridisation between the two subspecies, *L. s. svecica* and *L. s. cyanecula,* were detected based on genomic and mitochondrial Cytochrome B sequence data.

Symposium: S25. The positives and negatives of whole genome duplication: synthesizing polyploid evolution across organisms and disciplines (id: 969)

Abstract ID: 973
Poster board number:
P401

Polyploidization as an opportunistic mutation

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Whole-genome duplication is a common mutation in eukaryotes with far-reaching phenotypic effects. Both theory and data predict that polyploidy success is due to an increase in fitness, for example, due to higher tolerance to stressful conditions. Nevertheless, whole-genome doubling also arises with several costs in neo-polyploid lineages, like genomic instability, mitotic and meiotic abnormalities, and a reduction of fitness. Interestingly, the idea that polyploidization can fix by genetic drift, as a deleterious or neutral mutation is currently lacking in the literature. To test how and when polyploidy can invade a population by chance, we built a theoretical model in which polyploidization occurs through the production of unreduced gametes, modeled as a quantitative trait, which is allowed to vary through time. We found that when polyploid individuals are less or as fit as their diploid progenitors, the fixation of polyploidy is only possible when genetic drift is stronger than natural selection. Surprisingly, this result remains true even when polyploidy confers a selective advantage, with genetic drift being necessary for tetraploidy to invade, except when polyploids are highly better than their diploid progenitors. Finally, we found that self-fertilization is less beneficial than previously thought, as it increases the selection against unreduced gamete production compared to diploid populations when polyploids harbor an initial decrease in fitness. Our results bring new insight into how and when polyploidization occurs in natural populations, and help to understand the temporal and spatial distribution of polyploid species.

Abstract ID: 998
Poster board number:
P402

Niche differentiation after polyploidization?

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Aim

Although whole genome duplication (WGD) is an important speciation force, we still lack a consensus on the role of niche differentiation in polyploid evolution. One reason for this might be that the intraspecific genetic structure of polyploid complexes and interploidy gene flow is often neglected in ecological studies. Here, we aim to investigate to which extent these evolutionary processes impact our inference on niche differentiation of autopolyploids.

Methods

Leveraging a total of 352 cytotyped populations of diploid-autotetraploid *A. arenosa*, we examined differences among climatic niches of diploid and tetraploid lineages both globally, and independently for each tetraploid lineage with respect to the niche of its evolutionary closest relative. Then, we tested if there was an effect of additional interploidy introgression from other diploid lineages of *A. arenosa*.

Results

We found different patterns of climatic niche evolution in each tetraploid lineage when the assignment of populations to intraspecific genetic lineages is considered. We observed an effect of interploidy gene flow in patterns of climatic niche evolution of tetraploid ruderal plants of *A. arenosa*.

Main conclusions

The niche shift of tetraploids in *A. arenosa* is not driven by WGD per se but rather reflects dynamic post-WGD evolution in the species, involving tetraploid migration out of their ancestral area and interploidy introgression with other diploid lineages. Our study supports that evolutionary processes following WGD – which usually remain undetected by studies neglecting evolutionary history of polyploids – may play a key role in the adaptation of polyploids to challenging environments.

Abstract ID: 1313
Poster board number:
P403

Evolution of the meso-octoploid genome of *Heliophila variabilis* (Brassicaceae)

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There is broad consensus that whole genome duplications (WGDs) followed by post-polyploid diploidization (PPD) have contributed significantly to the evolution of land plants and, in particular, angiosperms. The Heliophileae, the most morphologically diverse lineage in the mustard family, remains largely unknown with respect to its genome origin, evolution, and phylogenetic relationships. Here, we report the chromosome-scale assembly of a first meso-octoploid crucifer genome, the meso-octoploid *Heliophila variabilis* (~300 Mb, 2n=22). Although the *H. variabilis* genome has shrunk considerably and the octoploid chromosome number was reduced, most of the homoeologous chromosomal regions have been identified in four copies, accompanied by biased divergence in gene density and phylogenetic relationships. These four genomic copies

were identified as two less fractionated (sub1 and sub2) and two more fractionated (sub3 and sub4) subgenomes. The putative ancestral genomes diverged during Oligocene-Miocene and their subsequent mergers may have occurred rapidly c. 18 million years ago. The biased subgenome fractionation was associated with extensive chromosomal rearrangements that mediated chromosome fusions and the activity of transposable elements. The progressive genome diploidization has enabled evolution of many important traits, including drought tolerance, disease resistance, leaf development, and flower color evolution. Our results provide a deeper understanding of the mid- and long-term evolutionary consequences of polyploidization and post-polyploid diploidization cycles. This work was supported by the Czech Science Foundation (project no. 19-07487S).

Abstract ID: 1363
Poster board number:
P404

The macro eco-evolutionary dynamics of mixed ploidy populations

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Polyploidy, i.e., having multiple sets of chromosomes, is generally thought as an important phenomenon underpinning plant ecology and evolution. Arguments regarding the establishment and persistence of polyploids rely on possible fitness advantages or niche divergence mechanisms experienced by these organisms. However, such advantages contrast with mounting evidences that higher ploidy taxa experience extinction rates superior to those of diploid species. Thus far, no explicit attempt to explain polyploid establishment and evolution has been made under the paradigm of neutral dynamics, and this is especially relevant in autopolyploids, which often share high niche overlaps with their diploid ancestors, and therefore coexistence cannot be easily explained by fitness differences among cytotypes. To gain a better understanding of the dynamics underlying mixed ploidy populations, we develop an eco-evolutionary model based on spatial populations with finite genomes to investigate whether neutral processes can explain both establishment, evolution and extinction rates in these populations. We present a general explanation to polyploid establishment, by showing that sexually reproducing organisms assemble in space in an iterative manner, reducing frequency dependent disadvantages and overcoming reduced fertility issues. Reduced fertility, which is an important feature of autopolyploid meiosis, along with unreduced gamete formation frequency, the main mechanism behind polyploid formation, are shown to control stability of coexisting cytotypes, possibly explaining rates of establishment, degrees of coexistence and elevated extinction rates. We also study speciation dynamics in different ploidy levels and discuss potential implications for the ecology and evolution of these organisms.

Abstract ID: 1364

Poster board number:
P405

Diploidization associates with cladogenesis, trait disparity and gene coevolution in Microlepidieae

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Angiosperm genome evolution was marked by many clade-specific whole-genome duplication (WGD) events. WGD is a trial-and-error process under natural selection, with subsequent genome diploidization proceeding with different intensities and being associated with speciation events. The Microlepidieae is a monophyletic tribe in the mustard family (Brassicaceae) formed after an ancient allotetraploidization, including c. 17 genera and 60 species endemic to Australia and New Zealand. Post-polyploid diploidization has resulted in the extant Microlepidieae genomes that differ in the extent of inter-subgenome reshuffling and the number of chromosomes (n=4 to n=12). To gain a deeper understanding of post-polyploid genome evolution in Microlepidieae, we analyzed phylogenetic relationships in this tribe using complete chloroplast sequences, entire 35S rDNA units, and abundant repetitive sequences. The four recovered intra-tribal clades mirror the varied diploidization of Microlepidieae genomes, suggesting that the intrinsic genomic features underlying the extent of diploidization are shared among genera and species within one clade. Nevertheless, even congeneric species may exert considerable morphological disparity (e.g., in fruit shape), whereas some species within different clades experience extensive morphological convergence despite the different pace of their genome diploidization. We showed that faster genome diploidization is positively correlated with mean morphological disparity and evolution of chloroplast genes (plastid-nuclear genome coevolution). Higher speciation rates in perennials than in annual species were observed. Altogether, the newly acquired results confirm the potential of Microlepidieae as a promising subject for the analysis of post-polyploid genome diploidization in Brassicaceae. This work was supported by a research grant from the Czech Science Foundation (20-03419Y).

Abstract ID: 1373
Poster board number:
P406

Are genes with variable expression more evolvable? Evidence from whole-genome duplication in fishes

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A classic view of gene duplication is that genetic redundancy can accelerate gene function evolution by relaxing pleiotropic constraints. Another, not mutually exclusive, possibility is that genes with higher evolutionary rates are more duplicable or more likely to be retained in duplicate in the first place. At the population level, it has been proposed that balancing selection predating duplication promotes the fixation of duplicate genes. Extending on this hypothesis, we speculated whether inter-individual expression variation could be associated with duplicate retention or function specialization. We generated transcriptome profiles spanning at least nine organs, with 4-12 replicates per sex (if known), in three species of ray-finned fishes: two which had undergone the teleost whole-genome duplication (WGD) around 230–315 MYA (*Danio rerio* (zebrafish) and *Esox lucius* (northern pike)), and one outgroup (*Lepisosteus oculatus* (spotted gar)). Per organ, we applied a mean-corrected measure of expression variation for each gene to investigate the potential role of variation on the evolution of genes after duplication. We found that single-copy gar orthologs of gene pairs retained after teleost-WGD have higher expression variation across multiple organs relative to orthologs of teleost singletons. Interestingly, we found a similar trend comparing pike genes to salmonid genes after their more recent WGD (80–100 MYA). Thus, this pattern holds across different evolutionary timescales. We also evaluated the relation between expression variation and functional divergence of ohnologs (sub/neofunctionalization). These findings could have broad implications for our understanding of the interplay between expression variation and evolvability of genes after duplication.

Abstract ID: 1435
Poster board number:
P407

Becoming polyploid in a diploid population: when size and metabolism change

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Polyploidization is the increase in chromosomal set size, arising mostly due to the fusion of unreduced gametes. Unreduced gamete formation is relatively common and while polyploid populations are widespread, the long-term establishment of polyploids is exceedingly rare and might coincide with changed environmental conditions. There are several hypotheses of why polyploids, compared to their diploid progenitors, might have a selective advantage during times of environmental turmoil. For example, changes in size and reproductive modes, alongside niche differences from the parental niche are often associated with polyploids. Current research links the evolution of body size to ecophysiological capacities and we seek to understand how body size increase in polyploids as a master trait governs changes in metabolic rates and development. Considering polyploidization as mutation that happens to a diploid individual's offspring, we constructed a spatially explicit individual-based model of polyploids arising and

establishing in a diploid population. Individuals are modelled as perennial plants, which grow from seed to maturity by consuming available nutrients, then respiring and growing somatic and reproductive tissue. Metabolic processes are functions of the individuals' sizes based on allometric scaling of metabolic rates and partitioning to somatic and reproductive energy budgets. We discuss how size-dependent metabolism influence polyploid establishment in different spatiotemporal scenarios and assess the implications for the evolution of alternative reproductive strategies. We seek to pair this theoretical population modeling with experimental data of newly synthesized polyploid *Chlamydomonas reinhardtii* and *Spirodella polyrhiza*.

Abstract ID: 1567
Poster board number:
P408

Introgression between diploid and tetraploid *Cardamine amara* in their secondary contact zone

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Polyploidisation was traditionally considered one of the strongest prezygotic isolation barriers, but recent studies have shown that opportunities for inter-ploidy gene flow still exist in many polyploid taxa. In a diploid – autotetraploid complex of *Cardamine amara* a secondary contact zone is formed in Czechia where mixed populations containing diploid, tetraploid, and intermediate triploid individuals, which are all morphologically indistinguishable and overlap in flowering, indicating a possibility of hybridisation. The aim of this study was to infer the strength and the direction of the introgressive gene flow across the ploidy barrier and to elucidate the formation and the potential role of triploid individuals as mediators. A combination of rigorous flow cytometry analyses, reciprocal crosses, and genomic analyses using sequence data obtained by whole-genome sequencing has been conducted to answer these questions. The genetic structure reveals well-differentiated diploids and tetraploids in allopatry with signatures of admixture in sympatry confirmed by a strong signal of introgression, while triploids are formed both by hybridization and fusion with an unreduced gamete. Furthermore, the interploidy crosses, regardless of gene dosage, yielded non-viable seeds pointing to formation via unreduced gametes and triploid block. Nevertheless, backcrossing of triploids with parental cytotypes yielded a few viable aneuploid and homoploid seeds. Finally, diploid, and tetraploid cytotypes of *C. amara* are genetically well differentiated as previous research has shown; however, the reproductive barrier is much more permeable than expected with strong signatures of introgression and a possible role of the triploid bridge further facilitating the gene flow between dominant cytotypes.

Abstract ID: 1595
Poster board number:
P409

Origin and evolutionary significance of autotriploids in *Butomus umbellatus*

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Contact zones of cytotypes harbour a unique opportunity to study the dynamics and evolution of mixed-ploidy systems. *Butomus umbellatus* (flowering rush) is one of a few species in which diploid and triploid cytotype is present in nature. The first known mixed-ploidy populations of *B. umbellatus* were discovered in south-eastern Slovakia during the previous studies. Common occurrence of the species in an area with substantially natural dynamics of wetland ecosystems represents a unique model system for unbiased comparisons of traits and genetic diversity between diploid and triploid individuals along with their dispersal capabilities on a landscape level.
The main aim was to uncover the truth behind evolutionary processes that are taking place in the contact zone of diploid and triplioid cytotype of *B. umbellatus* in south-eastern Slovakia. Using flow cytometry and analysis of microsatellite loci we discovered that the contact zone of cytotype is of both primary and secondary character and gene flow between cytotypes was also detected. These results were supported by high production and variability of offspring detected in triploid plants in mixed populations and extreme production of unreduced gametes in both cytotypes.

Abstract ID: 1694
Poster board number:
P410

The parasitoid wasp *Nasonia vitripennis* as a model for animal polyploid evolution

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Polyploidy is a paradoxical driver of evolution in eukaryotes. Polyploidization causes sterility, cell size changes, and gene expression disruptions. However, polyploidy also promotes gene network diversification, mass speciation, and adaptability. A major question in polyploid evolution is how initial disadvantages and evolutionary advantages are bridged. Key to investigating this is delineating mechanistic differences between more and less successful polyploid lines. Research on this has focused on plant polyploidy, which is easily induced and stabilized. Experimental evolution studies for animal polyploids have been difficult, due to inviability and greater consequences of e.g. sexual dosage effects. We exploited the biology of *Nasonia vitripennis*, a parasitoid wasp, to develop it into a comprehensive animal polyploid model. Like all hymenopteran insects, it has haplodiploid sex determination and so lacks specialized sex chromosomes. Unfertilized eggs develop into haploid males and fertilized eggs develop into diploid females. There exists a long-maintained Whiting polyploid line (WPL) derived from a spontaneous lab mutation, and means of creating neopolyploid lines through sex determination gene knockdowns. Unusually, both polyploid males (diploid) and females (triploid) have reproductive capacity, allowing for transgenerational study. We use this model to study several major topics in polyploid evolution:

1. How does variation in polyploid phenotypes among the different lines represent the likelihood of evolutionary success versus extinction?
2. Is there variation in polyploid cell number reduction and cell size reduction mechanisms?

3. Is there a pattern in the gene expression and/or dosage alteration in different polyploid lines, and does sexual dosage compensation exist in haplodiploids?

Abstract ID: 1727
Poster board number:
P411

How do different ploidies adapt? A case of *Arabidopsis* in non-extreme edaphic environment.

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Considering adaptation as mostly a genetic process, whole-genome duplication (WGD), a major mutation, represents a controversial but rather promising engine of adaptive evolution. Generally, polyploid organisms have the opportunity of tapping into a larger gene pool, where alleles are multiplied resulting in higher heterozygosity which can in turn work as a buffer against deleterious mutations and can lead to a higher diversification and evolvability. Furthermore, WGD is likely to affect gene flow between species, for example weakening or creating reproductive barriers and isolation between cytotypes. While adaptation to extreme environments has been largely investigated in plants, mechanisms of evolution in less deadly conditions received less attention. Theoretically, lower mortality rate is expected to slow genetic adaptation, imposing less steep selective clines. How different ploidies of the same species differ in their genetic evolution under such conditions was, so far, not addressed. We analyzed 608 resequenced genomes of two diploid-autotetraploid *Arabidopsis* species to uncover and compare ploidies' evolution of genomic basis underlying adaptation to non-extreme and common siliceous and calcareous substrates. Also coupling genomic data with ionomic results of locally sampled soil material, for each cytotype and species we identified candidate genes as mostly enriched in GO terms related to ions cellular transport. Finally, we assessed intraspecific ploidies' differences and parallelisms, investigated the evolutionary sources of trans-specific polymorphisms and measured the role of WGD caused interspecific gene-flow therein.

Abstract ID: 1824
Poster board number:
P412

Convergent evolution of DNA methylome in newly synthesized tetraploid towards natural tetraploid

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Epigenetic evolution should play a critical role in a newly synthesized allopolyploid to thrive *in natura* after polyploidization by controlling transcriptomic pattern and eventually phenotypes. We used a synthetic *Arabidopsis kamchatica* (prudeced by crossing *A. helleri* and *A. lyrata*) to explore how the DNA methylome pattern as well as gene expression pattern changes soon after the polyploidization event. The synthetic line was incubated for four generations in two different conditions, mild and hot, to compare them with progenitors and two genetic lines from natural habitats.

The subgenome-phased comparison of DNA methylome pattern between the synthetic line and progenitors showed divergent pattern according to generations, after the most drastic change at the first generation. Contrastingly, the synthetic lines showed convergence to natural lines over the course of generations. In addition, the synthetic line incubated at harsher condition showed faster change compared to the line at milder condition. In contrast to methylome pattern, the change of gene expression pattern was much more drastic in the synthetic lines, as approximately 10 to 30% of the genes are detected as differentially expressed. The number of differentially expressed genes was larger at harsher condition. These results imply that environmental condition may have an accelerating effect on the evolution of methylome and transcriptome of a new polyploid and also the existence of a stabilizing point of DNA methylome pattern defined by genotype of progenitors.

Abstract ID: 2159
Poster board number:
P413

Variation in the pathways and rates of diploid - polyploid gene flow across multiple plant systems

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Ploidy level differences are traditionally considered very efficient reproductive barriers. Indeed, the whole genome duplication directly provides first-generation polyploid mutants with postzygotic reproductive isolation from their diploid progenitors, known as the 'triploid block'. Here, we investigated how much the intensity of triploid block and its mechanisms differ among plant species and assessed population genetic signatures of inter-ploidy gene flow in natural diploid – polyploid contact zones. A strong triploid block was detected in *Arabidopsis arenosa* (Brassicaceae), which mainly manifested during the endosperm development but also translated into lower seed germination and survival of inter-ploidy hybrids. However, in two other study species, triploids were readily formed in mixed-ploidy populations or even stabilized by clonal reproduction as dominant cytotypes and did not exhibit lower vitality. Reproductive interactions involving triploids always resulted in profound karyological variation in the (predominantly aneuploid) progeny. However, occasional formation of euploids could be the key to facilitating inter-ploidy gene flow. Though the inter-ploidy gene flow never seemed to compromise integrity of the coexisting diploid and polyploid lineages, it might serve as a source of adaptive genetic variation. In *Tripleurospermum inodorum* (Asteraceae), even aneuploid F_2 hybrids participated in inter-ploidy crosses and signs of bidirectional gene flow between 2x and 4x were detected in natural populations. Genetic structure of *Butomus umbellatus* (Butomaceae) populations suggested both occasional genetic recombination between locally coexisting cytotypes and recurrent origins of triploids. Altogether, our results show that the strength of diploid – polyploid reproductive isolation varies profoundly among plant species, occasionally providing an opportunity for adaptive introgression.

Abstract ID: 2251
Poster board number:
P414

Evolution of vision in sturgeons

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Sturgeons are representatives of non-teleost fishes. Genomes of fishes in general have been modified by series of whole genome duplications (WGDs) and there have been at least three WGD events during the sturgeon evolution. Such changes strongly affected the evolution of sturgeon genomes, including the evolution of opsin genes. These genes encode opsine proteins, which are responsible for light detection. This study is focused mainly on the identification of opsin genes and the level of their expression. We found that one species, the Starry sturgeon (*Acipenser stellatus*) is particulary interesting, since this species does not express any rod opsins and seems to rely only on the cone opsin genes. All the other tested sturgeon species have both rods and cones in the retina. We further tested this phenomenon by the application of FISH (fluorescence in situ hybridization) and the distribution of photoreceptor cell types (rods/cones and their subtypes) is mapped. We have specifically focused on the interspecific hybrids with different WDG history and ecological preferences. We present results in opsin gene expression profiles of the Sterlet (*A. ruthenus*) and the Siberian sturgeon (*A. baerii),* their hybrids, normoploids and specimes with manipulated ploidy level, and, lastly, between pigmented and albino specimens.

Abstract ID: 2264
Poster board number:
P415

Eco-evolutionary dynamics in a polyploid establishment experiment

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Polyploidy, despite the huge costs, is ubiquitous in nature and reportedly drives biodiversity patterns. Therefore, there is interest in the processes behind polyploid establishment that overcome its inherent challenges. Theory and empirical findings that associate polyploids with stressful environments suggest a general road to polyploid success is niche differentiation through e.g. stress tolerance. Establishment in extant polyploids is, therefore, often inferred from climate and trait correlation but ignores the role competition with its ancestral population (and stochastic drivers) during the establishment process. We tested establishment of neopolyploid duckweed (Spirodela polyrhiza) in a population of majority diploid ancestors in benign and salt stress environment in replicated microcosm competition experiments. We used four clonal strains that previously underwent artificial polyploidization that avoided other genetic differences between cytotypes. We tracked cytotype frequency and dry weight to quantify population dynamics. We find that the slower growing but larger tetraploids only established in a few replicates, independent from strain identity. Salt-stressed replicates

tended to have a slightly higher polyploid establishment. This experiment showed the impact of neutral effects in polyploid establishment and a lack of inherent competitive advantage. However, we observed an immediate niche difference in neopolyploid duckweed related to whole genome duplication.

Abstract ID: 2365
Poster board number:
P416

How does the common barbel (*Barbus barbus*) see? The effect of the whole-genome duplication on vision

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Teleosts outstand among vertebrates in the number of visual pigments and photoreceptor types. Such extraordinary repertoire has evolved also thanks to the whole-genome duplication that occurred in their ancestor, approximately 350 million years ago. Here we explore teleost fish species that has recently experienced subsequent whole-genome duplication - the common barbel (*Barbus barbus*). We focus on the effect of tetraploidy on the visual system. We found 13 opsin genes in the common barbel genome – an unusually high number. We further investigate opsin gene expression to test if multiple opsin genes in the genome result in different visual system function. We present opsin expression profiles of adult specimens and larvae at different developmental stages and we have identified ontogenetic shifts specific for barbel, as well as shared among teleost fishes. Both copies of the opsin genes resulting from the barbel-specific whole-genome duplication are expressed in the retina, and for some opsins (SWS1, SWS2, RH2) we found alternative gene expression of the two copies during development. We also visualize opsin expression in adult retinae via fluorescence in situ hybridization to reveal the retinal cone mosaic and we discuss its functional consequences.

Abstract ID: 2366
Poster board number:
P417

Predictions from Fisher's geometric model on the effect of polyploidy on heterosis

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Polyploidization is thought to play an important role in the evolutionary history of many lineages, as well as in agricultural breeding practices. One reason for this is that polyploidization and crossing of polyploid lineages can give rise to heterosis. Birchler (2013) reviewed the available data and identified various ‘genetic rules’ of heterosis, concluding that no single model could account for all of the patterns observed. Here I will present a fitness landscape model predicting the fitness of hybrids between divergent

lines of arbitrary ploidy. We explore the effects of allopolyploidy on patterns of heterosis and compare these to the observations outlined by Birchler including the interplay between ploidy and genomic dosage, allelic diversity and homozygosity and their roles in heterosis.

Symposium: S26. The biological meaning of SNPs (id: 943)

Abstract ID: 1772
Poster board number:
P418

A pipeline for SNP genotyping in non-model species with various DNA sources and sequencing platforms

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Biodiversity research and monitoring of non-model, threatened and/or cryptic animals often rely on low-quality non-invasive genetic samples. Single Nucleotide Polymorphisms (SNP) are numerous, spread throughout the genome and can be amplified in short fragments, making them suitable for genotyping from low quality DNA. Many developing countries - which harbour the majority of the world's biodiversity - face grave resource limitations and a lack of access to affordable sequencing services. *In situ* conservation genomics can empower local researchers and needs. To do so, however, accessible and reproducible sequencing and genotyping alternatives are needed. We present a pipeline to develop a field-friendly genotyping approach for two species of Amazonian primates using both high and low quality DNA samples, and two different sequencing platforms, Illumina and Nanopore. We used 14 high-quality Illumina sequenced genomes to construct a set of 302 SNPs that allow for identification of species (20 SNPs), sex (18 SNPs) and individual identity (266 SNPs). Half of the SNPs used for individual identification are species-specific, the rest is shared between species - suitable in situations where species identity is difficult to discern based on the sample. Primers, adapters and indexes were designed in a Genotyping-in-Thousands by sequencing approach that is compatible with both sequencing platforms. This approach is based on sequencing multiplexed PCR products of a few hundred target SNPs to genotype thousands of individuals in a single sequencing run. In an effort to make conservation genomics more accessible, the reproducible pipeline to obtain the informative SNPs was modulated with Snakemake.

Abstract ID: 2232
Poster board number:
P419

Genome-wide SNPs reveals distinct population structuren the holoplanktonic snail *Limacina bulimoides*

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Many studies on population genomics have focused on terrestrial organisms. However, the seascape is a vast, interconnected three-dimensional habitat, which presents challenges for understanding the drivers of biodiversity in the open ocean. This is especially pressing given the threats of ocean warming, acidification and deoxygenation facing marine systems. We studied the distribution of genetic variation in the holoplanktonic pteropod *Limacina bulimoides* to gain insight into their population structure and adaptive potential. This species is found in (sub)tropical oceans globally, and is susceptible to ocean acidification due to their thin aragonitic shell. We developed a genome-wide target capture approach for 2,900 coding regions based on a draft transcriptome and genome of this non-model species. Based on the resulting 100,000 SNPs, we found that *L. bulimoides* is split into three populations within the Atlantic Ocean: North, Equatorial, and South, with two narrow dispersal barriers at 14-15°N and 15-18°S that coincide with regions of low abundance for this species. Despite the potential for basin-scale dispersal, physical connectivity modelling with particle release at sampling stations and subsequent tracking shows that limited mixing of populations is possible only at boundary regions within their estimated generation time of one year. To determine the nature of the dispersal barriers, we genotyped a comprehensive dataset of juveniles and adults found in the boundary regions. Selection, in addition to oceanography, are the likely drivers of divergence in this oceanic species, with functional variants identified across outlier loci in coding regions among the three populations.

Symposium: S27. Tandem repeats: their role in molecular evolution and methods (id: 33)

Abstract ID: 2088
Poster board number:
P420

Evolutionary dynamics of transposible elements in the poison frog *Dendrobates tinctorius*

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Poison frogs (Dendrobatidae) are used as evolutionary models to study predator-prey interactions, mimicry, mate-choice, and cognition. Recently, expression studies have identified genes associated with poison frog's colour patterning and parental behaviours; however, further genetic work has been hindered by a lack of genomic resources, likely due to the large and highly repetitive nature of Dendrobatid genomes. Here we use Pacific Bioscience HiFi reads to generate a high-quality genome assembly for the poison frog *Dendrobates tinctorius*. Using multiple annotation pipelines, we find that expansions of different transposable elements (TEs) have contributed to the evolution of the 6.5 Gbp genome of this species, with long terminal repeat (LTR) retroelements from the *Gypsy* class being particularly abundant. To gain insights into the dynamics of LTR evolution, we estimated insertion times by comparing substitution rates between left and right LTRs of individual LTR retroelements. Finally, we identify genes involved in adaptive colour polymorphism in this species using RNA-seq data, and explore whether TE insertion could have contributed to the evolution of this adaptive trait. Our results increase our understanding of the evolutionary dynamics of TEs in large vertebrate genomes and their role in contributing to adaptive genetic variation.

Abstract ID: 2295
Poster board number:
P422

Tandem repeats composing centromere, telomere and rDNA chromosome regions in the zebra finch

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Some chromosome regions (telomere, centromere, nucleolus organizer region) can be identified undoubtedly under a conventional microscope and therefore they are the first to be characterized during cytogenetic karyotyping of any object. Due to their heterochromatic nature and enrichment in repetitive DNA, they are the last to be deciphered during genome sequencing and assembly, being the subject of targeted analysis. Recently we specified the list of tandem repeats in zebra finch *Taeniopygia guttata*, a demanded model species in neurobiology and comparative genomics, and found *Tgut191A* and *Tgut716A* to be the major component of centromere regions. When high resolution FISH was performed on meiotic lampbrush chromosomes, we observed both repeats in the telomeric regions of microchromosomes as well as the Z and W sex chromosomes. To characterise the composition of ribosomal DNA in zebra finch we assembled and described the complete structure of the ~18 kb rRNA repeat including an intergenic spacer. 5S rRNA genes are found forming three main clusters on chromosomes 2, 4, and 9. 5S rRNA gene sequences on chromosomes 2 and 4 differ from those on chromosome 9 by 5%, and the intergenic spacers differ by more than 60%. It is unclear whether the variability of 5S rRNA sequences plays any functional role or whether there is any evolutionary significance of the phenomenon, but nothing similar has been found in the genomes of other birds.

Symposium: S28. Beyond transcription: the role of post-transcriptional gene regulation in adaptation and evolution (id: 945)

Abstract ID: 1161
Poster board number:
P424

The probability of smithRNAs: mitochondria can easily get involved in nuclear regulation

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In recent years it has been shown that short non-coding RNAs (sncRNAs) are involved in mitochondrion-to-nucleus communication, which is known as retrograde signaling. These elements were termed “small mitochondrial highly expressed RNAs” (smithRNAs) and were originally found in the Manila clam *Ruditapes philippinarum*; original *in silico* predictions have subsequently been confirmed by *in vivo* experiments. The key feature of smithRNAs is their combination of transcription loci and sources of target mRNAs: small RNAs were known from animal and plant mitochondria, but they have always been associated with mitochondrial targets. Notably, smithRNAs are transcribed from the mitochondrial genome, but they do regulate nuclear targets instead. How likely are smithRNAs across metazoans? We suggest that, as most sncRNAs, they may well be genetic elements that easily arise *de novo* during evolution. It is known that many such elements became adaptive microRNAs: we address the evolutionary probability of *de novo* evolution of smithRNAs, and, thus, the probability for mitochondria to evolve original and unprecedented (with respect to genetic legacy) ways to regulate and communicate with the nucleus. Moreover, we found clues of the presence of smithRNAs in other animal systems – far from being restricted to bivalves, smithRNAs were suggested to be present in distantly related bilaterian and we present broader evidence of smithRNAs encoded in species scattered throughout the metazoan evolutionary tree.

Abstract ID: 1414
Poster board number:
P425

Alternative splicing plasticity constrains genetic diversity and the potential for adaptation

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Plasticity is accomplished via tightly regulated developmental cascades that translate environmental cues into trait changes. While differential gene expression is a familiar component of this cascade, relatively little is known about how alternative splicing and other posttranscriptional molecular mechanisms contribute to plasticity or how these

mechanisms impact how plasticity evolves. We used transcriptomic data from two cases of seasonal plasticity (seasonal polyphenism in *Bicyclus anynana* and facultative diapause in *Pieris napi*) to compare the extent of differential splicing and expression between plastic phenotypes. We consistently found that differential splicing affects a smaller but functionally unique set of genes compared to differential expression. Further, using individual and pooled genomic data from wild populations, we found strong support for the novel hypothesis that spliced genes are highly susceptible to erosion of genetic variation, which we attribute to strong selection to maintain seasonally plastic phenotypes. Our results suggest that alternatevely spliced genes involved in seasonal plasticity are especially likely to experience genetic constraints that could affect the potential of wild populations to respond to rapidly changing environments.

Abstract ID: 1928
Poster board number:
P426

The biogenesis of mitochondrial short non-coding RNAs: an analysis of CLIP-seq data

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Interactions between organellar and nuclear genomes have played a central role in eukaryote evolution. Mitonulear genomic coadaptation has resulted in a network of regulative processes, which are not fully understood yet. Recently, we found a set of short non-coding RNAs that are transcribed by the mitochondrial genome and are predicted *in silico* to target nuclear transcripts (which we named Small MITochondrial Highly transcribed RNAs, smithRNAs). *In vivo* functionality of some of these smithRNAs has been proved in at least one species (i.e. *Ruditapes philippinarum*, the Manila clam), but their regulatory pathway and maturation are still unclear. In this study, we analyzed publicly available next-generation sequencing libraries of RNA immunoprecipitation (RIP) and cross-linking immunoprecipitation (CLIP) of the Argonaute family proteins and of other related proteins. We wanted to look at mitochondrial short non-coding RNAs that were enriched by co-immunoprecipitation with their interacting proteins. Our data revealed that in *Homo sapiens* and *Mus musculus* mitochondrial tRNA-derived smithRNAs are targets of AGO2, and that in *H. sapiens* of DROSHA and DGCR8 as well. Therefore, our *in silico* analysis predicts that smithRNAs might follow a miRNA-like canonical maturational pathway, at least in mammals. No significant interaction with smithRNAs was detected for ALG-1 and HRDE-1 in *Caenorhabditis elegans* and for PIWI and AGO1 in *Drosophila melanogaster*. However, we are willing to extend the analysis to the other species and other Argonaute proteins to further elucidate the maturational pathway of smithRNAs across Metazoa.

Abstract ID: 2178
Poster board number:
P427

Transcription factors and gene regulation in scent biosynthesis in *Ophrys* orchids

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The genus *Ophrys* is remarkable for its mimicry, whereby flower-lips closely resemble pollinator females in a species-specific manner. Therefore, floral traits associated with pollinator attraction, especially scent, are of special interest for understanding plant speciation and evolution. The Sphegodes-group (S) species *O. incubacea* and Fusca-group (F) species *O. iricolor*, both shift to the same pollinator. Preliminary data suggest that they have a comparable hydrocarbon profile in their scent, which is mainly composed of alkanes and alkenes. Genes encoding stearoyl-acyl carrier protein desaturases (SAD) involved in alkene biosynthesis have been identified in the S group. However, there is no information on the identity of functional homologs in the F group. This study aims to investigate the control and parallel evolution of ecologically significant alkene production in *Ophrys*. This is done by analyzing SAD and other very-long-chain fatty acid biosynthetic genes and their control using molecular biology techniques and in silico approaches. Owing to the central role those SAD genes play in determining positioning of alkene double-bonds, a detailed understanding of their functional mechanism and of regulatory aspects is of utmost importance. In order to understand, if the same genetic program has been repeatedly co-opted in evolution to carry out the same function, it is therefore essential to characterize the SAD alleles present in the F group. Here, we identified 5 transcription factors related to SAD in *O. Sphegodes*: MYB, DEF, GTE1, WRKY, and MADS. Ultimately, our results will contribute to understanding genes important in the regulatory control of floral scent synthesis.

Abstract ID: 2181
Poster board number:
P428

Interrogating the function of the avian germline-restricted chromosome through isoform analysis

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Studying gene expression in a complex evolutionary system can unveil mechanistic insight to its multifaceted regulation. The avian germline-restricted chromosome (GRC) is an odd case of programmed DNA elimination in early embryogenesis with an unresolved evolutionary history and a presence in more than half of all bird species. In essence, the GRC contains multi-copy paralogs from the “regular” chromosomes (A chromosomes) and is enriched in embryonic and gonad developmental genes, yet it remains poorly understood which of these genes are functional. Here, we utilized long-read and short-read transcriptomes to explore isoform variation between A-chromosomal and GRC-linked paralogs. The formation of identical gene copies can result in different fates for the amplified genes. The amplified copies may lose their function through pseudogenization, may partially preserve their function (subfunctionalization) or acquire a novel function (neofunctionalization). Unraveling the mechanisms acting on the preservation of the GRC-linked paralogs could be critical for understanding the impact of this chromosome on the complexity and diversification of songbirds. In this regard, we explored alternative

spliced variants of the GRC paralogs that might prevail in the germline, suggesting their subfunctionalization. Moreover, we found a higher expression of GRC-linked genes in ovaries compared to testes and also identified sex-biased isoform usage. Taken together, although the evolution of GRC remains rather mysterious, its spread in all songbirds indicates a potential cooption for a so far cryptic role, which we here investigated within the scope of post-transcriptional regulation.

Symposium: S29. Comparative genomics: a powerful tool for exploring broad evolutionary questions (id: 947)

Abstract ID: 1089
Poster board number:
P429

Finding genome-specific differences between pairs of genomes

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Differences between genomes have attracted research interest since the first genome sequences became available. However, it remains difficult to home in on functional genome-specific regions through sequence comparison alone. Prior work on individual genomes suggests that differences in high-complexity regions might be of particular interest. We are therefore developing a method for finding genome-specific high-complexity regions in mammalian genomes.
Our starting point is a method for quickly finding unique regions among samples of bacterial genomes. We iterate this method to make it applicable to pairs of mammalian genomes. Briefly, we extract from each of the two genomes the high-complexity regions not found in the other. Then we look up the genes whose promoters intersect these regions, which we subjected to enrichment analysis.
We have applied this approach to the genome of *Mus musculus* on the background of *M. spretus* and found 3.0 Mb high-complexity regions present in *M. musculus* but absent from *M.spretus*. The corresponding gene list contained 415 genes, which fell into 115 GO categories. These were enriched ($P < 10^4$) for anatomical structure morphogenesis, pattern specification and cell development. This enrichment for genome-specific function in the *M. musculus* genome agrees with the previous observation of enrichment of developmental genes in the full high-complexity moiety. We are currently carrying out the reciprocal analysis of the M.spretus genome.

Abstract ID: 1220
Poster board number:
P430

Characterising the genome of the spiny dogfish (*Squalus acanthias*)

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The third wave of novel sequencing techniques has taken over, yet shark genomes remain notoriously understudied. So far only eight Selachii genomes have been sequenced for currently 600 described species, mostly due to their large complex genomes. However, sharks are not only important contributors to the marine environment on multiple trophic levels, but are also set to play an increasingly important role in genomic research as the predecessors of bony fish. Therefore, greater efforts are needed to close this knowledge gap. Here, we present the ninth shark genome ever published, that of the spiny dogfish, *Squalus acanthias*. We employed third-generation sequencing, as well as evidence-based annotation, to assemble and annotate the 3.7 Gb genome. The resulting assembly is largely contiguous, complete and accurate (N50: 10.7 Mb, 91.0 % complete BUSCO, QV: 38.1). Furthermore, orthology-based functional annotation allowed the first insights into the evolutionary dynamics of the spiny dogfish genome. With this new genomic resource, we lay the groundwork for greatly facilitated research, and enhanced conservation management of this vulnerable species. Furthermore, we expect to significantly aid genomic research on sharks in general, by expanding the genomic representation from three to four of their nine orders.

Abstract ID: 1244
Poster board number:
P431

Evodictor: Prediction of prokaryotic gene gain/loss evolution

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Diverse organisms change their genomes during evolution, and prediction of those changes is a long-standing problem. While recent laboratory-evolution studies showed predictability of short-term and sequence-level evolution, that of long-term and system-level evolution has not been systematically examined. Here, we present a machine learning framework, Evodictor, that predicts gene gain/loss probabilities from a current gene content. To evaluate predictability of prokaryotic metabolic system evolution, we first reconstructed gene contents of ancestors based on that of ~3,000 bacterial species. Then, we assessed the gene gain/loss predictability at each branch in the phylogenetic tree using Evodictor. Cross-validation showed that gene gain and loss evolution were overall predictable, suggesting evolutionary pressures and constraints on metabolic systems are universally shared. Investigation of pathway architectures and metagenomic datasets confirmed that those evolutionary patterns have solid physiological and ecological bases such as functional dependencies among metabolic reactions and bacterial habitat changes. We further predicted archaeal gene gain/loss by Evodictor trained with the bacterial genome evolution and revealed gain and loss of >300 genes are predictable, suggesting evolutionary rules shared between different domains of life. Finally, we predicted future gene gain/loss for every extant species, applying Evodictor to antibiotic resistance genes as well as metabolic genes. Pangenomic analysis of intra-species gene-content variations demonstrated that even “ongoing” evolution in extant bacterial species is predictable by Evodictor. This study gives us insights into evolutionary rules of biological systems and clues for rational engineering of metabolic pathways and strategic control of drug resistance evolution.

Abstract ID: 1257
Poster board number:
P432

Exploring drivers of adaptive radiation using a comparative genomics framework

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Evolutionary radiations comprise much of Earth's biodiversity, however their intrinsic molecular drivers and their relative importance remain largely unknown. Recent work has indicated that highly dynamic genomes may play an important role in providing the necessary genetic variation for radiations. Using a comparative genomics framework, we investigate the role of genomic variation on different scales, such as rearrangements, gene duplication, adaptive sequence evolution and regulation, as drivers of differentiation between species of a radiating clade in *Tillandsia.* This group consists of more than 300 Central American, neotropical bromeliad plants that diverged 2-3 mya. Numerous adaptive traits segregate in this clade, among which we find multiple shifts in photosynthetic pathway (C3 vs. CAM). We report high-quality assembled genomes of two *Tillandsia* species which display different photosynthetic strategies (CAM vs. C3). We identify several events of chromosomal fusion and other large-scale rearrangements, TE dynamics driving changes in spatial gene distribution and gene family evolution, especially in the CAM lineage. We also used an RNA-seq experiment to identify differentially expressed genes between species across timepoints. This revealed several genes putatively involved in CAM photosynthesis. Additionally, differentially expressed genes are enriched for gene families with increased duplication in the CAM lineage and for intronic TE insertions. Lastly, we detect candidate genes with signals of adaptive sequence evolution, among which some are pleiotropic transcription factors. Our findings show that differentiation in the *Tillandsia* radiation occurred on many genomic levels, from large-scale rearrangements to gene family dynamics, to expression changes in single genes.

Abstract ID: 1271
Poster board number:
P433

Domestication of different varieties in the cheese-making fungus Geotrichum candidum

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Keywords: domestication, adaptive divergence, proteolysis, genomics, volatiles, laboratory experiments, *Galactomyces candidus*

Domestication is an excellent model for studying adaptation processes, constituting recent adaptation and diversification, as well as degeneration of unused functions. *Geotrichum candidum* is a fungus used for cheese making and is also found in other environments such as soil, wastewater and plants. By analyzing whole genome data from 98 strains, we found that all strains isolated from cheese formed a monophyletic clade. Within the cheese clade, we identified three differentiated populations and we detected footprints of recombination and hybridization. The genetic diversity in the cheese clade was the lowest but remained high compared to other domesticated fungi, suggesting milder bottlenecks. Commercial starter strains were scattered across the cheese clade, not constituting a single clonal lineage. The cheese clade was phenotypically differentiated from other populations, with a slower growth on all media even cheese, a reduced production of volatiles but a prominence of attractive cheese flavors and a lower proteolytic activity. Furthermore, cheese populations displayed contrasted phenotypes, with one cheese population displaying a blue cheese flavor (2-heptanone), and another one producing denser and fluffier colonies, excluding more efficiently spoilers.
Our findings suggest the existence of genuine domestication in *G. candidum*, which led to diversification into three varieties with contrasted phenotypes. Some of the traits acquired by cheese strains indicate convergence with other, distantly related fungi used for cheese maturation.

Abstract ID: 1276
Poster board number:
P434

Closely related *Tephritis* flies (Diptera: Tephritidae) have closely related host plants

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The interactions between insects and plants have rendered them among the most species rich eukaryotic species groups, making them an excellent system for studying processes driving diversification. The *Tephritis* peacock flies (160 described species) are one genus that has diversified following specialisation on different plant taxa in the family Asteraceae. The variation in the degree of specialisation within *Tephritis* makes the genus a great system for understanding how species colonise novel hosts, and the consequences of this process for diversification. However, to truly understand the diversification a solid understanding of the phylogeny of both the flies and the host plant taxa is needed. Here, we present the first well-supported molecular phylogeny of the genus *Tephritis* based on whole genome shotgun sequencing. The results suggest that there is a clear phylogenetic component to host use, as more closely related *Tephritis* species tend to have more closely related host plants. Interestingly, my

findings offer some support to the oscillation hypothesis, stating that repeated cycles of specialisation and generalisation can be important drivers of diversification.

Abstract ID: 1343
Poster board number:
P435

Signatures of balancing selection in genes associated with facial variation across great apes.

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We share >97% of our DNA and a large amount of homologous anatomy with our closest living relatives, the great apes. Despite this high level of similarity, the great ape face is a diverse phenotype between and within species. Our understanding of the evolutionary pressures that generate this diversity is limited, although previous studies have suggested that balancing selection could maintain facial diversity. GWAS have identified SNPs associated with facial morphology in humans, allowing us to test this interesting hypothesis using population genomics data. Specifically, we investigate, across all the great apes, the signatures of balancing selection in 155 genes that contain 155 SNPs associated with facial morphology in humans from GWAS studies. Using the non-central deviation (NCD) statistic, a neutrality test that measures allele frequency deviation from an expected target equilibrium frequency, we calculated genome-wide values in 1.5kb windows. We did not detect an excess of face genes with signatures of balancing selection, suggesting that balancing selection does not contribute to the evolution of face morphology in excess of expectations given the prevalence of balancing selection in the great ape genome. Still, ten genes display strong signatures of balancing selection in at least one great ape population. Of these, five genes showed strong signatures of balancing selection in multiple populations. Strikingly, this suggests that natural selection maintains polymorphisms contributing to facial morphology in several species.

Abstract ID: 1381
Poster board number:
P436

Revealing functional and genomic differences between two species of the megadiverse genus Begonia

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Begonia is one of the most diverse Angiosperm genera, with over 2000 described species. The wide morphological and ecological range in the genus makes it a good model for studying the generation and maintenance of diversity. We use transcriptomics to compare two closely related but morphologically and ecologically divergent species, *Begonia conchifolia* and *B. plebeja* to identify functional categories putatively involved in ecological divergence. Asking what genetic pathways showed species specific patterns of divergence, we used differential expression and gene ontology enrichment analyses to show species specific enrichment of light regulated functions in *B. plebeja*. Additionally, enrichment of ethylene and jasmonate pathways in *B.*

plebeja suggests an increased shade avoidance response, suggesting light availability may be a key factor in the divergent adaptation of *B. conchifolia* and *B. plebeja*. We further investigated the anthocyanin biosynthetic gene Chalcone Synthase (CHS) based on its previously reported importance in maximising the use of variable light levels. Results showed the CHS gene family has high duplicate turnover, all members of CHS identified in *Begonia* arising since the divergence of *Begonia* from cucumber, a close relative in the Cucurbitaceae. Sequence, expression and phylogenetic analysis showed evidence of pseudogenisation, lineage specific duplications, and relaxed selective constraints, showing that species specific differences have accumulated since the divergence of *Begonia conchifolia* and *B. plebeja*, and suggesting gene duplication may be a key mechanism for diversification in *Begonia*. While further investigation is needed, our work suggests genomic processes and ecological heterogeneity contribute to the high speciation rate in *Begonia*.

Abstract ID: 1496
Poster board number:
P437

The primordial MHC: insights from Cartilaginous fish genomes and comparative genomics

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The vertebrate adaptive immune system (AIS) is a complex system of molecules and cells that offer highly specific, fast responses against a wide array of pathogens. Despite its important function, the origin and evolution of the AIS is far from understood but is intimately tied to the evolution of Major Histocompatibility Complex (MHC) genes. These genes are essential in adaptive immune responses being responsible for antigen presentation to T cells. Here we provide the first comprehensive view of MHC genes and genomic region in Cartilaginous fish, the most basal jawed vertebrates to possess an AIS. We further compare the MHC genomic architectures across jawed vertebrates to gain insights into the primordial and derived features of the MHC. Notably, we found all classical and non-classical class I and II genes in the MHC of sharks (except W-type molecules), suggesting an MHC inception after the second round (2R) of whole genome duplication. The presence a “class I region” showing tight linkage among Class Ia/TAP1-2/PSMB8-9, adjacent to a “class II region” of alpha and beta genes was found in Cartilaginous fish and in basal ray-finned and lobe-finned fishes, implying the existence of a compact MHC gene cluster in the jawed vertebrate ancestor. Primitive synteny of classI/II genes and b2microglobulin, the required L chain for class I proteins, is also supported by cartilaginous fish and coelacanth genomes. These results challenge previous claims of MHC inception pre-2R and show co-location of classI/II/b2m and antigen-processing genes early in MHC evolution.

Abstract ID: 1523
Poster board number:

P438

Changes in immunological genes to explain intraspecie and interspecie parrot's evolution

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The evolutionary emergence of vertebrates was accompanied by a sudden change in the structure and function of the ancient metazoan immune system. Immune system is the functional cooperation of innate and adaptive cell types to orchestrate effective immune responses. It is known that dynamics of host–pathogen coevolution is due to pro-inflammatory and inflammatory processes, these cause changes in the immunological genes. Until now, only a few parrot's genomes have been sequenced and annotated, even so, and number of studies providing insights into the behavioural similarities between humans and parrots to understand mechanisms of the evolution of cognitive abilities. Also, a better understanding of parrot's immune systems evolution promises to lead to the development of new strategies for medical interventions targeting the consequences of faulty immune functions and mental disorder. Here, we have designed degenerated primers, and we have sequenced nine immunological genes for different parrot's species by Sanger. Intraspecie and interspecies genome features have been described, and these results have been compared with the phylogenetic analysis already published

Abstract ID: 1527
Poster board number:
P439

Museomics versus the taxonomic gap: a type-specimen explicit protocol to resolve cophyline phylogeny

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Narrow-mouthed frogs (Cophylinae) currently comprise 115 described species that are found exclusively on Madagascar. Most of them have been described rather recently, when the completion of the inventory of DNA barcodes of Madagascar's frogs revealed a considerable taxonomic underestimation of cophyline biodiversity. However, many species are still awaiting description, including species currently blocked by unresolved species complexes and uncertain affiliation of taxonomic names. Genetic data from type specimens thus represents a valuable source of information for the resolution of taxonomic groups, as removing ambiguity from their identity would allow for the unambiguous allocation of taxonomic names. However, sequencing genetic markers from archival samples proves to be challenging due to postmortem DNA damage and preservation techniques used.

We aim to overcome these taxonomic impediments by using a state-of-the-art hybrid-enrichment sequencing method: FrogCap. FrogCap is a recently released bait set for frogs targeting about 13,000 nuclear markers, which will be applied to fresh material from all available species. Subsequently, a newly developed bait set, called MuseoFrogCap, will be used on type material. Low-coverage shotgun sequencing has shown that extractions were successful and already suffices for some preliminary conclusions for most museomic specimens. Once sequences are available from modern and museomic material, we will be able to integrate them in both phylogenomic and species delimitation approaches. This is the first part of our newly established type-specimen explicit protocol for integrative species delimitation, which will allow us to eventually resolve cophyline phylogeny, and which hopefully will serve as a model for other taxonomic studies.

Abstract ID: 1564
Poster board number:
P440

Identifying the genomic basis of the ecological transition to life out of sea in molluscs

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The expansion of the ecological niche of animals out of marine environments constitutes one of the most dramatic ecological and evolutionary events in Earth's history. Noticeably, this transition occurred repeatedly across numerous animal lineages, providing the opportunity to study the genomic underpinnings of such convergent adaptive processes. Here we performed a comparative genomic analysis of the Mollusca radiation, a highly diverse group of invertebrates, to explore lineage-specific genomic changes associated with transitions to life in non-marine environments. To do so, we de novo assembled high-quality transcriptomic and genomic data from 107 species, encompassing all major molluscan clades (i.e. orders) and several evolutionary independent transitions out of marine environments. We identified and reconstructed the evolutionary dynamics of gene families along the phylogeny of the phylum, and estimated gene gain and loss rates across these gene families. We identified several gene families with significantly elevated rates of change in size in lineages where transitions to life out of the sea have occurred. Moreover, through selection analyses, we further identified genes with footprints of positive selection associated with this ecological transition. Finally, we explored putative functions of these genetic elements through Gene Ontology enrichment analyses. Here we present, explore and discuss the potential functional and adaptive significance of these findings. Our results set the road towards understanding the genomic underpinnings of transitions out of marine environments at a deeper level.

Abstract ID: 1566
Poster board number:
P441

Chromosome rearrangements and evolutionary diversification of duplicated genomes

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Chromosome rearrangements (CRs) are known to promote the reduction of genome size and chromosome numbers (i.e, diploidization) in plants undergoing recurrent whole-genome duplications. Such phenomenon appears decisive for the evolutionary diversification of plants, however the genomic basis of chromosomal restructuring remains underexplored.
In our study, we combine cutting-edge sequencing technologies (Oxford Nanopore, PacBio Iso-Seq and Hi-C) to build, annotate, and compare near chromosome-scale genome assemblies of closely related *Biscutella* species. These plant species diversified independently following a whole genome duplication event and colonized different environmental niches, making the *Biscutella* genus a unique system for understanding the impact of diploidization on plant adaptation in natural populations.
The availability of chromosome-scale genome assemblies is crucial for investigating structural variation. However, the complexity of large and repetitive plant genomes often hinders such analyses, and it is crucial to provide guidelines for the assembly and annotation of high-quality genomes. Furthermore, we shed light on the molecular mechanisms underlying CRs (with a special focus on transposable elements, TEs) and their impact on genome divergence. Through comparative genomics, we quantify the impact of different restructuring events. We assess molecular processes that alter genome size and content, and determine to what extent different types of restructuring events affect the gene space vs the TE fraction during diploidization and species diversification.

Abstract ID: 1571
Poster board number:
P442

The evolution of mutualistic dependence – a case study using a diverse ant/plant symbiotic system

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Mutualistic dependence – the level of fitness lost when a mutualist partner is removed – is poorly understood compared to other aspects of mutualism. Specifically, why do some species become highly dependent whereas some species remain independent? The ant genus *Philidris* (Dolichoderinae) provides an ideal system to investigate this question as it forms a wide spectrum symbioses with epiphytic plants. One species (*Philidris nagasau*) engages in plant agriculture, obligately depending upon plants for nesting space due to having lost the ability to build their own nests; several species of *Philidris* engage in facultative mutualisms with plants, benefiting from additional nesting space in the form of plant-made structures for ant nesting called domatia but retaining the ability to build their own carton nests and others do not engage in any mutualism with plants. During my PhD I aim to investigate how differences in mutualist strategy affect genome evolution. Specifically, I will compare gene family expansion and contraction, as well as host fast they evolve in obligate mutualists, facultative mutualists and non-mutualists. I will also investigate genes relating to the evolution of agriculture, with some candidate areas are genes relating to olfactory receptors, the nervous system and aggression as well as investigating potential genes losses. My work will thus illuminate the evolution of mutualistic dependence, showcasing an iconic example of ant agriculture.

Abstract ID: 1614
Poster board number:
P443

MicroRNA expansion in cephalopods and the evolution of the complex nervous system

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Coleoid cephalopods (squids, cuttlefishes, and octopuses) possess one of the most elaborate nervous systems among invertebrates. These animals employ extensive A-to-I RNA editing to re-code mRNAs in their nervous systems, but knowledge about non-coding RNAs in cephalopods is scarce. We thus profiled mRNAs and small RNAs in 18 tissues of the common octopus (*O. vulgaris*). We show that the major RNA innovation of coleoid lineage is a massive expansion of the miRNA gene repertoire comparable in magnitude only to that of vertebrates. Evolutionary novel miRNAs were primarily expressed in neuronal tissues, during development, and have conserved and thus likely functional target sites. Coleoid cephalopods set a new record of miRNAome diversity for invertebrates, raising the possibility that miRNAs are key components for shaping the complexity of animal brains.

Abstract ID: 1636
Poster board number:
P444

Characterization of the genetic basis of resistance to (bio)pesticides in *Cydia pomonella* (L.)

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The codling moth, Cydia pomonella, is a major pest of apple and pear orchards worldwide. Despite the development of alternative control methods and biopesticides, the use of chemical insecticides remains the most used control method in conventional agriculture. However, an increasing number of resistant phenotypes related to this use are emerging. In this context, the main objective of this study is the identification of genetic markers associated with resistance to different (bio)pesticides in C. pomonella to allow fast and high-throughput molecular detection of resistances in natural populations.
An artificial evolution experiment was conducted on a multi-resistant population in order to segregate the alleles associated with resistance to 3 pesticides: spinosad, deltamethrin and chlorantraniliprole. Three different lines were obtained by exercising

different selection pressures with the three active substances of interest. Then, RNA and DNA pool-sequencing of the resulting lines were made, in order to identify the genetic variations associated with the resistant phenotypes.
Through RNA sequencing, we identified candidate genes within each selected line whose expression profile was associated with insecticide resistance, among which genes known to be involved in detoxification pathways. Variant calling on transcript and whole-genome sequencing data, as well as GWAS between resistant and susceptible lines, also allowed us to link polymorphisms in coding and non-coding regions with resistance, providing candidate markers to track resistance.
These results contribute to a better understanding of the complex mechanisms associated with insecticide resistance and provide a basis for the development of new resistance detection tools, based on genomic approaches.

Abstract ID: 1646
Poster board number:
P445

Genome-scale reconstructions of *Wolbachia* to elucidate horizontal transfer in Lepidoptera

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Wolbachia is one of the most widespread intracellular bacteria worldwide, estimated to infect over half of all arthropod species. *Wolbachia* is primarily transmitted vertically, from mother to offspring. However, phylogenetic incongruences between the trees of host species and their *Wolbachia* strains suggest that horizontal transfer of the symbiont from one species to another is common in arthropods. For such transfer to occur, intimate interactions between the donor and recipient hosts are supposedly required.
Lepidoptera is one of the four most diverse insect orders. They include economically and ecologically important species on all continents (except Antarctica) and key members of complex species communities. The numerous associations with diverse organisms and the high incidence of *Wolbachia* infections make Lepidoptera a good system for investigating the interspecific transfer of the endosymbiont, however, the magnitude of this phenomenon in the order remains to be determined.
Here we present a comprehensive screening of over 6,000 publicly available DNA sequencing samples from lepidopteran hosts, from which we assembled over 100 partial *Wolbachia* genomes, significantly expanding the number of *Wolbachia* genomes isolated in Lepidoptera. The resulting *Wolbachia* phylogenetic reconstructions revealed novel strains and supported several horizontal transfer events between both distantly and closely related host species, further confirming the complex transmission dynamics of *Wolbachia* across Lepidoptera in particular, and insects in general.

Abstract ID: 1671
Poster board number:
P446

Towards a better understanding of Lepidoptera phylogeny

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Butterflies and moths comprise together the order Lepidoptera, the second largest group of macroscopic organisms on Earth. It is relevant to study their phylogeny for many reasons including their vital ecological roles as pollinators, food source and pests. There have been several phylogenetic/phylogenomic studies focusing on Lepidoptera with datasets of varying size, with respect to both taxon sampling and alignment length. However, one common theme to all of these studies is that there are ambiguities in the backbone of the tree: major clades can jump to seemingly unexpected places within the tree depending on the nature of the data used. Whether these conflicts arise from insufficient taxon sampling, the limitations of current inference methods in the age of large-scale genomic data, or the convoluted patterns of evolution inherent to the data at hand remains to be investigated. This work aims to arrive at a reliable backbone phylogenetic hypothesis using data from thousands of single-copy orthologous genes across the whole order and to identify sources of aforementioned conflicts. Studying these conflicts will not only help resolving the phylogeny, but also hopefully yield highly useful and generalizable methodological information regarding phylogenetic best practices in taxon sampling, dataset generation and alternative inference methods, with the side benefit of having a core set of alignments from thousands of genes across more than 350 taxa. The aim is to develop an autonomous pipeline for new data to be integrated into the existing alignments and in turn having a self-improving phylogeny as new data emerge.

Abstract ID: 1672
Poster board number:
P447

Speciation without gene-flow in hybridizing deer

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Hybridisation in nature can be viewed as part of the continuum of speciation. Under the ecological speciation model, divergent selection acts on ecological differences between populations, gradually creating barriers to gene flow and ultimately leading to reproductive isolation. Here, we use white-tailed (*Odocoileus virginianus*) and mule deer (*O. hemionus*) to investigate patterns of speciation in hybridising sister species. We quantified genome-wide introgression and performed genome scans to look for signs of four different evolutionary scenarios. We found no sign of introgression, no signature of divergence with gene flow and restricted patterns of allopatric speciation. The absence of introgression signs could suggest Dobzhansky-Muller incompatibilities and selection against hybrids which would contribute to the reinforcement of reproductive isolation. The deficiency of patterns of allopatry suggests that white-tailed and mule deer were spatially separated during the glaciation cycles of the Pleistocene where genome wide differentiation accrued via drift, both species are now far along the speciation continuum. The major evolutionary pattern in the genome was balancing selection related to immunity and MHC or sensory perception of smell, the latter of which is consistent with deer biology. Our results suggests that WTD & MD do not conform to a speciation with gene flow scenario, but that they evolved via drift in allopatry during the Quaternary and that both species are currently advanced along the speciation continuum.

Abstract ID: 1677
Poster board number:
P448

Multiple expansion and contraction events in two major chemosensory gene families in aphids

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Olfaction and taste (chemosensation) play a crucial role in the interactions between phytophagous insects and their hosts. Phytophagous insects recognize the plants' chemical cues through the activation of specific proteins that are encoded by multigene families. For instance, the odorant receptors (ORs) and gustatory receptors (GRs) play a key role in aphid chemoreception. Here, we have reconstructed the evolutionary history of OR and GR genes for 12 aphid species and one aphid-like species, to understand the processes underlying the diversification of these two major gene families. We assembled a high-quality genome of the major apple aphid pest, *Dysaphis plantaginea,* and retrieved genomes of 11 aphids and one aphid-like species with contrasting geographical distributions, ecological preferences, and host specificities. The genome assembly was of high quality (486 Mb, N50=17.7 Mb, 96% of conserved Hemipteran genes based on BUSCO analysis). Using annotator tools and manual curation, we annotated 40 OR and 23 GR genes in *D. plantaginea* and detected a variable number of chemosensory receptor genes in the other aphid species. We detected a high evolution rate along with expansion and contraction events during the evolution of ORs and GRs in the aphid and aphid-like species. We also identified recurrent signatures of positive selection in OR and GR genes supporting their potential role in adaptation. The high-quality *D. plantaginea* genome and the chemosensory receptor gene annotations provide insight into the mechanisms underlying the adaptation of insects to their host plants and an unprecedented database for studying phytophagous insect evolution.

Abstract ID: 1704

Poster board number:
P449

De novo gene emergence: A large-scale investigation of the enabling mutations

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Genome evolution is driven by the emergence of new genes. Several mechanisms give rise to gene birth, duplication being the most frequent one. In the last couple of years, however, a mechanism, called "de novo" gene birth, has been increasingly described. De novo genes are new genes found to have emerged in genomes from previously non-coding sequences. Since their initial discovery, there has been mounting evidence of their essential functions in some species.
Although the existence of de novo genes is nowadays undoubtable, it remains difficult to evaluate their mechanisms of emergence. In our works, we created a methodology to further understand the emergence mechanisms of de novo genes on a large scale, from seven populations of Drosophila melanogaster.
De novo genes were detected in each population, and our results suggest they exhibit high birth and death rates. We found non-coding homologs to de novo genes, and showed that their emergence was due to different processes. The appearance of open reading frame (ORF) first, followed by a transcription event, seems to be the most widely observed pattern. We describe the putative mutations giving rise to ORF emergence, and also show that transposable element insertions are another important motor in proto-gene emergence. We provide here the missing key to understanding de novo gene birth, and a large-scale demonstration of their emergence from scratch.

Abstract ID: 1775
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P450

Whole-genome duplication boosts parvalbumin gene diversity in teleost fishes

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Parvalbumin is considered a major fish allergen and the parvalbumin gene repertoire in bony fishes are more diverse than in other vertebrates. In our study, we were able to identify the evolutionary history of the parvalbumin genes and provide an evolutionary

reconstruction of the fish parvalbumins using whole genomic and transcriptomic data. Here, we report the molecular evolution of the parvalbumin genes in bony fishes based on 19 whole genomes and 70 transcriptomes. Further, we investigated parvalbumin gene expression in the common carp, a species with 21 (19 unique) parvalbumin genes in its genome and identified two pvalb-α and eight pvalb-β2 copies abundantly expressed in the muscles, while the alternative copies dominate pvalb expression in other tissues (brain, testes, kidney, retina, and thymus). We were also able to assign certain copies to the teleost-specific genome duplication on species with additional whole-genome duplications, such as the common carp (Cyprinus carpio) serving as a comprehensive genomic overview, allowing future studies to target and focus on the functional aspects of parvalbumin, including, for example, allergenicity, and its possible identification and diagnosis.

Abstract ID: 1832
Poster board number:
P451

Convergent decay of the CTCF paralog BORIS in neognathous birds

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BORIS (brother of the regulator of imprinted sites), the paralog of the genome architectural protein CTCF, originated in the ancestor of amniotes (mammals, reptiles, and birds) 318 million years ago (Mya). Its expression is complementary to CTCF and restricted to germline tissue in mammals. By comparative genomics of 59 bird species, we show that birds, in contrast to other amniotes, experience a severe degradation of the BORIS gene. The degradation events are restricted to neognathous birds, specific for the BORIS coding sequence, and occur multiple times independently. They comprise a wide range of molecular decay, from single point mutations to the inactivation of particular zinc fingers, to the almost complete disintegration of the gene. The decay cannot be explained by the action of repetitive elements or other obvious sequence elements within the affected loci. To our knowledge, this is the first description of a presently ongoing, convergent, and specific gene loss. In analogy to the decay of enamelin genes in different orders of placental mammals, we speculate that changes in the life history of neognathous birds render BORIS dispensable in this lineage. More generally, our findings imply that complex evolutionary histories may hide behind the frequent observation of gene loss across organisms.

Abstract ID: 1848
Poster board number:
P452

Comparative genomics & transcriptomics reveal rapid evolution of novel reproductive genes in insects

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Advances in sequencing technologies facilitate ‘omics driven investigations of both microevolutionary processes and macroevolutionary patterns of diversification. Genome-wide sequencing and RNAseq-based transcriptomics elucidate how new genes are born,

how genomes evolve, and how populations diverge. Illumina, a leader in *de novo* transcriptomics, produces high-quality data that trades-off against short reads requiring assembly. In contrast, Oxford Nanopore Technologies (ONT) offer long reads, end-to-end transcripts and isoform-level resolution of genes and expression. However, the uptake of ONT transcriptomics among non-model species is still low due to high error rates, lack of references, and bioinformatics challenges. Here, we implement *de novo* ONT and Illumina transcriptomics pipelines to study the evolution of novel genes in reproductive tissues of non-model insects, the dung beetle *Catharsius molossus* and the dung fly *Sepsis punctum.* Insect reproductive tissues such as accessory glands of male insects are responsible for seminal fluid synthesis, and are hotspots for rapidly evolving genes that play a crucial role in postcopulatory sexual selection and may even mediate diversification. Our results show the birth of scores of completely novel reproductive genes followed by their recruitment for high expression, especially in the accessory glands. Evolutionary analysis suggests that these genes evolve through rapid innovation at the genomic level even among closely related species, and that genomic expansion and contraction can drive divergence of male reproductive traits and their functions. Congruence of results between technologies demonstrates the usefulness of both ONT and Illumina for investigating the origin, evolution, and function of novel phenotypic traits in non-model organisms.

Abstract ID: 1893
Poster board number:
P453

Comparative study of the evolution of human cancer gene duplications across fish

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Comparative studies of cancer-related genes provide novel information about their evolution and function, but also an understanding of cancer as a driving force in biological systems and species life histories. So far these studies have focused on mammals. Here, we provide the first comparative study of cancer-related gene copy number variation in fish. As fish are evolutionarily older and genetically more diverse than mammals, their tumour suppression mechanisms should include most of the mammalian mechanisms, but also reveal novel (but potentially phylogenetically older) previously undetected mechanisms. We have matched the sequenced genomes of 65 fish species from the Ensemble database with the cancer gene information from the COSMIC database. By calculating the number of gene copies across species using the Ensembl CAFE data (providing species trees for gene copy number counts), we developed a novel, less resource demanding method for ortholog identification. Our analysis demonstrates a masked relationship with cancer-related gene copy number variation (CNV) and maximum lifespan in fish species, suggesting that higher tumour suppressor gene CNV lengthens and oncogene CNV shortens lifespan. Based on the correlation between tumour suppressor and oncogene CNV, we show which species have more tumour suppressors in relation to oncogenes. It could be suggested that these species have stronger genetic defences against oncogenic processes. Fish studies could be a largely unexplored treasure trove for understanding the evolution and ecology of cancer, providing novel insights into the study of cancer and tumour suppression, in addition to fish evolution, life-history trade-offs, and ecology.

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P454

Clustered gene orientation bias on Gemmatimonadota chromosomes

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On most bacterial chromosomes, the majority of genes is coded on the leading strand. One explanation for this phenomenon is the reduction of collisions between the DNA and RNA Polymerase complexes which can cause detrimental mutations. The extent of this gene orientation-bias ranges from up to 85% in some Firmicutes to little more than 50% in some Proteobacteria.
The understudied phylum Gemmatimonadota has currently only four closed genomes available that share a remarkable chromosome architecture. While most of the chromosome shows only a modest gene orientation bias, the vast majority of genes in an approx. 600kb region surrounding the putative terminus of replication are coded on the leading strand. They show a consistently high expression level, while expression of genes outside this region is more variable. Remarkably this region is also extremely poor in repetitive elements compared to the rest of the chromosome. The evolutionary pressure to maintain a strong gene orientation bias only on part of the chromosome needs to be clarified.

Abstract ID: 2066
Poster board number:
P455

Comparative genomics identify major shifts in LINE content associated with bivalve diversification

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Transposable elements (TEs) can represent one of the major sources of genomic variations across eukaryotes, providing novel raw material for species diversification and innovations. While considerable effort has been made to study their evolutionary dynamics across vertebrates, arthropods, and plants, molluscs represent a substantially understudied phylum, with few comparative analyses focused only on a small subset of species. Here we adopted an automated TE annotation pipeline to widely characterize TE evolutionary dynamics across 36 molluscan genomes, of which 28 representative bivalve species, as well as three additional annelida. We identified multiple instances of bivalve restricted TE emergence and expansion, identifying important shifts in TE composition coupled with their diversification. Some notable examples are represented by Rolling Circle and Long Interspersed Nuclear Elements (LINEs) elements belonging to the RTE and Jockey superfamilies. Additionally, we adopted an ORF-based extraction and tree-based classification to deeply characterize 93,872 reverse transcriptase-containing LINE loci and to manually curate more than 1,000 putative autonomous families. Our results confirm the bivalve-restricted emergence of RTE-X, CR1-Zenon, and Proto2 lineages, among the others, and provide the first freely available public library of putative autonomous LINE families. Finally, we take advantage of the wide taxon

sampling to decouple the interplay between TE content, TE diversity, and genome size variation. Our results provide further support for a prominent role of TEs in genome size evolution as well as a tendency of LINE-rich genomes to include a smaller proportion of putative active elements than poorer ones, as previously suggested by simulation studies.

Abstract ID: 2118
Poster board number:
P456

Host specialization of the pathogenic fungus Zymoseptoria passerinii in wild and domesticated barley

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Zymoseptoria passerinii causes Septoria Speckled Leaf Blotch (SSLB) disease in domesticated and wild barley species and is a sister species of the prominent wheat pathogen *Zymoseptoria tritici* responsible for the disease Septoria tritici blotch. Although SSLB is a serious but sporadic disease of barley, the broader host range of *Z. passerinii* and the diploid nature of barley make it an excellent model for studying host specialization and septoriasis in cereals. We established *Z. passerinii* as a new pathogen system for barley and analyzed whole-genome sequences of 40 haploid strains: nine from domesticated barley from North America and the remaining from wild grasses from northern Iran. Domesticated and wild barley were susceptible to infection by *Z. passerinii* isolates obtained from domesticated barley. However, isolates from wild hosts led to the establishment of SSLB only on wild barley, without sporulation on domesticated barley. In contrast to patterns observed in *Z. tritici*, we observed a high extent of clonality among *Z. passerinii* genomes and identified four populations based on analyses of SNP data. The isolates from domesticated barley clustered into a single population with high differentiation across the genome with respect to the isolates from wild hosts (*FST*= 0.38±0.06). Populations isolated from wild hosts showed a higher extent of genetic variation (π) compared to those coming from domesticated barley, also contrasting the pattern observed for *Z. tritici*. The prevailing evidence supports that host specialization of *Z. passerinni* on domesticated barley occurred by different evolutionary processes than for *Z. tritici* on wheat.

Abstract ID: 2262
Poster board number:
P457

Machine learning assisted gene annotation of a nematode phylogeny by proteotranscriptomics

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Quality of gene annotation plays a key role in distinguishing artifacts from real biological effects in comparative genomics. This is a common problem especially in nematode and invertebrate genomics.[PMID: 33045985] and constitutes an impediment in recent

decades' comprehensive picture of the evolution of species related to one of the most studied nematodes, the model organism *Caenorhabditis elegans*. Given that the comparison between genomes of very close relatives can provide understanding of the mechanistic level of the genetic pathways, we focused to resolve this problem using proteotranscriptomics, a multi-omics approach which integrates in-depth transcriptome sequencing and high-resolution mass spectrometry combined with a supervised machine learning algorithm which detects incomplete assembly of transcripts independent of former annotation information. Using this approach, we were able to provide comprehensive assemblies of protein-coding genes in 6 Caenorhabditis and 7 nematode species of phylogenetic interest. For five of these species which lack a reference genome we provide annotations with similar quality as *C. elegans. Using* this high-quality data we dissect homology relationships among the genes in these 12 species and combine it with a comprehensive study of positive selection. The results of these deep comparisons shed light on evolutionary forces acting in the studied recently diverged species.

Abstract ID: 2312
Poster board number:
P458

What makes a tree a tree? Evolution of the gene regulatory network underlying wood formation

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One of the great mysteries of the plant world is the many and rapid evolutionary shifts between woody and herbaceous growth forms. The ability to produce wood is likely ancestral to all seed plants, but has been lost and gained several times throughout plant evolutionary history. Intriguingly, there are likely no major genetic modifications associated with these shifts, but rather unique gene regulation causing rapid evolutionary change. This means that if we could understand the gene regulatory network underlying wood formation in plants, we could potentially answer one of the major questions within plant evolution - what makes a tree a tree? In this project, we will therefore characterize and compare the regulatory networks orchestrating the differentiation of stem cells into woody tissues in three gymnosperm and three angiosperm species. Specifically, we will i) generate high resolution regulatory atlases across wood forming tissues and ii) use a novel computational framework to infer and compare regulatory networks and thus deduce the regulatory mechanisms explaining the evolution of trees. In parallel, we will identify important candidate genes for wood formation by conducting comparative phylogenomic analyses in a large set of woody and non-woody angiosperms. By testing for convergent shifts in selection pressure in transitions from woody to non-woody growth forms, we can identify previously undetected non-regulatory gene evolution of

importance to wood-formation. Together, these studies will help us understand the evolution of growth form variation in plants.

Abstract ID: 2409
Poster board number:
P459

Evidence of horizontal transmission of *Wolbachia* within the *Drosophila saltans* group (Drosophilidae)

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Wolbachia is the most widespread endosymbiont on Earth, it infects a wide range of arthropods and nematodes. As an endosymbiont, this bacterium is transmitted vertically, however, horizontal transmission has been commonly reported. The *Wolbachia* horizontal transmission can occur through different ways in nature, such as parasitism, cannibalism and predation of infected individuals, or even through hybrid introgression and sharing of ecological niches. In the present work, we analysed the horizontal acquisition of *Wolbachia* within the *Drosophila saltans* group, through *w*Stv, *w*Stv-like, *w*Spt, *w*Psd, *w*Pro strains, infecting the respective hosts *D. sturtevanti, D. lehrmanae, D. septentriosaltans, D. pseudosaltans* and *D. prosaltans*. We inferred a phylogenetic tree of the *Wolbachia* supergroup A, in IQTree, to 71 *Wolbachia* genomes and compared it with the hosts' phylogeny, reconstructed using 122 single copy orthologs genes identified in OrthoFinder. Our results demonstrate an incongruity between the phylogenies of hosts and strains, in which the *w*Stv (host *D. sturtevanti*) and *w*Stv-like (host *D. lehrmanae*) strains were phylogenetically distant from *w*Pro (*D. prosaltans*), *w*Psd (*D. pseudosaltans*) and *w*Spt (*D. septentriosaltans*) and the latter were allocated close to other infecting strains of *Drosophila* (*w*Mel, *w*Yak, *w*Tei, *w*Ara, *w*Rec, *w*Bor and others). The *w*Stv and *w*Stv-like were grouped into a clade with the *w*Adent (*Apterostigma dentigerum,* Formicidae), *w*Agra (*Anoplolepis gracilipes,* Formicidae) and *w*Nik (*Drosophila nikananu*, *melanogaster* group) strains. These incongruities suggest horizontal transmission of the strains *w*Stv and *w*Stv-like. However, the transmission route remains open, to which new studies are being carried out to better answer this question.

Symposium: S30. Characterizing genomic landscapes of recombination and their evolution (id: 951)

Abstract ID: 1078
Poster board number:
P460

Population genomics reveal PRDM9-dependent recombination landscapes in salmonids

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In most mammals, the genomic localization of recombination hotspots is directed by the PRDM9 protein. The complete or partial loss of PRDM9 in other taxa such as birds, some teleost fishes or invertebrates, results in a different localization of hotspots and an apparently more stable dynamics of recombination landscapes than in mammals. The existence of mammalian-like recombination landscapes in taxa that have retained a functional PRDM9 remains unclear, raising questions about the ancestral role of PRDM9 in animals. Salmonid fishes have a full-copy of the PRDM9 gene - Is it involved in the regulation of recombination as in humans and mice? To address this question, we used linkage disequilibrium information from whole-genome polymorphism data to build fine-scale population-based recombination maps in three Salmonid species: *Oncorhynchus kisutch*, *O. mykiss* and *Salmo salar*. The three species showed recombination rate variation at both broad and fine scales, with a tendency for hotspots to be localized away from transcription start sites, similarly to mammals. Moreover, the comparison of recombination landscapes among species of salmonids revealed a rapid evolution of the recombination rate distribution. These findings strongly suggest that PRDM9 has a function of directing DNA double strand breaks in salmonids, arguing in favor of an ancestrally PRDM9-mediated recombination process in vertebrates. Confirmation of these results via ChipSeq and binding motif analysis is on its way.

Abstract ID: 1268
Poster board number:
P461

Influence of nutrient deficiency on meiotic recombination and pollen size variation in rye

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Meiotic recombination increases allelic diversity via crossover or gene conversion and is therefore a major driver of the evolution of organisms. Studying meiotic recombination allows us to better understand how speciation proceeds and is also valuable for plant breeding for creating new varieties providing food security. Another important mechanism generating novel allelic combinations enabling adaptation to changing environments is cross-pollination. Past studies have shown that meiotic recombination and pollen size are depending on environmental factors and nutrient balance, but the underlying genetic architecture is remaining elusive. The goal of our study is to investigate meiotic recombination and pollen size variation in a heterogeneous population under nutrient deficiency caused by 140 years of monoculture in rye (*Secale cereale*) to understand the genetic architecture underlying these stress response interactions. We will investigate the meiotic recombination rate variation by genotyping single pollen nuclei of individual plants. This method directly determines the crossover events in haploid DNA samples derived from diploid heterozygous plants. In order to unravel the genetic architecture of abiotic stress responses of the meiotic recombination, we will use GWAS to identify genes involved in that process. Further on, we will study the pollen size variation by flow cytometry which will enable a high-throughput measurement of thousands of pollen grains per plant. Our study will help to extend our

knowledge of the molecular and evolutionary mechanisms of allelic diversity generated by recombination in plants.

Abstract ID: 1449
Poster board number:
P462

Effects of recombination rate variation on efficacy of selection in butterflies.

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Recombination is an important mechanism for reshuffling genetic variants, thereby giving rise to novel allele combinations that natural selection can target. Hence, recombination can decouple alleles with opposing selection coefficients and increase the efficacy of both positive and negative selection. As a consequence, a relative increase in the recombination rate should lead to a higher probability of fixation for adaptive mutations and a lower proportion of segregating deleterious variants. In this study, we investigate the link between karyotype structure, recombination rate variation and the efficacy of selection. The common wood white butterfly (*Leptidea sinapis*) shows extreme intraspecific geographical variation in karyotype; chromosome numbers range from n = 27 - 32 in northern and central Eurasia to n = 53 - 55 in southwestern Europe. Here, we use high-density linkage maps to assess how karyotype is associated with recombination rate variation, using two populations of *L. sinapis* with distinct karyomorphs. We characterize the effects of chromosome rearrangements on the global and regional recombination landscapes and estimate the effects on genetic diversity and efficacy of selection. Our results show that the population with a higher number of chromosomes has a significantly higher overall recombination rate and that there is a negative correlation between chromosome size and recombination rate. In addition, we find that there is substantial recombination rate variation along chromosomes. How the differences in recombination rate between karyomorphs and chromosome regions affect the maintenance of genetic diversity and the efficacy of selection is discussed.

Abstract ID: 1475
Poster board number:
P463

Genetic basis of individual recombination rate variation in a wild house sparrow population

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Meiotic recombination is an essential mechanism in sexual reproduction and performs a key role in diversity of eukaryotic genomes. Recombination is both evolutionarily and mechanistically beneficial as it prevents the accumulation of deleterious alleles, increases genetic variance for fitness, and ensures proper segregation of chromosomes

during meiosis. However, recombination carries significant costs as it increases the risk of local mutation, chromosomal rearrangements, and breakdown of favourable allele combinations previously built up by selection. This cost/benefit dynamic is likely to vary depending on evolutionary context leading to an expectation of variation in recombination rate at the individual, population, and species levels. A key step to understanding this phenomenon is to determine the landscapes and genetic architecture of recombination rate variation. In this study, we integrated pedigree and dense genome-wide SNP data to characterise genome-wide recombination landscapes and individual recombination rates in a wild population of house sparrows (*Passer domesticus*). Linkage maps revealed heterogeneity of recombination landscapes both between and within chromosomes and differences in recombination rates and landscapes between the sexes. Individual recombination rates were heritable in both sexes, with genome-wide association analyses suggesting that rate variation is polygenic i.e. driven by many small-effect loci. These findings add to the growing body of research on trends in recombination variation and serve as a stepping-stone for further analysis into associations between individual recombination rate and fitness.

Abstract ID: 1699
Poster board number:
P464

Combination of recombination inference methods in a wild owl population

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The frequency of genetic recombination can vary between chromosomes and individuals, as well as between sexes and populations. Examples of recombination frequency variation in nature are manyfold but the underlying causes are only poorly understood. While expanding the taxonomic sampling will help characterise how recombination rates vary within and among species, the data required to quantify recombination are hard to generate. Here, we present the recombination landscape of the European barn owl (*Tyto alba*). By utilising whole genome sequencing of 264 birds we constructed the first linkage map of an owl species. The linkage map helped create the first chromosome-level assembly in the Strigiformes order and shows evidence of heterochiasmy in a wild population with females exhibiting a higher rate of recombination along the genome. We complemented the linkage map with an LD-based recombination map using a sample of unrelated individuals. The increased resolution of the LD-based map allowed us to quantify fine-scale variation in recombination, identify hotspot locations and associate them with genomic elements. This is the first characterization of the recombination landscape in an owl species and one of the few in bird species outside the order of Passeriformes. Thus, it proves to be not only an important resource for the species but an asset for between-species comparisons as well.

Abstract ID: 1770
Poster board number:
P465

High-throughput gamete-based inference of recombination and variation within species

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Genome-wide recombination rate has been recognised as an important evolutionary process, facilitating phenotypic novelty and defining local adaptation rate. However, for the most part, its empirical inference is laboriously demanding and, in many instances, experimentally challenging. As a result, recombination rate inference has been primarily restricted to a single average parameter per species, and comparative studies have focused on a long evolutionary scale contrasting rates between species. In this work, we implemented 10X single cell RNA and ATAC sequencing in a pool of multiples crosses (hybrids), aiming to reconstruct recombinant haplotypes and to build linkages maps per individual simultaneously. We tested the method in two independent instances: *i) Arabidopsis thaliana* pollen obtained from crosses between multiple Eurasian populations; and *ii)* Fission yeast haploid cells (*Schizosaccharomyces pombe*) with a known history of recent natural hybridization between two ancestral populations. We found that the resolution of the linkage map and the potential to pool multiple hybrids vary between species/systems, being RNA content and divergence between pooled samples mayor criteria to consider. In both cases, we show that the method allows the differentiation of hybrids within the pool, the subsequent reconstruction of recombinant haplotypes, and the inference of a mean genome wide recombination rate. Our understanding on the evolution of recombination rate can be potentially improved by this method, with promising application to a large variety of systems.

Abstract ID: 1944
Poster board number:
P466

The interplay between selection and the genomic landscape during the domestication of grain amaranth

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The process of adaptation is vital for populations facing changing environments. A number of potentially adaptive traits have been studied intensively, but intrinsic traits like the genomic landscape i.e., the composition and structure of the genome, have received less attention. Multiple features of the genomic landscape influence the molecular outcome of adaptation and recent evidence indicates that some features might be under selection themselves. However, the interplay between the genomic landscape and adaptation remains unclear. The domestication of crops is a well-suited model to study adaptation, as selection intensities and some target traits are known and the wild ancestors coexist. Our goal is to understand how parallel selection during the three independent domestications of grain amaranth changed their genomic landscape. We combine quantitative and comparative genomics to estimate the recombination rates and chromatin structures along this adaptive gradient. Changes in the recombination rate will be determined through the construction of genetic maps for each of the three grain species and the two closest wild relatives. To determine changes in the chromatin landscape of all five species, we apply ATAC sequencing of seedling and leaf tissue from 20 diverse accessions. The comparison of open chromatin and recombination regions in the genomes along the selection gradient from wild to domesticated populations will reveal potential signals of selection on the genomic landscape and between the three

grain amaranths the convergence of such signals. Hence, our model of repeated adaptation provides the opportunity to understand the interplay between selection and the genomic landscape.

Abstract ID: 2007
Poster board number:
P467

Inferring recombination from population genomic datasets: from simulation to real data

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Meiotic recombination is one of the central parameters considered in evolutionary theory. While until recently technological challenges limited empirical estimation of fine-scale recombination rates, sequencing technology and methods development now permit us to infer its variations on a genome-wide scale.
Genetic polymorphism within population provides information on linkage disequilibrium among loci and permits the inference of the recombination history within populations, including of non-model organisms. However, this information is sensitive to other evolutionary processes than recombination, e.g., changes in demography, selection, or migration. Disentangling the relative contribution of each of these phenomena on the linkage and diversity patterns is of prime importance when looking at the effect of recombination in evolutionary studies, for example while studying speciation.
In this talk, I propose to discuss how good are the fine-scale recombination maps inferred from population genetic data, using recombination maps that I inferred from simulations under different evolutionary scenarios and technical criterions. I will then use these insights to interpret the fine-scale recombination maps obtained from two ecotypes of the cichlid fish species *Astatotilapia calliptera*, that are on the path to speciation. Finally, I'll discuss how recombination and selection interacted to shape the genomic differentiation landscape of these populations (e.g., Fst and D_{xy} measures).

Abstract ID: 2064
Poster board number:
P468

Yeast recombination specificity impact on demography inference

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The canonical life cycle of Saccharomyces cerevisiae consists of an alternation between mitosis (clonal reproduction) and meiosis events (outcrossing and intratetrad mating). In this life cycle, meiosis events and then recombination events are known to be rare. This raises questions because it is known that genetic recombination favors genetic diversity.
However, recent studies start to show that heterozygosity in yeast would be greater than previously thought, which implies that recombination events might be more frequent than anticipated.
Indeed, these events are estimated at frequencies ranging from 1 per 50000 generations to 1 per 1000 generations (the difficulty to estimate these frequencies makes it hard to give a more accurate range).

Using SLiM and dadi, we investigate if we can correctly infer demographic parameters given the frequency of recombination events. We test multiple demographic scenarios from simple ones (exponential growth or bottleneck in a single population) to more complex ones (multiple populations with migration, …).
For instance, we observe interesting results such as an excess of polymorphic sites at frequency 0.5 for simulations of populations with bottleneck demography and recombination events every 1000 generations.

Abstract ID: 2158
Poster board number:
P469

PRDM9 diversity and function in salmonids

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What controls the location of meiotic recombination sites along the genome is a long-standing question that has been partially addressed with the discovery of PRDM9, a zinc finger (ZnF) histone methyltransferase which directs recombination at its binding sites in mice and humans. Not all species have PRDM9: it is absent in plants and fungi and in spite of its presence in the ancestor of metazoans, it has been lost partly or totally in several lineages. Recent investigations suggested that only full-length PRDM9 (containing all KRAB, SSXRD, PR/SET and ZnF domains) is able to specify the localization of recombination sites. This remains to be analyzed and tested accross the tree of life. We thus explored the role of PRDM9 in directing recombination sites in salmonids using different approaches. First, we analysed the diversity of PRDM9-ZnF across populations of two species: *Salmo salar* and *Oncorhynchus mykiss*, both having different PRDM9 paralogs, either full-length or KRAB-less. We identified different *Prdm9* alleles and a high diversity of ZnF for both species, all with strong positive selection for the amino-acids involved in DNA binding specificity. Our results argue for an involvement of full-length PRDM9 in hotspots localisation but also suggest that KRAB-less paralogs have either recently lost their activity or are involved in other regulatory activities. We are currently carrying out the genomic localisation of hotspots by molecular mapping to determine if those are determined by PRDM9.

Abstract ID: 2394
Poster board number:
P470

The interplay of selection and recombination on the genomic level

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Recombination and natural selection are central processes in both genetics and evolution. By breaking linkage and shuffling alleles, recombination generates the diversity of haplotypes that natural selection acts upon, in turn also shaping the patterns of genetic diversity at linked neutral sites. Recombination and natural selection therefore influence each other on the genomic level in complex ways. Local recombination rates modulate the effects of selection while selection can also act to modulate recombination rates. Moreover, the genomic signatures of selection affect our ability to infer

recombination rates from population genomic data. For example, the signature of a selective sweep produces a false signal of low recombination. Here I am going to report on my efforts to disentangle these processes, using both population genetic data and direct estimates from a gamete sequencing approach.

Symposium: S31. Limits to adaptation: linking evolution, ecology, and genetics (id: 956)

Abstract ID: 1093
Poster board number:
P471

Maternal effects do not resolve the paradox of stasis in birth weight in a wild mammal

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The ultimate goal of evolutionary biologists is to understand and predict genetic change, particularly those occurring in response to natural selection. While evolutionary models frequently predict that adaptive evolution should occur in natural populations, such adaptive responses are rarely observed. This discrepancy highlights our inability to predict evolutionary change in nature. One particularly promising hypothesis to explain the lack of evolutionary responses in a key offspring trait, body size, is that positive selection on juveniles is counterbalanced by selection against maternal investment in offspring growth, given that reproduction is costly for the mothers. Yet, no study has managed to fully validate or reject this hypothesis, as it requires knowledge on the genetic architecture of maternal effects and estimates of selection on maternal investment, information that is not easily accessible in wild systems. Here, we used data from one of the longest individual-based studies of a wild mammal population, the red deer population of Rùm, to estimate these key evolutionary parameters. We first showed that despite positive directional selection on birth weight, and heritable variation for this trait, no genetic change has been observed for birth weight over the last 47 years in the study population. Contrarily to our expectation, we found no evidence of selection against maternal investment in birth weight. We used a fully parameterize maternal effect model to demonstrate that maternal effects cannot explain the lack of evolutionary response observed for birth weight; ultimately our analysis here only deepens rather than resolves the paradox of stasis.

Abstract ID: 1114
Poster board number:
P472

Experimental evolution in Drosophila–parasitoid networks as a tool to study evolution in communities

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Evolution in nature unfolds in the context of complex communities and webs of interactions. However, most evolutionary studies focus on a single species and a single selective pressure, leading to a biased understanding of evolution. Moreover, single species studies overlook the eco-evolutionary dynamics that occur in communities and are driven by rapid adaptation to biotic factors. We aim to address this gap by investigating the interactive effects of multiple selective pressures that typically occur in communities. To understand the mechanisms of evolution in communities, we will use experimental evolution in a controlled environment coupled with genomic analysis. Experimental evolution in a microcosm or mesocosm allows us to increase the complexity of the environment while still controlling the number of confounding factors. We will study the adaptation of Australian *Drosophila* species in small communities with their parasitoid wasps, which are natural drivers of *Drosophila* population dynamics and local adaptation. Specifically, in our experimental evolution, we aim to investigate the effects of parasitism, intraspecific and interspecific competition, and warming on *Drosophila* adaptation by applying the appropriate selective pressures. Additionally, we intend to reproduce eco-evolutionary dynamics in the laboratory and investigate their mechanisms and the parameters that influence them. Understanding the evolutionary dynamics of populations in a community will advance our understanding of nature and has concrete implications for conservation strategies. Species adaptation must be considered in the context of a community, where the loss of one species can have cascading effects on the entire community.

Abstract ID: 1137
Poster board number:
P473

Genetic drift and the architecture of polygenic adaptive divergence under gene flow

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Environmental adaptation often involves spatially heterogeneous selection at many genetic loci. Thus, the evolutionary consequences of hybridisation between populations adapted to different environments depend on the coupled dynamics of multiple loci under selection, migration and genetic drift, making them challenging to predict. In this talk, I will outline simple theoretical approximations that capture the combined effects of linkage disequilibria (LD) and drift on polygenic adaptive divergence in the face of gene flow. This analysis allow us to clarify how genetic architecture (i.e., the numbers, selective and dominance effects and linkage relationships of adaptive variants) influences adaptive divergence, and the conditions under which genetic drift might significantly constrain local adaptation.

Abstract ID: 1269
Poster board number:
P474

Fisheries induced evolutionary changes recover slowly but surely over time.

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Overfishing is one of the greatest threats to fish populations. Size-selective harvesting favours faster juvenile growth, younger maturation, small adult body size and low reproductive output. These changes might be slow to recover and ultimately threaten population's survival. To study the recovery potential of exploited experimental populations, we compared life-history traits in three differently size-selected experimental lines (large-selected, small-selected, randomly-selected) after five generations of harvesting and ten subsequent generations of recovery. We show that after a recovery period twice as long as the harvesting period, the differences in adult body size among the selection lines have eroded. While there was still a significant body size difference among the selection lines, this did not translate to differences in reproductive success. Our experimental results demonstrate that, despite that size-selective harvesting can cause contemporary evolutionary changes in exploited fish populations, these changes can be reversible if populations are allowed to recover long enough.

Abstract ID: 1287
Poster board number:
P475

The genomic consequences of 10,000 generations of isolation of Orkney voles

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Islands are ideal test grounds to observe the progress of adaptation to a new environment under the tangled forces of genetic drift and selection. Population genetics theory can provide detailed predictions for the genetic patterns expected for isolated populations yet empirical studies of the effects of long-term isolation under natural conditions are very limited. Here we examine the genomic consequences of more than 5000 years of isolation experienced by common voles (*Microtus arvalis*) that were introduced to the Orkney archipelago off Northern Scotland by Neolithic settlers from continental Europe. Orkney voles derive from an introduction wave originating at the northern coast of France or Belgium and have remained isolated since introduction, without detectable gene flow for about 10,000 generations. This extreme demography has left strong signatures in the genome. Depending on the island, Orkney vole genomes only contain 8-29% of the heterozygosity of continental conspecifics despite large modern population sizes. Homozygosity of deleterious alleles accumulated and fixed to a dramatic degree particularly on smaller islands. The Orkney vole population also showed evidence of genome-wide relaxation of selection, and the marked increase of body size in Orkney may relate to the relaxation of positive selection on related genes. This natural system demonstrates that long isolation in vertebrate populations is associated with strong loss of genetic diversity, accumulation of homozygous deleterious alleles and lower efficacy of selection. Yet the potential negative effects of this exceptional genomic background can be overcome even in complete isolation.

Abstract ID: 1377
Poster board number:
P476

Genotypes selected for early and late avian lay date differ in phenotype but not fitness in the wild

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Global warming has shifted phenology traits in many species, but not sufficient to track changes in their environment. Despite directional selection on phenology, species fail to further shift their phenology, indicating that fitness might not increase with further shifts in phenology. To test this, we measured lay dates and fitness of great tits (*Parus major*) with extreme early and late genotypes for lay dates, obtained from a genomic selection experiment where birds were selected based on their genomic breeding value (GEBV) for lay dates. We reintroduced selected females of the fourth-generation into our wild study population, making our study the first application of genomic selection in the wild. Females with early genotypes indeed advanced their lay dates relative to females with late genotypes, but did not advance lay dates beyond the earliest local females, while females with late genotypes delayed lay dates relative to local females. Albeit advanced lay dates of females with early genotypes translated into a better synchrony with the environment, there was no difference in the number of fledglings produce between females with early and late genotypes, in line with an overall weak effect of lay date on the number of fledglings in the study population in the years of the experiment. Our study constitutes the first application of genomic selection in the wild and led to an asymmetric phenotypic response between early and late genotypes, that did not translate into a difference in fitness indicating the presence of additional fitness components that remain to be identified.

Abstract ID: 1591
Poster board number:
P477

Evolution of developmental constraints: lessons from a classic case of fish resource polymorphism

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Developmental constraints such as canalisation (the buffering of phenotypic variability from environmental and genetic perturbations) and morphological integration can bias the production of phenotypic variation and in turn affect the rate and direction of evolution. How phenotypic variability is affected during adaptive divergence is poorly understood as knowledge of the molecular mechanisms underlying canalisation is sparse. Here, we assessed if/how expression variability evolves in diverging populations. We further investigated how hybridisation would affect such divergence in gene expression variability when considering the effects of dominance. Our study system is the Arctic charr morphs (*Salvelinus alpinus*) in lake Thingvallavatn, a classic case of resource polymorphism involving trophic niches. We estimated gene expression

variability in the offspring of two contrasting morphs (benthic/limnetic) and their hybrids reared in common-garden and sampled during two key points of craniofacial development. The two morphs exhibited distinct profiles of gene expression variability for both coding and non-coding RNAs (microRNAs), suggesting that multiple pathways have undergone canalisation in either morph. In the hybrids, gene expression variability was substantially affected by maternal effects or was similar to the limnetic morph. Futhermore under- and overdominance patterns in expression variability were also observed for a fraction of the genes. In all, we show that divergence in gene expression variability can evolve rapidly in sympatry. Furthermore, the multiple dominance patterns associated with gene expression variability indicate that many developmental pathways may mediate the effects of hybridisation on phenotypic variation.

Abstract ID: 1729
Poster board number:
P478

Random segregation as a constraint on the evolution of multidrug resistance on bacterial plasmids

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Bacterial plasmids and other extra-chromosomal DNA elements may carry genes that have adaptive functions for their hosts, in particular antibiotic resistance genes. Because plasmids often exist in multiple copies, different plasmid copies can carry distinct alleles, allowing for heterozygosity not possible for loci on a haploid bacterial chromosome. This plasmid-mediated heterozygosity of resistance alleles can contribute to multidrug resistance, a serious problem in the clinical context. However, the evolution and maintenance of multidrug resistance through plasmid-mediated heterozygosity is constrained by the constant loss of heterozygosity due to random segregation of plasmids on cell division: each division has some probability of producing a homozygous daughter cell. We present mathematical models of the establishment of a novel resistance allele on a plasmid in a bacterial population already adapted to one antibiotic but undergoing demographic decline due to simultaneous treatment with multiple antibiotics (an evolutionary rescue scenario). We derive the minimum threshold on the selective advantage of heterozygotes required to overcome segregative loss and make population persistence (rescue) possible; this threshold decreases with increasing copy number of the plasmid. We further show that the formation of cointegrates from the fusion of plasmids increases the probability of rescue, as multiple alleles on cointegrated plasmids are less subject to stochastic loss. These results contribute to understanding the contribution of plasmids to the evolution of antibiotic resistance in complex selective environments, particularly the limits to that contribution imposed by the constraints of plasmid biology.

Abstract ID: 1798
Poster board number:
P479

How does ecology shape phenotypic and genomic divergence on a small spatial scale?

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Rapidly changing environments across the globe pose challenges for organisms to either adapt or risk extinction. High rates of gene flow are expected to prevent populations from adapting to their local ecological environments, but an increasing number of studies show that even at small geographical scales, natural or sexual selection can counteract the homogenizing effect of gene flow. Here we show that different populations and habitats (i.e., coastal vs. inland populations) of the common bluetail damselfly (*Ischnura elegans*) differ in their competitor and predator faunas (i.e., the potential for biotic antagonistic interactions), potentially causing divergent selection and phenotypic divergence in wing-size allometric relationships. We found no evidence for pre-reproductive barriers between populations or habitats, but, unexpectedly, migrant males and males originating from coastal populations had a higher probability of mating with resident females, potentially opposing population divergence and accelerating gene flow. Whole-genome resequencing (WGS) data analysed with population genetic and bioinformatics tools revealed weak and variable molecular divergence between habitats, with one population being particularly divergent from the other populations. Our results suggest that differences in ecology and biotic conditions between habitats and populations provide opportunity for different selection regimes and can potentially drive phenotypic divergence even in the presence of high dispersal and extensive gene flow.

Abstract ID: 1838
Poster board number:
P480

Rapid adaptation of a novel butterfly biocontrol in the Cook Islands (New Zealand)

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The realisation that evolution can happen in short timescales, has changed the way we think about the natural world. Remote islands are particularly vulnerable to the effects of globalisation and invasive species, due to their unique biodiversity. In an attempt to reduce the use of chemical pesticides, biocontrol agents have long been used to manage alien species. The introduction of organisms into novel environments to control others creates the potential for adaptive evolution and drastic ecological changes, thus making biocontrol programmes excellent systems to study rapid evolution. In this study, we are tracking evolutionary and ecological change in a novel biocontrol agent, the butterfly *Heliconius erato cyrbia*. This butterfly was introduced to the Cook Islands (New Zealand) in 2016 to halt the spread of one of its natural host plants, the invasive passionflower vine *Passiflora rubra*. We have whole-genome sequenced a total of 150 individuals from the founding population, as well as two later timepoints in the established population (2019, 2021). With this unique dataset, we model the effects of strong but short bottlenecks imposed by biocontrol programs, as well as the impact of small founder populations and drift on the potential for adaptive evolution. We search for signatures of local adaptation or relaxed selection pressures in these remote islands with genomic and phenotypic approaches. Relating the constraints of rapid evolution to ecological and demographic processes in nature is an essential step towards empowering conservationists to realistically integrate evolution into biocontrol programs.

Abstract ID: 1870
Poster board number:
P481

Unraveling the impact of compensatory evolution on metabolic divergence

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Deleterious mutations exerting a strong selection pressure are continuously purged from the population. However, the harmful effect of such mutations can also be suppressed by compensatory genetic changes elsewhere in the genome, resulting in evolutionary divergence between lineages. Indeed, several instances showed the role of compensatory genetic changes in the between-species divergence of single RNA or protein molecules. However, little is known about the effect of compensatory evolution on the divergence of complex molecular networks. This is an important gap in our knowledge, because traditionally between-species differences in molecular networks are assumed to arise through the accumulation of beneficial or neutral mutations. Here we propose that compensatory adaptation is a key evolutionary force with a profound impact on cellular networks. The present project aims to investigate the impact of compensatory adaptation on the evolution of metabolic networks. Specifically, we apply advanced phenotyping and molecular biology techniques on a set of laboratory-evolved single-gene knockout *E. coli* strains to explore how compensatory mutations shape cellular metabolism and the phenotypic consequences of such metabolic rewiring. Our work demonstrates that compensatory evolution altered the carbon utilization profile of *E. coli* strains, yielding some genotypes with fitness advantage in novel environments. These findings suggest that rudimentary forms of new adaptive traits emerge through gene loss and subsequent compensatory adaptation, without direct selection on them. Our work also has relevance for biotechnology, as genetic modifications introduced towards a desired industrial phenotype may often induce detrimental side effects and thereby create ample opportunity for compensatory adaptation.

Abstract ID: 1940
Poster board number:
P482

Coarse-graining model for the evolution of cooperative breeding

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Cooperative breeding occurs when an individual helps to raise the offspring of others. It is typically considered to be costly for helpers who lose or post-pone the opportunity of personal fitness gains. This behaviour is widespread, occurring in a variety of different taxa, and ecological settings. Moreover, phy-logenetic data suggests that environmental conditions play a role in promoting and hindering cooperative breeding. The complex interplay between environ-mental constraints and population interaction makes it challenging to model

cooperative breeding in a satisfying way. In order to better understand the influence of environment on cooperative breeding while having reasonable computations, we built a coarse-graining model for the group augmentation effect. That way, this population model allows us to have more complex relations between the environment and the population and thus to better understand their role. Specifically, by computing the inclusive fitness of this kin selection model, we were able to show that environment-individuals relations, for instance the intraspecific competition, have an influence over the emergence and development of altruistic behaviour in the population.

Abstract ID: 2119
Poster board number:
P483

Genome-wide changes caused by fishing in experimentally exploited fish populations

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Unsustainable fishing can be considered as one of the most pervasive threats to wild fish populations globally. Exploited populations do not only experience very high mortality rates but fishing typically also exhibits a strong selection pressure against large body size. Simultaneously, fishing can induce evolutionary changes in many other traits and ultimately change life-history strategies. We demonstrate life-history and behavioral changes in size-selectively harvested zebrafish (*Danio rerio*) populations together with broad-scale gene expression changes, genomic shifts, and epigenetic changes. Five generations of size-selective harvesting induced phenotypic changes in body size, growth rate, reproductive output, activity, and exploration. Fish selected for small body size were smaller, less successful spawners and less explorative than the control fish. Transcriptome sequencing revealed that the expression of 4000 genes was significantly altered after five generations of size-selective harvesting. We further studied fishing-induced genome-wide changes across 3.5 million SNPs and identified over 13 000 outlier SNPs responding to size-selective harvesting. These occurred within genes contributing to various major biological processes, such as muscle development, regulation of metabolic processes and morphogenesis. Interestingly, size-selective harvesting appeared to push replicated populations toward different evolutionary trajectories despite similar phenotypic responses. We also demonstrated large-scale epigenetic changes in size-selectively exploited populations. The extent and rapid pace of the changes in gene expression and sequence level together with epigenetic changes caused by size-selective harvesting emphasizes the need of evolutionary enlightened management towards sustainable fisheries.

Abstract ID: 2282
Poster board number:
P484

Bill length variation in great tits (*Parus major*): Are there any fitness consequences?

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Bird bills vary greatly in shape, size, and colour and this variability is strongly associated with feeding ecology and species differentiation. Various studies show that bill length and shape is a true polygenic trait, with up to 100 different genes implicated. In great tits bill length varies across populations with persistent differences between UK and Dutch birds. Structural differences were shown to be due to selection for larger bills in the UK population, associated to human bird feeding. We hypothesized the Dutch population too would experience selection of larger bills and aimed to catch 'evolution in the act'. We measured potential fitness consequences of bill length, studied the underlying genetic variation and the associated developmental processes using a multi-disciplinary approach. Our data consist of multi-year observations of bill length, other phenotypic and life history traits in four long-term study populations of the great tit, embryonal bill gene expression data from a selection experiment, and whole genome sequencing data from phenotypic extreme wild individuals. Our results show that bill length is a heritable trait that varies between sites and years but without any fitness consequences or evidence of selection. The genetic data hints at involvement of the same developmental pathways previously implicated, however with variation in different genes, further strengthening the view that bill length is a polygenic trait. Thus, in contrast to our expectations, bill size is not under selection and hence, despite it being heritable, is not expected to evolve to larger bills, as the UK population has.

Abstract ID: 2377
Poster board number:
P485

Trade-off between mimicry and thermoregulation: an experimental study in hoverflies

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Thermoregulation plays an important role in the lives of organisms during foraging, antipredator behaviour, courting behaviour, or overwintering. Moreover, thermoregulatory requirements could also affect species on an evolutionary level. For instance, in hoverflies (Diptera, Syrphidae), it was hypothesized that the trade-off between antipredator coloration and efficient thermoregulation maintains inaccurate mimicry in some species. Our aim was to look for experimental evidence of the trade-off between thermoregulatory abilities and mimetic accuracy in hoverflies. We examined the temperature excess (TE, difference between body temperature and ambient temperature) of 566 specimens of 47 species in the field, using a thermistor microprobe. Interestingly, we did not find any correlation between temperature excess and mimetic accuracy. However, we observed a strong sexual dimorphism. Females showed lower TE, which was independent on most internal and external factors, whereas males showed consistently higher TE, which was further influenced by activity type (flying > sitting) and resembled model (bumblebee-mimics > honeybee-mimics > wasp-mimics > small solitary bee-mimics). Our results indicate that males are likely pushed to a higher

temperature excess by sexual selection, as better thermoregulation provides advantage during the lekking flights. We conclude that the trade-off between thermoregulation and mimicry might not be the strongest maintaining mechanism of imperfect mimicry in hoverflies, although selection pressure on thermoregulation might affect the coloration and its plasticity to some extent.

Symposium: S32. Inferring macroevolutionary patterns from microevolutionary processes: methods and practices (id: 22)

Abstract ID: 1365
Poster board number:
P486

Effects of distinct drivers on the phylogenetic structure of forests in the Eastern Czech Republic

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The evaluation of cross-effects (direct and indirect) of predictors on the phylogenetic structure of natural communities requires the use of efficient approaches in explanatory-predictive power, which are not based only on macroevolutionary models such as Brownian Motion. We analyzed the influence of predictors representing climate, soil, land use (historical coppicing) and topography on the phylogenetic diversity (PD) and structure (MPD-mean pair distance and MTND-nearest taxonomic distance) of 4,600 forest plots distributed along the Eastern Czech Republic, applying structural equation modeling (SEM). For phylogenetic metrics (target variables), we used their standardized effect size (ses), while for predictors we used their summarized information extracted from the first two axes of a principal component ordination (PCA) and classifying them as two distinct gradients. Our findings showed that extreme and average climate, high elevation and soil drainage gradients led to a significant increase ($p<0.05$) in sesPD, sesMPD and sesMTND, ie, phylogenetic overdispersion and consequent increase in phylogenetic diversity in the forest plots. On the other hand, acidic and drained soils and elevation gradients led to an increase in sesMTND, ie, stronger environmental filters grouping closer phylogenetic species and decreasing phylogenetic diversity in the forest plots. Historical coppicing significantly increased sesMPD, demonstrating the widespread effect of this important land management even on phylogenetically distant clades. Therefore, SEM modeling can clearly highlight cross-effects in different patterns (i.e. clustering or overdispersion) at distinct levels of phylogenetic relationships (i.e. sesMPD - entire phylogeny, from oldest to shallowest clades; sesMNTD - shallower clades and nodes).

Abstract ID: 1398
Poster board number:
P487

Consistent phenotypic variation across biological levels: from developmental noise to macroevolution

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Though the phenotypic diversity across the tree of life seems endless, there is emerging evidence that phenotypic evolution is constrained by the genetic architecture underlying these traits. Assuming that the genetic architecture, often described in the form of genetic (co)variance matrix (**G**), is relatively conservative, phenotypic divergence is predicted to occur in the direction that has the most genetic variation in phenotypic space (i.e., $\boldsymbol{g}_{max}$). In addition to **G**, phenotypic evolution can also be guided by phenotypic plasticity and developmental noise, which are potentially interacting with **G**. However, little is known about the relationship between the pattern of variation among these biological hierarchies. Here we aimed at quantifying the pattern of variation at four levels–developmental noise, genetic variance, plasticity, and macroevolution–and comparing them with each other in multidimensional morphospace using the wings morphology of *Drosophila* flies as a model system. The patterns of variations in each biological hierarchy were similar and well aligned with each other in the wing morphospace. These results suggest that phenotypic variations in the lower biological hierarchy, including developmental noise, plasticity, and genetic variation may interactively constrain the pattern of macroevolution, though at this time we do not have explanations for what factors underlie these patterns of variation. We will discuss the relationship between hierarchies and the relationship between the patterns of variation and their implications for our current understandings of the causes and consequences of evolutionary constraints in micro- and macroevolutionary time scales.

Abstract ID: 1456
Poster board number:
P488

A spectrum of verticality across genes

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Prokaryotes are known to constantly transfer genetic material between lineages. This process has historically fueled discussion about the validity of prokaryotic species and if genes are able to show the identity of a lineage. Some genes, however, seem to defy the general tendency of horizontal gene transfer (HGT), making them valuable tools for phylogenetic studies. They tend to evolve vertically by generational splits instead of transfers between branches in the gene tree. Surprisingly, this tendency has never been quantified or shown on a large scale. Thus, we created a measure of verticality by looking for HGT events in high level taxonomic groups. This measure is based on the simple idea that more vertically evolving genes should have trees with more monophyletic groups. By calculating this measure on over 100,000 possible trees from a prokaryotic proteins sequence clustering encompassing 5,655 genomes, we were able to compare the verticality between different protein families. Protein families that were more prevalent among all genomes showed higher verticality. As the distribution of a gene among all genomes in this dataset is an indicator for universality of the gene among all genomes in nature, verticality seems to rise with universality of a gene. Moreover, these more universal genes often showed important functions for the cell, e.g. ribosomal

proteins. Further comparing these protein families allows insights into the general tendency of a group to undergo HGT, verticality of single genomes and also possible HGT in the ancestors of mitochondria and cyanobacteria.

Abstract ID: 1573
Poster board number:
P489

Innovation and elaboration on the avian tree of life across evolutionary scales

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The origins of biological diversity remains a central question in mega-, macro- and micro-evolutionary biology. A long-standing proposal is that the majority of diversity at the species level and at nested taxonomic levels arises from elaboration - where new species' traits evolve along an 'evolutionary line of least resistance'. An alternative is that diversity can arise via innovation - where species evolve orthogonally to that 'line of least resistance'. Here we apply new multi-trait methods to evaluate the magnitude and distribution of elaboration and innovation among superorders, orders and species of birds. Our analyses reveal that diversification has arisen via different patterns of elaboration and innovation at all scales. Furthermore, we reveal a nested structure of these patterns at the mega-, macro- and micro-evolutionary levels. These results suggest that both elaboration and innovation are ubiquitous across evolutionary scales and that our new method can be used to unpick heterogeneous patterns in the origins and maintenance of biodiversity.

Abstract ID: 1695
Poster board number:
P490

The role of nutrients in the evolution of multicellularity in green algae

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The transition to multicellularity represents a leap in evolutionary innovation, enabling rapid diversification of complex life forms. The initial step towards multicellularity is predicted to convey ecological benefits, such as the acquisition and storage of nutrients. However, experimental evidence of the nutrient conditions that unicellular and multicellular species are adapted to are lacking. Here we test the selective advantage of multicellularity under a range of nutrient conditions using 17 species (11 unicellular and 6 multicellular) of freshwater green algae. Species were exposed to nutrient replete, nitrogen deplete and phosphorus deplete media in a fully factorial design and their growth and survival measured to quantify the fitness landscape of multicellularity. At the onset of the stationary growth phase, each species' cell sizes, proportion of multicellular colonies, production of reactive oxygen species (ROS) and neutral lipids were measured.These traits indicate direct physiological and morphological responses of algal cells under varied nutrient availability, which offer further clues of why cells either form or break up groups. The results of this experiment show how the environment can

favour group living in some green algae species but not others, providing new insights into the mechanisms underlying the transition to multicellularity.

Abstract ID: 2002
Poster board number:
P491

Modeling the diversification of species interaction networks

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Species interactions are ubiquitous in the natural world, forming networks at various levels of organization. In recent years, clade-based networks, i.e. networks formed by all species of a clade and their interaction partners, have been increasingly studied. Some general patterns such as phylogenetic conservatism in interactions partners have been characterized for such networks. However, there lacks a mechanistic understanding of how the processes of speciation, extinction, and dispersal shape the diversification of such networks. Here, we present an individual-based mechanistic model for the macroevolutionary diversification of clade-based networks, whereby speciation, extinction, and dispersal are underlain by various microevolutionary processes such as coevolutionary selection, local adaptation, genetic drift, and geographic isolation. The broader goals of this research are to (i) understand the diversification of species interaction networks under diverse biotic and abiotic conditions (ii) generate new hypotheses for future empirical studies, which are difficult to develop without computational methods due to the large number of integrated processes and potential non-linearities, and (iii) caution against inferring processes that cannot be inferred from present-day empirical networks, if different processes are shown to produce similar patterns.

Abstract ID: 2254
Poster board number:
P492

Elucidation the systematic status of *Orestias agassii* (Cyprinodontinae): Altiplano, South America

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The ichthyofauna of the genus *Orestias* (Cyprinodontinae: Tribe Orestiini) inhabit the bodies of water of the Altiplano, South America. The current topology of the Altiplano is fragmented into 4 main hydrological systems (Lake Titicaca, Lake Poopó, Coipasa saltpan, and Uyuni saltpan). These systems have been historically connected through Paleolakes, the most current one, paleolake Tauca. In this genus there are 5 species complexes described: *cuvieri*, *mulleri*, *gilsoni*, *lutea*, and *agassii*. From these, the species

complex *agassii* is the most diverse, including 22 species. This complex is based on *Orestias agassii*, described for the locality of Corocoro, Bolivia. Additionally, this species is described in 100 localities from Peru, Chile and Bolivia, having a widespread distribution (Lat: -13°S – -23°S). Recent phylogenetic and morphological evidence suggest that the populations assigned as *O. agassii* are not a monophyletic group. This study will attempt to clarify the systematic of *Orestias agassii* including samples covering the majority of its distribution. For this, we performed a molecular approach using mitochondrial (*dloop* and *cytb*) and a nuclear gene (*glyt*). Our main results show that *O. agassii* sensu stricto is limited to Corocoro (type locality), and localities from lower altitudes of the Altiplano, including Lake Titicaca, Lake Poopó and Coipasa Saltpan. The other linages found are restricted to higher altitudes and/or closed basins. Which suggest that the taxonomy and systematics of *O. agassii* needs to be reevaluated, including its distribution, since it is lower than suggested by other studies.

Abstract ID: 2437
Poster board number:
P493

Analysis of evolutionary regimes of mammals under the mixed Gaussian phylogenetic model

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Phylogenetic comparative methods (PCMs) account for a class of methods utilized to study evolutionary processes of phenotypic traits given measurements on extant species and their shared history described in a phylogenetic tree. Gaussian phylogenetic model, such as Brownian Motion (BM) or Ornstein-Uhlenbeck (OU) process, has been commonly used to model the evolution of the traits over time along the tree. In a large phylogenetic tree, a single model is often not sufficient to consider the diversity of the species. Rather, the tree is partitioned into several evolutionary regimes which has its own type of process and parameters. Recent developments have made it possible to model the evolution of traits using different Gaussian phylogenetic models which correspond to different evolutionary regimes. At the same time, it is also possible to infer the parameters in each regime and to measure the model's goodness-of-fit. Here, we analyze the pruned mammalian phylogeny with brain and testicles mass measurements. Using evolutionary regimes based on sperm competition level (SCL), we considered different configurations of Mixed Gaussian Phylogenetic Model (MGPM) and used the PCMFit software to infer evolutionary parameters and measure the likelihood and AIC score for each model. We also performed inference of regimes location and found that the composition of regimes based on the distinction of rodents and non-rodents has better scores than the regimes based on SCL.

Abstract ID: 2450
Poster board number:
P494

Is there a trend in evolvability? Testing the theory of frozen evolution

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The morphological disparity of evolutionary lineages usually increases after their formation. It is not surprising – if it did not, clades would soon extinct. It is the parameters of this process that is remarkable. According to paleobiologists, the first option is a gradual, not necessarily monotonous, increase in disparity with the age of the clade. The second option is a rapid increase followed by a slow decrease in disparity over time. The third eventuality is a rapid increase in disparity at the beginning of the existence of the clade, which is not followed by any prevailing trend. An overview of studies shows that most lineages are characterized by the second or third option. At least sometimes, this can result from the fact that we only encounter lineages that have successfully diversified in the past. Alternatively, more potential ecological niches might have been free to occupy at the beginning of clades' evolution than later. However, there is evidence that the evolution of evolvability probably plays a key role in the process, making a growing number of traits and developmental pathways robust but effectively unchangeable. This is exactly the prediction of the theory of frozen evolution, according to which stable, further effectively unchangeable structures and traits accumulate in time by the process of stability-based sorting. We test the hypothesis that the evolution of evolvability is responsible for trends in disparity using the fossil material of Palaeozoic invertebrates because of its accessibility, abundance, time span, and the number of distinguishable morphological features.

Symposium: S33. Domestication: Fresh insights from ancient genomics (id: 944)

Abstract ID: 1264
Poster board number:
P495

The founding feathers: the true ancestry of the Barbary dove

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Since the 16th century, Barbary dove has been known, but its domestication is unclear and poorly understood. Today, Barbary dove is considered to be the long-domesticated form of African Collared dove (*Streptopelia roseogrisea*), but no molecular work has been done to confirm this until now. Here, we generated 26 whole-genome sequences of modern and historical Barbary doves as well as African Collared doves and Eurasian Collared doves (*S. decaocto*). Using a population genomics approach, we were able to confirm that the main ancestry of Barbary dove derives from African Collared dove, specifically, from populations of the subspecies *S. r. arabica* distributed around The Red Sea region. This suggests that The Red Sea region could be the possible geographic origin of its domestication. Also, we identified signals of admixture between Barbary dove and Eurasian Collared dove; a possible early admixture event after the domestication of the Barbary dove. Furthermore, in modern times, a more extended admixture possibly related to the recent Eurasian Collared dove expansion through Europe. In this

study, we have not only clarified the ancestry of Barbary dove, but also discovered a complex history of admixture that shaped the genetic background of Barbary dove.

Abstract ID: 1383
Poster board number:
P496

How would you recognize an aurochs if you sequenced one?

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Ancient DNA is a powerful tool for studying the history and evolution of domestic animals and their wild relatives. Yet, it is not always straightforward to discriminate between domestic and wild species based on DNA data alone, especially when the true extent of genetic diversity among both early domesticates and their wild ancestral species is unknown. Morphological species identification might miss hybrid individuals and, thus, usually only samples pre-dating the introduction of domestic animals can be considered definitively wild. One such case is that of aurochs (*Bos primigenius*) and domestic taurine cattle (*B. taurus*) across Europe; while aurochs existed in sympatry with domestic cattle across Eurasia for millennia, only a handful of definitively aurochs sequences have been published. Because divergence between different geographically distant aurochs populations may be deeper than between domestic cattle and a given aurochs population, one cannot simply use any aurochs genome as a reference for all *B. primigenius* populations. This creates a problem; if you sequence ancient *Bos* DNA from a locality with no available aurochs sequences, can you tell if your sample represents a domestic cattle, an aurochs, or a hybrid? Can you quantify introgression? This problem is explored in the process of cattle domestication in European regions for which no definitively aurochs samples have been sequenced. I will survey various approaches for low coverage shotgun sequencing data that have been used in other species and discuss them in a case study context.

Abstract ID: 1518
Poster board number:
P497

An archaeogenomic perspective into sheep evolution and local breeds in the Baltic Sea area

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Sheep were domesticated 10-12 thousand years ago (kya) in western Asia. Sheep spread across Europe with the Neolithic expansion and had reached Scandinavia by 5 kya. At the same time the first wool economies started to become established in the Near East, probably associated with new types of sheep breeds which later expanded across Europe. Northern European short-tailed sheep are believed to be remnants of the first expansion of meat sheep. Very little is known about the genomics of early sheep in

northern Europe with most studies to date focusing on uniparental markers or retrovirus genotypes. In this study we investigate the genomic history of sheep in the Baltic-sea area with a focus on Sweden and Finland. We present five new high quality ancient sheep genomes (0.54X-16.8X) from two islands, Gotland and Åland, dating from ~3600 calBP (Late Neolithic - Early Bronze age) to ~435 calBP (late Medieval/early Vasa periods). We compare these genomes to a large panel of modern breeds from across the world with a focus on northern European breeds. We investigate what happened genetically in Scandinavian sheep from their introduction up until modern times both in terms of demographic history and in regard to wool-associated loci. We put specific emphasis on how these ancient samples relate to the landraces we can find now on these islands, as well as the more commercial Gotland breed. This previously un-opened window is bound to shed light on the evolution of characteristic Northern European sheep breeds.

Abstract ID: 1606
Poster board number:
P498

Deciphering the evolutionary history of a domesticated red alga using population genomic

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Gracilaria chilensis is one of the few seaweeds that present sign of incipient domestication. The species presents a disjunct distribution across the South Pacific Ocean, with populations located in New Zealand, Chatham Island, Chile and Peru but cultivation is occurring only in Chile where signs of domestication have been identified. The reduced genetic diversity observed in Chilean populations compared to other parts of its distribution, has been associated with recent over-exploitation of natural beds and/or a founder effect that occurred during the post-glacial colonization from New Zealand. The magnitude of these two events on the species' evolutionary trajectory is poorly understood. We used 2,232 SNPs genotyped for 687 individuals collected over the whole species range to perform population genomic analyses. We detected high genetic diversity and strong spatial structure in New Zealand that attest to the importance of Pliocene/Pleistocene events on populations and species diversification in its area of origin. ABC analyses support complex scenario of transoceanic dispersal with Chatham Island and South America colonized independently near the end of the Last Glacial Maximum. Furthermore, ABC analyses also inferred the existence two strong bottlenecks in Chile confirming that both the founder effect linked to transoceanic dispersion and colonization of South America, and the recent over-exploitation of natural populations have influenced the genetic architecture of *G. chilensis*. Predomestication history, including recurrent genetic bottlenecks, strongly eroded the genetic diversity of *G.*

chilensis prior to its cultivation, raising important challenges for the management of genetic resources in this incipiently domesticated species.

Abstract ID: 2100
Poster board number:
P499

Spread of donkeys into Asia Minor: archaeogenomic evidence

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Donkeys were domesticated from African wild asses in ancient Egypt. Neither their domestication history nor how they spread to other areas of the world has yet been fully understood. Due to its proximity to putative domestication centers, Anatolia can be regarded as an important station in donkey dispersal. Previous ancient DNA studies presented evidence of selective breeding of kungas, a F1 hybrid of female donkey and male Syrian wild ass, in mid-3rd millennium BC in Northern Syria, providing a dispersal date for this region, but not for Anatolia. In order to elucidate the history of the earliest donkeys of Anatolia, we sequenced 39 equid samples from Arslantepe and Kuriki Höyük from Central-East Anatolia, and generated ancient genomes of 6 individuals. These samples were found to cluster with modern donkeys in population genetic analyses. One of the Arslantepe donkeys, which was excavated from a Late Chalcolithic context, suggests the arrival of donkeys into Anatolia between 3900-3400 BC, contemporary with Early and Middle Uruk cultures in Mesopotamia, and represents the oldest known genetically confirmed donkey on Anatolian landscape so far.

Abstract ID: 2253
Poster board number:
P500

Animal domestication by humans as a case of correlated evolution

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Correlated evolution occurs when two or more traits evolve together, although sometimes only one is targeted by selection and others evolve indirectly. One example is the domestication process in vertebrates, in which humans imposed a selection favoring individuals with less defensive behaviors that might be correlated with other

modifications such as reduced cranium size and depigmentation. However, the generality of these correlations is debatable, partly, because it is unknown how much these correlated traits changed in domesticated vertebrates when compared to their ancestral forms, and if different domestication contexts affected the correlated evolution. Here, we investigated whether correlated evolution is a general process in domesticated vertebrates using comparative meta-analysis. We analyzed trait differences between domesticated and ancestral forms of several vertebrate species, considering traits were targeted and non-targeted by domestication. Additionally, we considered the domestication contexts for each species. We found that traits targeted by domestication showed greater difference between domesticated and ancestral forms when compared to non-targeted traits. We also found that contexts in which species were domesticated before having strong contact with human societies showed lower trait differences from their ancestral forms than species that were experimentally domesticated or that lived as commensals of human societies before domestication. Therefore, we showed that correlated evolution might be pervasive, although its magnitude may differ according to the context in which each species was domesticated. We suggest that such variation is the result of imposed selective pressure intensity on each species and the time that each one had to accumulate modifications.

Abstract ID: 2299
Poster board number:
P501

The history of domestic cat in Central Europe

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Progress in paleogenomic studies provided new information about domesticated animals, but cats are still veiled by mystery. Until now, it was known that in Europe domestic cats spread from two domestication centres, the Near East and Egypt but still it is unclear when and how. It was assumed that the main role in cat's expansion through the northern part of Europe had Roman legions. However, we found that cats that bore mitochondrial DNA (mtDNA) haplotypes of near- Eastern wildcats were already present in Central in the Neolithic. This indicates that the cats' route from the domestication center to Central Europe might have been more complex than previously thought. The newest mtDNA analyses show that cats with A1 haplotype, which was assumed to be characteristic for non-domesticated Near Eastern wildcats, were present in Central Europe even in the pre-Neolithic period. It could suggest that the range of the Near Eastern wildcat was much broader. We expect that our ongoing nuclear DNA analyses will elucidate whether the appearance of mtDNA of the Near Eastern wildcats in Central Europe was a natural admixture between two subspecies or it was human mediated dispersal.

Abstract ID: 2399
Poster board number:

P502

Early European tomato genomes reveal a mixed origin and private variation at domestication genes

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The tomato (*Solanum lycopersicum*) was brought to Europe in the 16th century after the conquest of the Americas. Historical sources suggest that the earliest European tomatoes appeared fully domesticated and displayed a large variation in fruit morphology. However, the origins of these tomatoes remain largely unknown. Their names in the literature imply both a Mexican and a Peruvian origin. A 16th-century genome sequenced at low coverage grouped with both Mexican and South American cherry tomatoes, and thus remained inconclusive. To shed further light on the ancestry of European tomatoes, we sequenced 21 herbarium genomes from between 1596 and 1915. Mean alignment depths at filtered SNPs ranged from 8.7 to 21.4. Including published sequences from 166 modern accessions, we found that the historical specimens split into one group associated with Mexican cherries, and one with Mexican large-fruited tomatoes. However, the latter group shares substantial genomic ancestry with Peruvian cherries. Both groups were already represented among our oldest four specimens from around 1600. We also explored variation at 116 domestication genes and identified haplotypes missing in modern cultivated tomatoes at 21 (18%) of these genes. Most of these genes (12) are associated with fruit flavour, and one with late-blight resistance. Our results support historical sources pointing to a Mexican origin of European tomatoes and previous findings of admixture between South American and Mexican tomatoes. Some of the flavour alleles we found only in historical genomes might have been lost as a side-effect of efforts to improve other traits.

Symposium: S34. How have biomarkers improved our understanding of health and the evolution of senescence? (id: 15)

Abstract ID: 1065
Poster board number:
P503

Ageing and age-specific effects of deletions on Drosophila life history

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Established evolutionary theories of ageing are based on the assumptions that the strength of selection declines with advancing age and the presence of mutations with age-specific effects. According to these theories mutations contributing to ageing have deleterious effects late in life, and either neutral or beneficial effects early in life. While many studies support these theories, our understanding of the age-specificity of individual mutations is still very limited, and the commonly observed positive pleiotropy across ages is not immediately compatible with mutations with age-specific effects and, consequently, with either established theory. To advance our knowledge on the age-specificity of individual mutations, here, we study a set of genomic deletions, which we measure for their effects on egg-to-adult survival, development time, fecundity at three ages (from young to moderately old) and adult survival. Most deletions show age-specific effects on performance, and many follow a pattern where their deleterious effect increases with age. Point estimates of correlational effects between ages were positive in all cases but one, but only significant towards higher ages. Our results thus indicate that ageing may also be caused by deleterious mutations with increasing negative effects with age. Such mutations are compatible with evolution of ageing under positive pleiotropy and are further supported by novel theory.

Abstract ID: 1205
Poster board number:
P504

Does evolution of ageing feedback (positively or negatively) on itself?

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Evolutionary theories of senescence are well established and evidenced, with ample support for the existence of ageing mutations, i.e., with only late life deleterious effects. However, we still lack a proper understanding of how, and if,the effects of deleterious mutations change with age. Since aged individuals are expected to be in a poorer condition than young individuals, new deleterious mutations should cause relatively greater harm in old vs young individuals. Infact, aged individuals can also be considered as being away from their optimal fitness, burdened by ageing mutations, compared to young ones. However, according to Fisher's geometric model of adaptive evolution, new mutations are less likely to be deleterious when an organism is away from its optimal fitness. This would suggest that new deleterious mutations would be less harmful in old than in young individuals. These contradictory ideas then suggest either an increase or a decrease in the relative fitness loss late in life due to new deleterious mutations, which would then speed up or slow down the evolution of senescence, respectively. We test these hypotheses in our study by exposing an outbred, laboratory adapted *Drosophila melanogaster* population to six stressful environments at different ages (to emulate temporally controlled 'deleterious mutations', i.e., the animal being maladapted to the environment), and measure relative changes in age-specific fecundity. Our study reveals mixed patterns of age-specificity of these 'mutations' and advances our understanding of mutational effects and the evolution of senescence.

Abstract ID: 1584
Poster board number:
P505

Parental age effects on offspring performance exacerbate reproductive senescence in European badgers

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Reproductive senescence is an age related decline in reproductive performance, and is commonly studied in terms of age-related patterns of offspring production. However, parental fitness arises via offspring performance as well as production, so both components require attention to gain a more complete understanding of the trajectory and fitness consequences of reproductive senescence. Here we utilise a longitudinal dataset from a long-term study of European badgers (*Meles meles*) to investigate maternal and paternal reproductive senescence, and quantify how both offspring production and lifetime performance vary with parental age. First, we show that badgers of both sexes experience a senescent decline in annual offspring production, which occurs with a similar age of onset in the two sexes. Second, we show evidence of deleterious maternal age effects on offspring performance; offspring mortality risk increases and offspring lifespan and life-time reproductive success decreases with within-mother increases in maternal age. Crucially, the maternal ages of onset of these declines in offspring performance are significantly earlier than those for offspring production, such that failure to account for them would lead to underestimation of the severity (in terms of timing and fitness consequences) of maternal reproductive senescence. Finally, we found no evidence of paternal age effects on offspring mortality, lifespan or life-time reproductive success. Overall, our findings illustrate the potential importance of attending to parental age-related changes in offspring performance as well as production, and the potential for sex differences in the relative contributions of these two components to the overall fitness consequences of reproductive senescence.

Abstract ID: 1588
Poster board number:
P506

Transient early-life downregulation of nutrient-sensing signalling improves late-life survival

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Life history theory posits that trade-off between reproduction and survival underpins the evolution of ageing and lifespan. However, recent research suggests that increased survival and reduced reproduction may not be as inextricably linked as previously thought. Some current evolutionary theories of ageing suggest that selection optimises gene expression for early-life fitness, but the same levels of expression may have damaging effects in late-life when selection is too weak to optimise them. Such theories predict that age-specific modification of gene expression can increase survival without reducing reproduction. Here we test this prediction by transient age-specific downregulation of insulin/IGF-1 nutrient-sensing signalling (IIS) pathway along the life cycle of *C. elegans.* IIS is an evolutionarily conserved genetic pathway that regulates

development, growth, reproduction, and longevity. Using RNA interference (RNAi) approach to knockdown expression of *daf-2* - a key receptor in the IIS pathway, a well-described method for lifespan extension in *C. elegans,* we investigated whether brief transient knockdowns in early-life can increase late-life survival without fitness costs. We first showed that transient 24-hour exposure to *daf-2* RNAi results in gradual recovery of normal gene expression levels within 48 hours. We then found that even such a brief downregulation of the IIS pathway across different ages increases late-life survival. Transient knockdown at any age did not result in a cost to lifetime reproductive output but pre-adult knockdown reduced individual fitness. These findings lend support to theories which propose that ageing evolves due to weak selection on gene expression in late-life.

Abstract ID: 1897
Poster board number:
P507

The use of cave-dwelling animals as models in senescence studies

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Subterranean environments harbour diverse species, which usually show astonishing, and sometimes bizarre, adaptive traits. One of these may be the elongation of lifespan, although it has not been established as a classical cave-related trait yet. Our literature review revealed that, when comparing subterranean species with their closest surface relatives, the former shows a substantial increase in longevity. These findings have been obtained from both vertebrate and invertebrate species, indicating a broad convergence in the evolution of longevity as one of the adaptive traits in cave-dwelling species. Increased longevity in cave animals is often in discordance with known predictors. For example, small-bodied subterranean species can live much longer than closely-related surface species of larger size. However, some of the environmental features which characterize subterranean environments (e.g., limited food resources, hypoxia and lack of UV irradiation), are consistent with known ecological predictors of longevity. Model species that have both surface and subterranean populations, and can be easily bred in laboratories such as the Mexican tetra (*Astyanax mexicanus*) can be utilized to disentangle the environmental vs. genetic contributors to longevity. The extensive convergent occurrence of longevity potentially enables researchers to discover different pathways for lifespan extension. Therefore, the use of cave-dwelling animals in ageing studies may represent a new frontier that can shed light on some of the mechanisms responsible for senescence.

Abstract ID: 1902
Poster board number:
P508

Biomarkers in a social fluid reveal social rewiring of metabolism and aging in superorganismal ants

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Many successes in life are based on collaboration. Microorganisms exchange nutrients through cross-feeding, and multicellular organisms are made up of tissues with different

metabolic roles and needs. Social insects, take this collaboration still further: Many ant colonies engage in social transfers of experimentally accessible fluids that contain both exogenously sourced and endogenously produced materials in a behavior called trophallaxis. We have shown that the endogenously produced proteins transmitted are biomarkers of the colony life in the carpenter ant *Camponotus floridanus*. Different stages of the colony life cycle circulate different types of proteins: young colonies prioritize direct carbohydrate processing; mature colonies prioritize consolidation and transmission of stored resources. Further, colonies circulate proteins classically implicated in oxidative stress, aging, and social insect caste determination, indicating that these molecules may act as superorganismal hormones. Comparing the trophallactic fluid of different individuals within a colony, we find that protein abundance and gene expression in relevant tissues rarely correlate, indicating division of metabolic labor across the superorganism, where some individuals produce while others use. We observe notable disparities in storage proteins and antioxidants. Thus, trophallaxis behavior provides a mechanism for distributed metabolism in social insect societies. Further, it may enable a fundamental rewiring of nutrient-sensing and reproduction gene networks resulting in the subversion of the longevity-fecundity trade-off in social insects through the shift of the metabolic burden of reproduction to workers.

Abstract ID: 1913
Poster board number:
P509

Inheritance of senescence-associated methylation patterns in the short-lived turquoise killifish

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As we are now starting to understand the processes underlying senescence, the mechanisms by which parental senescence can affect offspring are still unexplored. The turquoise killifish (*Notobranchius furzerii*) is characterized by a fast pace of life, resulting from adaptation to life in ephemeral savannah pools. With a rapid growth, a sexual maturity reached within two weeks after hatching and a lifespan of six months, this species is a particularly interesting model to study transgenerational effects of senescence. This study is part of a larger scale longitudinal experiment in which we rear killifish in captivity to investigate senescence effects on life history traits throughout the lifespan of individuals, and their transmission across generations. We aim to explore changes in DNA methylation as a parent-to-offspring transmission route of senescence effects by comparing young and senescing parents, and their offspring. We will identify senescence-associated alterations of DNA methylation patterns in the parental generation and whether and how (via maternal or paternal transmission) these patterns are inherited by employing the EpiRADseq method. This novel approach is derived from ddRAD sequencing and specifically adapted to the discovery of methylated loci. We will present here our experimental design, hypotheses and preliminary results on the methylation profiles of fin and ovary tissues of individual females.

Abstract ID: 2226
Poster board number:
P510

Synchronization of senescence across phenotypic traits and sex difference in the Alpine swift

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Senescence can be defined as a general deterioration of the organism, which can be observed in a large number of traits (e.g. physiology, morphology, reproduction), and which results in the death of the organism. Although senescence has now been widely described in wild animals, studies are mostly restricted to survival and reproductive traits, with a focus on female individuals. Whether senescence is affecting all the traits, whether this process is synchronised across traits, and whether males and females are affected in the same way, remain under-researched questions. However, this knowledge is essential for understanding the evolution of senescence. Using a long-term individual-based monitoring of free-living Alpine swifts (*Tachymarptis melba*), we investigated synchronicity and sex-specificity in senescence of 11 traits, including biometric traits, parasite burden, and reproductive traits, while accounting for selective disappearance and terminal effects. Overall, our results provide general support for senescence in 10 out of the 11 traits investigated. Although there was little variation across traits in the onset of senescence, some traits showed much stronger senescence patterns than others, and we observe significant differences in patterns of senescence between males and females. In particular, we found strong evidence of reproductive senescence in females but not in males. Our results suggest that natural or sexual selection may lead to sex-specific patterns of senescence, and to asynchrony between phenotypic traits. This study thus provides new insights for the understanding of the evolution of senescence.

Abstract ID: 2234
Poster board number:
P511

Reproductive death and the delay of the selection shadow in ants

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The way an organism ages (the onset and speed of senescence) depends on the strength of selection against age-specific mortality. This strength of selection is affected by the proportion of newborns from parents attaining an advanced age. Theory predicts that this proportion always decreases, therefore aging unfolds under a selection shadow. Social insects are an interesting case for gerontology, as queens achieve a highly productive, and at the same time, very long life in comparison to solitary species. We show that colonies of the ant *Cardiocondyla obscurior* shift to the production of sexuals late in life, following a prior investment into workers. Furthermore, transcriptomic data show that queens experience senescence only past this reproductive peak. We conclude that fitness returns late in life delay the selection shadow, and underlie the aging patterns of social insect queens. We argue that “Continuusparity” combines characteristics life history strategies of iteroparous and semelparous species and evolved together with superorganismality.

Abstract ID: 2036
Poster board number:
P512

Biomarkers for immunosenescence and inflammaging in wild passerine birds

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In immune defence, the first-line effector mechanisms including inflammation importantly contribute to host resistance to infections. Whether these immune responses undergo any age-related changes is currently unknown in most wild vertebrates. Here, we tracked selected inflammatory biomarkers in 54 individuals of free-living great tits (*Parus major*) of known age repeatedly captured during three subsequent years. The aim was to investigate long-term stability and age-dependent changes in oxidative burst responsiveness upon *in vitro* stimulation with bacterial lipopolysaccharide (LPS) and their links to leukotriene B4 (LTB4) levels and haematological traits. Furthermore, we linked these immunological traits to selected physiological markers (antioxidants, oxidative stress, and testosterone), and condition-related traits (carotenoid- and melanin-based plumage ornamentation, ptilochronological feather growth rate, and body mass). The LTB4 levels and absolute granulocyte counts increased with age, consistently with the *Inflammaging hypothesis*. In contrast, in line with the *Immunosenescence hypothesis*, the cellular oxidative burst showed quadratic dependency on age, with a peak in midlife individuals. Interestingly, the LTB4 levels were positively associated with the oxidative damage while negatively with glutathione peroxidase activity indicating links to redox balance. The cellular oxidative burst responsiveness was negatively linked to plasma testosterone levels in both sexes, indicating the immunosuppressive effect of testosterone. Individuals with elevated total oxidative burst responsiveness expressed significantly higher lightness of their carotenoid-pigmented yellow plumage and males showed narrower breast stripes suggesting a role in mate choice consistent with the *Indicator hypothesis*. This longitudinal study demonstrates in birds the contrasting age-related changes in markers of pro-inflammatory immunity contributing to immunosenescence.

Abstract ID: 2038
Poster board number:
P513

The effect of germline senescence on life history evolution

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Reproductive success shows age-associated patterns across the tree of life. An individual's reproductive success can increase with age, due to e.g. gaining experience or attaining a larger body size. However, increasing age can also associate with a

decline in reproductive success; having old parents leads to reduced offspring quality in various species. The latter can arise due to deterioration of parents' body condition with age and the resulting decrease in parental investment. Alternatively, or additionally, reduced offspring quality can result from deterioration of parents' germline with age, i.e. germline senescence. Various mechanisms can underlie germline senescence, including mutation accumulation, telomere attrition, and mitochondrial senescence. Importantly, while both somatic and germline deterioration in parents can affect offspring quality, alterations in germline can potentially be inherited and create a cumulative effect across generations. Here we ask: how does germline senescence affect the evolution of life histories? We model the two aspects of parental deterioration (somatic and germline) explicitly and perform simulations to investigate how reproductive strategies and allocation to germline maintenance evolve under different scenarios. We conclude that disentangling the effect of parental somatic deterioration from that of germline senescence can increase our understanding of parental age effects, and more empirical and theoretical studies are needed to help us better understand the mechanisms underlying senescence across generations.

Symposium: S35. The art of microscopic war: interference competition in microbes (id: 9)

Abstract ID: 1024
Poster board number:
P514

Siderophore-mediated social interactions drive invasion dynamics in natural Pseudomonas communities

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Invasions by alien species can have drastic effects on resident community composition and general ecosystem functioning. While the mechanisms and consequences of invasion have been widely studied in macroscopic communities, invasions in microbial communities have only recently received attention, and it remains thus unclear which microbial traits help invaders to successfully establish themselves in a community. Here, we examine the role of siderophores, iron-scavenging ligands, in shaping invasions of the pathogen *Pseudomonas aeruginosa* into resident communities of environmental pseudomonads. Siderophores can act as 'public goods' by making iron available to cells possessing matching receptors; but they can also act as 'public bads' by impeding access to iron to competitors lacking these receptors. Therefore, we predict siderophores to either promote or prevent invasions, depending on their effects on invader and resident growth. We performed supernatant and cross-feeding experiments and show that the invader is most successful when its siderophores inhibit the resident's growth. Conversely, invasion success is the lowest the more the invader is inhibited by resident siderophores. Finally, we also found that both invader and residents plastically adjust their own siderophore production depending on whether their opponent's acts as a

"public bad" or "public good". Strains downregulate their siderophore production if the other's is a "public good", and upregulate if the other's is a "public bad". Our findings show that a single secreted compound can have a major impact on bacterial community assembly and invasion dynamics, through its dual role as growth promotor versus inhibitor.

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P515

Collective protection against the type VI secretion system in bacteria

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Bacteria commonly face attacks from other strains via a wide range of antibacterial mechanisms and toxins. One of the most widespread attack mechanisms is the type VI secretion system (T6SS), a molecular speargun used by bacteria to stab and intoxicate competitors. A key strategy open to bacteria in the face of these attacks is to work together, but examples for collective defence mechanisms against the T6SS remain scarce. We serendipitously identified a putative collective defence mechanism against the T6SS while developing a computer game of bacterial warfare for an outreach activity. In agent-based simulations made for the game, we noticed that one strategy ("Slimy") that made extracellular polymeric substances (EPS) was able to resist attacks from another strategy that employed the T6SS ("Stabby"). Further dedicated simulation work revealed that this was a collective defence mechanism, whereby the production of EPS protected not only the producing cells, but also other cells nearby, even if they did not make EPS. We tested our model empirically using engineered strains representing the key strategies in the simulation: a T6SS-wielding attacker *(Acinetobacter baylyi*), and two T6SS-sensitive target strains (*Escherichia coli*) that either secrete EPS or not. This revealed that there was indeed collective protection, which occurred in part because secreted EPS shielded nearby non-producer cells from the T6SS. Our work identifies a key mechanism by which EPS-producing bacteria can work together to defend themselves from attackers.

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P516

A plasmid-borne antibacterial T6SS effector in *Vibrio campbellii*

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Climate change and the rise in ocean water temperatures is thought to result in the observed increase in the abundance of aquatic bacteria of the family *Vibrionaceae*, many of which are emerging pathogens. Most vibrios employ a tightly regulated type VI secretion systems (T6SS) to deliver antibacterial and anti-eukaryotic toxins, called

effectors, into neighboring cells to outcompete rivals and to manipulate hosts and predators, respectively. The function and regulation of T6SSs remain uncharacterized in many bacterial species. In this study, we investigated the environmental conditions that activate T6SS in *Vibrio campbellii* strain ATCC 25920. Using secretion and interbacterial competition assays, we determined that this T6SS is active under warm, marine-like conditions in which it mediates antibacterial toxicity. Interestingly, the publicly available genome sequence of this strain revealed a plasmid with many mobile genetic elements. When we inspected the genes found on this plasmid, we identified two putative T6SS effector and immunity pairs that may mediate antibacterial toxicity. One effector contains a DUF2335 phospholipase domain, whereas the activity of the second effector is unknown. Interbacterial competition assays confirmed that the novel effector and immunity pair mediates antibacterial toxicity via T6SS. We further confirmed that the effector exerts its toxicity in the bacterial cytoplasm upon ectopic expression in *E. coli*. Protein structure predictions indicated that it may be an ADP-ribosyltransferase. Taken together, our findings suggest that *V. campbellii* acquired T6SS effectors via horizontal gene transfer, and that it utilizes its T6SS during interbacterial competitions in its natural marine environment.

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P517

A novel antibacterial T6SS effector restricted to a subset of Vibrio parahaemolyticus isolates

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Vibrio parahaemolyticus are Gram-negative marine pathogens that can lead to gastroenteritis upon consumption of contaminated undercooked or raw seafood. Like most vibrios, *V. parahaemolyticus* employ T6SSs as antibacterial weapons in competition against rivals to establish themselves in an ecological niche. T6SSs are complex apparatuses that translocate toxic proteins, called effectors, into neighboring cells. The clinical type strain, *V. parahaemolyticus* RIMD 2210633, encodes two T6SSs. T6SS1 regulation and activity are well studied, whereas T6SS2 remains understudied. Here, we established that T6SS2 is an antibacterial system regulated by TfoX. Using comparative proteomics along with bioinformatic and genetic analyses, we identified three orphan operons encoding putative effectors. Competition assays confirmed that two of these operon encode T6SS2 antibacterial effectors and their cognate immunity proteins. One of these effectors contains a predicted nuclease domain and an Rhs repeats region; it is required for T6SS2 overall activity. The second effector, homologs of which are restricted to a subset *V. parahaemolyticus* isolates, interestingly contains two predicted domains: an N-terminal Par-E like nuclease and a C-terminal HDH lipase. We found that this effector is toxic when expressed in the bacterial cytoplasm. We aim to determine which of these two domains is responsible for the toxic activity of this novel T6SS effector.

Abstract ID: 1238
Poster board number:
P518

Engineering a customizable antibacterial T6SS-based platform in *Vibrio natriegens*

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Bacterial pathogens are a major risk to human, animal, and plant health. During evolution, bacteria have developed resistance against classic antibiotics. Therefore, alternative antibacterial strategies are urgently needed to treat infections. Many Gram-negative bacteria outcompete rival bacteria using a contact-dependent protein secretion apparatus, termed the type VI secretion system (T6SS), to deliver antibacterial toxins, called effectors, into neighboring cells. Thus, we reasoned that T6SS can be utilized as an antibacterial agent. In this study, we constructed a proof-of-concept customizable, modular, and inducible antibacterial toxin delivery platform. By engineering a T6SS that is controlled by an externally induced on/off switch, we transformed the safe bacterium, *Vibrio natriegens*, into an effective antibacterial weapon. Furthermore, we demonstrated that the delivered effector repertoire, and thus the toxicity range of this platform, can be easily manipulated and tested. We believe that this platform can serve as a foundation for novel antibacterial bio-treatments, as well as a unique tool to study antibacterial toxins.

Abstract ID: 1753
Poster board number:
P519

Systematic identification of novel genetic targets for fungal-bacterial antagonism

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Fungi and bacteria often occupy the same niches, where they compete against each other for resources. Such fungal-bacterial interactions have broad implications for human health and agriculture, but our understanding of the fungal-bacterial competition is very limited. We are interested in the antagonism between the fungus *Candida albicans* and the bacterium *Pseudomonas aeruginosa*, two opportunistic pathogens that frequently co-colonize and compete within infected tissues in humans. We hypothesize that the antagonism between these two species is driven by genes in conflict. Using these two microbes as an experimental model, we sought to identify genes participating in this inter-kingdom antagonism. We established a co-culture system in which the fungus suppresses bacterial viability and growth. To ask which bacterial genes are involved in this suppression, we screened *P. aeruginosa* transposon mutants in the presence and absence of *C. albicans*. We identified 13 bacterial genes required to defend against *C. albicans*. Three of them were involved in bacterial magnesium transport, suggesting that competition for magnesium underlies one of the antagonistic interactions. Furthermore, we identified 23 genes that became dispensable in co-culture with *C. albicans*, indicating that they function as mediators or direct targets of fungal antagonism. Many of these dispensable genes regulate essential bacterial physiology, like cell division and translation, while other genes remain functionally uncharacterized. These results suggest that the antagonism between these two microbes can affect bacterial physiology or virulence. Overall, our work highlights the power of functional genomics to discover multiple and novel antagonistic interactions across microbial kingdoms.

Abstract ID: 1828
Poster board number:
P520

Competition between two contagious cancers for one host: the Tasmanian devil (Sarcophilus harrisii)

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Tasmanian devil populations have decreased due to a contagious form of cancer (Devil Facial Tumour 1; DFT1) first reported in 1996. In addition, a second transmissible cancer (DFT2) discovered in 2016 is threatening this already endangered species. In the area where DFT1 and DFT2 co-occur and compete for hosts, they likely engage in an evolutionary arms race. To determine the competitive abilities of these two cancers, in vitro co-culture assays were performed. Using GFP-transduced DFT1 and DFT2 cell lines, different seeding ratios of cells were co-cultured for two weeks and counted using flow cytometry. Compared to mono-cultures, co-cultured DFT2 cells reached similar carrying capacities and growth rates but had longer lag phases. Overall, the number of co-cultured DFT1 cells decreased over time, never reaching the exponential growth seen in mono-cultured DFT1 cells, suggesting that the presence of DFT2 limits the growth of DFT1 cells. To understand whether the competitive advantage of DFT2 relies on physical interactions (e.g. ligand-mediated cellular recognition or mechanical stress), DFT1 and DFT2 cells were co-cultured in transwells, physically separating cell lines by a semi-permeable membrane. Transwell co-cultures showed no difference in growth between mono-cultured and co-cultured cells. The combined results from these experiments indicate DFT2 might be a better competitor than DFT1, at least in a contact dependent manner. The underlying mechanisms are being investigated with transcriptomics data. Although these results are in vitro, they will allow epidemiological modelling of disease trajectories and outcomes, and thus aid the conservation management of this endangered species.

Abstract ID: 1976
Poster board number:
P521

The evolution & ecology of bacteriocins in natural populations of *Staphylococcus aureus*

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Bacteriocins are toxins produced by bacteria to kill unrelated strains and species. Theory and laboratory experiments suggest that bacteriocin production is important in determining the competitive dynamics of bacterial strains. However, there is a lack of evidence supporting this in natural populations. Here, we examined the role of

bacteriocin-mediated competition in longitudinally sampled populations of *Staphylococcus aureus* from the human nasal cavity, allowing us to track within-host evolution over time. Using phenotypic assays, we assessed the ability of *S. aureus* to kill other *S. aureus* strains and commensal species co-inhabiting the nasal cavity. We then sequenced the genomes of our isolates to determine the identity of bacteriocin genes causing inhibition. We found that: (i) while only 25% of *S. aureus* strains could produce bacteriocins, they did play a role in colonisation success: bacteriocin producers were more likely to displace and outcompete other *S. aureus* strains compared to non-producers; (ii) *S. aureus* bacteriocins were more effective against interspecific competitors compared to intraspecific competitors; (iii) *S. aureus* strains carried a diverse range of bacteriocin genes to perform this inhibition. Overall, we provide evidence that the production of bacteriocins, especially those with a broad-spectrum of activity, is important in determining competitive dynamics in natural populations of bacteria from the human nasal cavity.

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Poster board number:
P522

Inter-species competition and resource availability can limit the evolution of pathogen virulence

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Understanding ecological factors driving pathogen evolution is critical in understanding emerging diseases. Pathogens both inside and outside hosts are subjected to selection imposed by the environmental conditions (presence of other microbial competitors & available resources) and various evolutionary trade-offs therein. Does evolution of better competitiveness trade-off with pathogenicity? Do the direction and strength of such trade-offs depend on the available resource? We addressed these questions using experimental evolution lines, where an entomopathogen *Bacillus thuringiensis* (Bt) evolved in the presence (co-culture) and absence (mono-culture) of another entomopathogen *Pseudomonas entomophila* (Pe). We grew them under two resource conditions, standard nutrient-rich 100 % Luria broth vs nutrient-poor 10% Luria Broth; followed by regular transfers to fresh media every 24 hours for 74 days. Although Pe could outcompete Bt when cocultured together at the beginning (before coevolution), the effect was reversed when Bt coevolved with Pe under high resource conditions. Coevolved Bt showed higher competitiveness against Pe than their control counterparts (monoculture), along with increased intrinsic growth rate. Next, we infected *Tribolium castaneum* (natural hosts) with coevolved Bt to test whether evolving higher competitive ability and growth interfered with their pathogenicity. We saw lesser mortality in beetles infected with coevolved Bt, suggesting a trade-off between higher competitive ability vs pathogenicity. We did not find all these effects in Bt lines coevolved under low resources, indicating that resource availability might impact the evolution of competitiveness and pathogenicity. We are also examining the genetic basis of the adaptive evolution of higher competitiveness vs reduced pathogenicity, using whole-genome sequencing.

Symposium: S36. Evolution of antibiotic resistance: from lab to clinic (id: 953)

Abstract ID: 1056
Poster board number:
P523

Quantifying stress-induced mutagenesis using fluctuation assays

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Bacteria are commonly exposed to low concentrations of antibiotics, for example due to imperfect adherence to a prescribed treatment or antibiotic residues in the external environment. Such low-dose exposure selects for resistance mutations, but also induces stress responses in bacteria. Some of these responses increase the mutation rate, called stress-induced mutagenesis (SIM). SIM potentially facilitates the evolution of antibiotic resistance and it has been proposed to prescribe “anti-evolvability drugs” in conjunction with antibiotics. However, besides the mutation rate, stress responses also alter other cellular properties like death or division rate and are often heterogeneously expressed across a population. Therefore, stress responses influence the whole population dynamic and it is unclear whether they actually result in more or fewer resistant mutants. Moreover, they affect mutation rate estimates via the standard approach of fluctuation assays because underlying modelling assumptions are not met. Current methods are only able to estimate the mean population mutation rate and potentially produce inaccurate estimates under stressful conditions.
We describe a population dynamic model which includes bacterial stress responses and is informed by single-cell data. Based on this, we develop a computational method for inferring mutation rates under stress. Our method allows estimation of the distinct mutation rate of cells with a high stress response level, which is important as theoretical work suggests that mutation rate variation can speed up multi-locus adaptation.
Taking stress responses into account when measuring mutation rates in the lab is a step towards better understanding how populations evolve resistance during antibiotic treatment.

Abstract ID: 1248
Poster board number:
P524

Combining antibiotics to curb antibiotic resistance: A systematic review and meta-analysis

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Antibiotic resistance is a major public health concern and combination therapy (CT) is discussed frequently as a potential treatment strategy to slow down resistance development. For some infectious diseases such as HIV and tuberculosis CT has been successfully applied to slow down resistance development. Theoretical studies and in vitro experiments suggest that CT is a promising general strategy to slow down antibiotic resistance evolution. However, there has been clinical evidence published that indicates no benefit of using a higher number of antibiotics over fewer. To assess whether clinical evidence is in line with non-clinical studies, we systematically summarise and assess data across a wide range of bacterial pathogens and antibiotic combinations from randomised controlled trials (RCTs). Our systematic review und meta-analysis shows that the current clinical evidence based on RCTs cannot generally reinforce CT as a universal superior strategy for bacterial infections with regard of resistance development. As assessing resistance development is not a common main aim of RCTs, these trials are typically not specifically designed to detect a difference of resistance development in treatment arms implying that they are often strongly underpowered. Therefore, the non-significant effect we found does not necessarily support the absence of a relevant effect of using a different number of antibiotics. Our study rather highlights the absence of adequate evidence from RCTs to properly estimate the effect. Our results suggest that there is a need for further clinical research to produce reliable estimates and to understand which factors determine the performance of antibiotic CT.

Abstract ID: 1652
Poster board number:
P525

Evolutionary paths to high-level ampicillin resistance

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The widespread use of beta-lactams has resulted in a growing prevalence of highly resistant pathogens. Indeed, clinical isolates can have very high resistance to beta-lactams, most prominently to ampicillin where resistance levels could even exceed 1,000 µg/ml. Yet, in striking contrast, bacteria evolved in laboratory settings, typically plateau on much lower levels of resistance. Here, evolving *Escherichia coli* on the Microbial Evolution and Growth Arena (MEGA) plate, we found that large population sizes circumvent the previously observed saturation of resistance under ampicillin selection, selecting for mutants resistant to ampicillin at over 8,192 µg/ml. Whole-genome sequencing of resistant isolates revealed that this high ampicillin resistance was acquired via a combination of single-point mutations and an increasingly focused gene amplification of the beta-lactamase enzyme AmpC. Importantly though, blocking AmpC-mediated resistance only slightly reduced the adaptive potential: strains deleted for *ampC* were able to evolve high-level resistance through combinations of genetic changes in genes involved in multidrug resistance such as efflux pumps, transcriptional regulators, and porins. Our results reveal that combinations of distinct genetic mutations, accessible at large population sizes, can drive high-level resistance to ampicillin even independently of beta-lactamases.

Abstract ID: 1666
Poster board number:
P526

Antibiotic resistance fitness landscapes are surprisingly predictable across environments

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Much of our understanding of antibiotic resistance (ABR) evolution comes from culturing bacteria with single focal mutations in one lab environment. However, evidence is mounting on the importance of interactions at dictating real world ABR evolution: in addition to genotype-by-environment (GxE) effects, also gene-by-gene (GxG or epistatic) and gene-by-gene-by environment (GxGxE) effects seem to be prevalent. To quantify GxGxE effects in Escherichia coli, we studied how ABR fitness landscapes change across environmental gradients. We created intergenic fitness landscapes using gene knockouts and single nucleotide ABR mutations a priori identified to vary in the extent of GxE effects and we measured competitive fitness across a full combinatorial set of temperature and antibiotic dosage gradients. This way, we assessed the predictability of 15 small fitness landscapes across 12 different, but related, environments. Surprisingly, we found little evidence of interactions overall. Most of the variation in our data is explained by the additive effects of mutations and environments. Nevertheless, the patterns of epistasis were strikingly different between ABR mutations and gene knock-outs. For ABR genotypes, epistasis decreases as antibiotic concentration increases. Gene knock-outs exhibit the opposite trend. Despite setting out to promote the role of GxGxE interactions on evolution, our work reiterates that ABR single mutants can have consistent effects across genotypes. Furthermore, our work suggests that GxG interactions between gene knockouts and amino-acid (ABR) mutations may be smaller than between other mutational classes, perhaps due to evolved mutational robustness in E. coli.

Abstract ID: 1732
Poster board number:
P527

One strategy to treat them all? The "hit hard" dogma in view of antibiotic resistance evolution

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The prevailing dogma of antibiotic treatment "hit early and hit hard" dates back to the discovery of antibiotics and their first medical application. In this treatment strategy antibiotics are administered as early as possible during an infection, and at a dose as high as possible to kill the infectious agents quickly. In recent years the "hit hard" part of this strategy has been questioned when analyzed in the light of evolution of antibiotic resistance, e.g. by Day and Read in 2016. The argued that a concentration as low as possible could in some situations be the optimal treatment concentration to prevent the emergence of an antibiotic resistant subpopulation. We revisit this question theoretically and study the location of the optimal treatment concentration to prevent the establishment and, more importantly from a host population perspective, to minimize the

spread of antibiotic resistant pathogens. We find that the optimal antibiotic concentration to minimize the spread of resistance is very often the highest possible dose. This indicates that even when looked at through an evolutionary lense, the old wisdom of "hit hard" seems to be the best strategy to prevent the spread of antibiotic resistance in many situations. Additionally, we study the differing effects of biostatic, i.e. growth inhibiting, and biocidal, i.e. bacteria killing, drug types. We find that generally biostatic antibiotics limit the spread of resistance more than biocidal drugs. Overall, the presented theoretical results can be translated directly into hypotheses amenable to experimental validation.

Abstract ID: 1803
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P528

Antibiotic persistence is not defined by bacterial population growth phase

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Subpopulations of quiescent bacterial cells, known as persister cells, can survive high doses of antibiotics despite being genetically susceptible. The lack of an identified genetic mechanism raises questions about how persistence evolves: why do persister cells form; is there variation in the rate of formation; and can we explain this variation by observing population growth dynamics and interactions with abiotic stressors such as different antibiotics? The majority of evidence presented in the literature suggests that persister cell formation rate peaks when cell growth rate is slow, such as during stationary phase or in biofilms. However, we still lack definitive evidence comparing how persistence changes across physiological stages of a growth curve. In addition, little attention has been paid to the antibiotic-specific effects driving variation in persistence. We measured persister cell formation at two-hourly intervals across a growth curve in response to three antibiotic stressors in cultures of *P. aeruginosa*, an opportunistic pathogen. In contrast to previous observations, we observed that persistence can peak significantly during exponential growth when population growth rates are highest. This persistence peak during exponential growth occurred independently in two antibiotic treatments (ciprofloxacin and tobramycin). The response to the beta-lactam, meropenem, differed in that persistence was greatest during stationary phase growth. By varying inoculation density, we found that increased persister cell formation during stationary phase mainly occurs in cultures with higher inoculation densities. Taken together, our results suggest that persister cell formation is not simply the result of slow growth as is commonly assumed.

Abstract ID: 1818
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P529

Exploring the boundaries and mechanisms of cellular negative hysteresis

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Novel treatment strategies using existing antibiotics more sustainably are urgently required to combat the antibiotic crisis and constrain the evolution of antibiotic resistance. The potential of negative cellular hysteresis to increase efficiency of sequential antibiotic treatment was tested in a previous study. Short exposure to the β-lactam carbenicillin was shown to sensitize *Pseudomonas aeruginosa* PA14 towards the aminoglycoside gentamicin. However, the molecular mechanisms of this phenomenon and its distribution across *P. aeruginosa* and other Gram-negative bacteria remained unknown. In this study – using a high-throughput screen – we find that negative hysteresis is widespread across the whole phylogeny of *P. aeruginosa* and several strains of *Escherichia coli, Acinetobacter baumannii*, and *Klebsiella pneumoniae.* It is also expressed across a variety of clinically relevant antibiotics. Moreover, the genetic basis of cellular hysteresis was investigated with a focus on the Cpx envelope stress response system. Although well described for *E. coli*, this two-component system has not been characterized for *P. aeruginosa* previously. Our findings provide insights into the mechanisms underlying negative hysteresis. In addition, the concept of negative hysteresis is likely to be applicable for a variety of infections and thus offers a promising focus for improving evolution-informed antibiotic therapy.

Abstract ID: 2449
Poster board number:
P530

Ecologically mediated mutation rate plasticity provides new insights on microbial evolution

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Spontaneous point mutations are the ultimate source of genetic variation and, for microbes, can confer resistance to most antibiotics. Understanding mutation rates is both essential for a fundamental understanding of microbial evolution, and suggests sustainable routes to mitigating antimicrobial resistance. Mutation rate is, in part, determined by microbes' ecological environment. Density-associated mutation rate plasticity (DAMP) is a widespread phenomenon resulting in populations at low population density mutate at elevated rates. However, the mechanisms producing DAMP remain elusive. Here we bring together dynamic ODE modelling with experimental measurements of mutation rates and natural mutagens (reactive oxygen species, ROS), to get insights into the DAMP mechanism. ODE modelling predicts that, when individuals' production and/or degradation rates of ROS respond to density, the population shows DAMP. Our experiments in *Escherichia coli* confirmed that reducing ROS production through anaerobic growth or reducing degradation rates via deletion of *katE*, *katG*, *ahpC* and *ahpF* (all involved in ROS, specifically hydrogen peroxide, removal) eliminates DAMP. Previous work also links the activity of MutT, responsible for

the removal of ROS-damaged nucleotides, to the DAMP phenotype. Further, we show that cells lacking the *fur* gene have high mutation rates and no DAMP. These cells have an elevated free iron pool, which increases the intracellular concentration of highly mutagenic hydroxyl radicals. Finally, we link DAMP to dynamic fluctuations in the external hydrogen peroxide concentrations generated during the culture cycle. Thus, DAMP mechanisms provide new insights into how ecological factors determine the spontaneous mutation rate.

Symposium: S37. Microbiomes in the wild: the drivers and evolutionary consequences of microbiome variation (id: 948)

Abstract ID: 999
Poster board number:
P531

Feedback loop: microbiome, immunity, stress and fitness

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Microbial composition/colonisation of the gut - gut microbiome - during the first stages of life has been shown to have major influences on physiology, immunity and fitness of the host. Recent studies also show that long exposure to stress may disrupt the gut microbiota affecting the immune system and fitness.
Using a wild population of the common buzzard (Buteo buteo), we propose to study the gut microbiota development during the first weeks of life and its effects on fitness, immunocapacity and stress. We investigated not only gut bacteria, but also fungal and microbial eukaryotes through a combination of 16S rRNA, 18S rRNA and 28S rRNA gene sequencing. Hemolysis/Hemaglutination and Bacterial killing assays will be used to assess immunocapacity. Long-term exposure to stress will be measured via glucocorticoide secretion.
We expect our results to show that buzzard chicks with good body condition will have higher diversity of gut microbiota, will score higher in the immunocapacity assays and would be subjected to lower long term levels of stress.
A large number of studies have focused on some aspects of this system but none looked at the system as a whole and as far as we know this will be the first of its kind done in a wild population.

Abstract ID: 1017
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P532

Effect of temperature in the microbiota composition of a parasitoid wasp

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Insects' gut harbours diverse microorganisms — this community, also called the gut microbiota —affects their hosts' functional and ecological roles. It has been shown that environmental shifts caused by climate change, such as temperature variation, can disrupt the stability of the gut microbiota of insect hosts, with consequences for the host fitness. However, few datasets on restricted systems are available to explore this question further. Thus, we still know little about how temperature alters the microbiota of wild insect populations and the consequences of such changes for species community ecology. Here, we investigate the effect of environmental temperature in the bacterial community of individuals of the parasitoid wasp *Hyposoter horticola*. Insects were reared in two different temperatures (26 and 28 °C) under controlled laboratory settings from larval to adult stages. We compared sequenced amplicons of the bacterial 16S rRNA gene of 39 individuals reared at 26 °C and 79 wasps reared at 28 °C. This study will help us understand how environmental temperature affects the diversity of bacterial symbionts associated with a parasitoid wasp and will bring new insights into the effects of climate change on the microbiota of wild populations.

Abstract ID: 1187
Poster board number:
P533

Infection by a eukaryotic gut parasite in wild zooplankton associates with a distinct microbiome

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Host-associated bacterial communities (or microbiomes) play an integral role in defense against parasites. Yet, few studies investigate tripartite interaction between a host, a parasite and host microbiomes, particularly in the wild. We investigated such interactions using the zooplankter water flea belonging to the *Daphnia longispina* species complex and its highly virulent, eukaryotic gut parasite *Caullerya mesnili*.
We performed two experiments using 16S amplicon sequencing to compare microbiomes associated with infected and uninfected hosts in the Swiss eutrophic lake Greifensee during (1) a natural epidemic in 2020, in the host gut and body tissue and (2) six past natural epidemics spanning 13 years (2007, 2011, 2013, 2014, 2017 and 2020), in whole individuals. Overall, our sequence data represents the microbiomes of 250 infected and 214 uninfected animals. Infected host gut microbiomes showed classic community-level changes consistent with dysbiosis (decreased alpha-diversity and increased beta diversity) compared to uninfected hosts; and some bacterial abundance shifts also occurred in the body tissue with gut infection. However, variation in beta diversity by disease status in whole individual microbiomes was inconsistent across epidemics. Further, distinct sets of bacterial taxa differed in abundance by infection

status from year to year, but some taxa specifically associated with infected or uninfected hosts across epidemics.
Our results show that the microbiomes of a dominant zooplankton species change across years and during natural epidemics of a gut parasite, raising questions about the functional role of bacteria associated with infected hosts and their role in host disease ecology.

Abstract ID: 1204
Poster board number:
P534

How immune priming affects host microbiome and *vice versa*

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An animals' microbiome can have strong effects on host biology and fitness. Moreover, the microbiome itself, as well as microbiome-related host traits, might affect coevolving pathogens. In the red flour beetle, *Tribolium castaneum*, we have previously shown that the removal of the hosts' microbiome abolishes oral immune priming. Priming is an important and widespread form of innate immune memory in invertebrates, leading to increased resistance after a prior exposure. Here we asked, whether immune priming of *T. castaneum* with the insect pathogen *Bacillus thuringiensis* affects the hosts' microbiome, and whether micro-evolution of this pathogen differs in primed as compared to non-primed hosts. Using 16S rRNA sequencing of the host microbiome following two different, established routes of immune priming treatment (orally via ingestion of bacterial culture supernatants, and septically via injection of heat-killed bacteria), we found that only oral priming led to changes in the host microbiome, in particular an increase in the abundance of *Bacillus* species. Experimental evolution of *B. thuringiensis* via serial passage in orally primed and non-primed hosts resulted in a strong divergence in the replicate lines with respect to bacterial virulence (i.e., host killing), especially in lines evolved in primed hosts, some of which lost virulence. Whole genome resequencing of the evolved bacteria revealed genomic changes that are currently being analysed to gain deeper knowledge of the underlying evolutionary changes. Taken together, our study provides urgently needed, but rare knowledge about the relevance of the host microbiome for both, host and pathogen fitness.

Abstract ID: 1346
Poster board number:
P535

Using flow cytometry to quantify and describe the gut microbiome of wild mice

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The composition of the microbiome can profoundly affect an animal's biology, and so accurate determination of its composition is critical. As such, absolute quantification of microbial cell number by flow cytometry is advantageous compared with the more commonly used measurement of relative abundance of taxa. Flow cytometry can also identify and sort different component cell populations of the microbiome, which allows new questions to be asked about the composition of the microbiome and interactions among different components. Two such different components of the microbiome are microbes that are bound by or not bound by host immunoglobulin A (IgA). Previous studies in humans have shown that IgA-bound taxa are more pathogenic than non-IgA bound taxa. Therefore, our first question was: to what extent are IgA-bound and non-IgA-bound microbial taxa the same taxa among different hosts. Two other components of the microbiome are prokaryotic and eukaryotic cells. Eukaryotic cells are often overlooked in the microbiome studies, despite being able to interact with both the host and prokaryotic cells. Therefore, our second question was: how does the abundance and composition of eukaryotic taxa vary among different hosts, and how do eukaryotic taxa interact with prokaryotic taxa. To address these questions, we designed novel methods to survey the gut microbiome of three UK populations of wild house mice (*Mus musculus domesticus*) using flow cytometry and amplicon sequencing. Initial findings suggest that mice vary according to number of IgA-bound microbes and that flow cytometry can be used to better identify fungal taxa in the microbiome.

Abstract ID: 1348
Poster board number:
P536

Gut microbiota at the interface of host energy needs and food availability

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Vertebrate hosts and their associated microbiota evolve in interaction with one another and with the environment. Importantly, gut microbiota can facilitate host adaptation and plastic responses to the local resource environment by contributing to the acquisition, metabolism, and allocation of energy from food. We examined the possible role for gut microbiota in mediating between host physiology and food availability, using an experiment that combined experimental evolution and a food availability manipulation. Hosts with different evolved metabolic rate and energy demand (bank vole selection lines for high metabolic capacity vs. unselected lines) were released into large field enclosures with or without food supplementation. Host reproductive success and survival as well as changes in their gut microbiota (via 16S V4-region amplicon sequencing) were monitored throughout the summer season. While the food treatment strongly shaped both host fitness and the diversity and composition of gut microbiota, the microbiota of the selection lines largely overlapped in both treatments and did not predict fitness in surviving voles. Thus, gut microbiota rapidly adapted to the environment but had little impact in matching differing host energy needs with the food availability. The results suggest that gut microbiota may be crucial for host phenotypic plasticity in adjusting to the prevailing resource environment, with the environmental conditions shaping the resulting microbiota more than the host genotype.

Abstract ID: 1354
Poster board number:
P537

Global comparative analysis of virome composition in ants

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Viruses are the most abundant and diverse biological entity on our planet. Over the past decade, advances in sequencing technology and bioinformatic tools have opened up entirely new opportunities in the field of insect viromics, with unprecedented insights into the diversity and evolution of insect-associated viruses. Within the framework of the Global Ant Genomics Alliance, we identified and analyzed viral sequences in the metagenomes of 162 ant species across 12 subfamilies, 27 tribes and 99 genera, using short and long read data from whole-genome next generation sequencing. Our results show that natural ant populations harbor a diverse array of viruses, including entomopathogenic viruses, phages of associated microbes, and viruses likely associated with species specific diets. Characterizing the viral diversity within a taxonomic and phylogenetic framework will allow investigating host-virus coevolution, horizontal transmission, and the eco-evolutionary dynamics related to eg, variation in nutrition, habitat types, or social organization in ants. Together, these analyses will significantly expand our knowledge and understanding of ant virus diversity and evolution.

Abstract ID: 1378
Poster board number:
P538

Defensive symbiosis “in the wild”: seasonal dynamics of parasitism and symbiont-conferred resistance

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Resistance to parasites rarely comes for free. If it trades off with other components of fitness, being resistant can result in either a net benefit or a net cost to the host, depending on the ecological context. In our model system, black bean aphids (*Aphis fabae*) benefit from increased resistance to parasitoids when carrying the defensive bacterial endosymbiont *Hamiltonella defensa*, which is however costly in the absence of parasitoids. Balancing selection may thus explain why only part of the individuals in natural aphid populations carry *H. defensa,* despite the protection it provides. In a 2-year field study, we set out to look for signatures of balancing selection in three natural populations. We collected temporally well-resolved data on the prevalence of *H. defensa* in *A. fabae* and we estimated the risk imposed by aphid parasitoids using bait hosts. Despite a marked early summer peak in parasitism risk in both years, the prevalence of *H. defensa* remained surprisingly stable. Only in one of the two years we found suggestive evidence for the expected increase of *H. defensa*-protected aphids in response to selection by parasitoids. We discuss these results in the light of seasonally variable parasitism pressure as well as other environmental factors potentially imposing selection for or against aphids carrying *H. defensa*.

Abstract ID: 1404
Poster board number:
P539

Coping with anthropogenic stress: the role of gut-associated bacteria in a freshwater isopod

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Human activity is a major driver of environmental change and can act as a significant evolutionary force. Although responses of organisms to anthropogenic changes are extensively studied, most work to date does not integrate responses of host-associated microbiomes, even though they can be a key determinant of host fitness. Chemical pollutants - often introduced to streams via wastewater treatment plant effluents - are pervasive anthropogenic stressors that can affect the fate of individuals, populations, and ecosystems. We use *Asellus aquaticus*, a freshwater isopod with high environmental tolerance, to study the impact of pollution on organismal fitness and to explore the hypothesis that the gut-microbiome may mediate adaptation to environmental stress. We specifically aim to understand how wastewater contaminants, including chemical compounds and microbes, affect *A. aquaticus* performance and microbiome. For this, we combine laboratory and semi-natural flume experiments with the study of wild populations that inhabit areas with varying degrees of pollution. Our results show that chemical pollution can lead to mortality of the host at high concentrations, while more realistic concentrations affect growth and feeding rates (i.e. host performance). 16S amplicon sequencing of midguts and hindguts further reveals that the composition of the gut microbiota is altered in the presence of wastewater, and differs between animals from polluted and non-polluted habitats. Our results provide insight into host-microbiome responses to anthropogenic change, contributing to an ongoing discussion about the extent to which the microbiome may mediate host adaptation to stress.

Abstract ID: 1463
Poster board number:
P540

Pollution-related bird-microbe associations

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Host-associated microbial communities and their functions relevant to the host physiology can be disturbed by exposure to anthropogenic pollution. Several toxic heavy metals, such as arsenic and cadmium that are commonly detected in the surroundings of industrial activities, have been associated with altered microbiota composition in animals; including increase in pathogenic bacteria. However, wild avian microbiota in relation to pollution are poorly studied, despite their relevance for avian health, pathogen transmission, and conservation. We study the effects of anthropogenic metal pollution (Cu, Ni, As, Cd, Pb) on the nest and gut microbial composition of three common passerine birds (great tit *Parus major,* blue tit *Cyanistes caeruleus,* and pied flycatcher *Ficedula hypoleuca*) around a copper-nickel smelter in Harjavalta, Finland. We

inspected 15 nests per each study species from polluted and unpolluted areas to collect data of brood variables (i.e., all together 3 species x 2 areas x 15 nests = 90 nests). Nest swabs and fecal samples (pooled by brood) were collected, and the fecal samples were split for microbial (16S rRNA sequencing) and metal (ICP-OES) analyses. Blood samples were further collected to measure oxidative stress responses (enzymatic antioxidants and glutathione). We expect to see differences in the nest and gut microbiota between metal exposed and non-exposed nestlings. We also expect metal-related interspecific variation in the microbial colonization of nests and nestlings, due to differences in nest composition, diet, and metal tolerance. Pollution-related changes in the wild avian microbiota is a novel approach to bird ecotoxicology and requires further investigation.

Abstract ID: 1512
Poster board number:
P541

The drivers of gut microbiota in wild great tit: effects of health and heavy metal contamination

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The gastrointestinal tract of vertebrates is inhabited by taxonomically and functionally diverse bacterial communities, which can influence host health and fitness. Consequently, gut microbiota composition and richness can potentially serve as an indicator of host health status. In urban environments, heavy metals can be an important source of impaired health state in free living animal populations. In addition, the exposure to heavy metals can disrupt symbiotic bacterial communities. Current research on the consequences of heavy metal exposure on health of the host and its symbiotic microbiota, aims chiefly on humans and model organisms, but the knowledge in non-mammalian free living vertebrates is still insufficient. Using samples collected between 2015 and 2018 in repeatedly captured individuals we studied the interactions between health-related traits (heterophiles to lymphocytes ratio, relative number of immature erythrocytes, relative basophile count), the gut microbiota (analysed by 16S rRNA Illumina sequencing) and the exposure to heavy metals (blood concentrations of Cd, Pb, Zn) in free-living population of great tits (*Parus major*) inhabiting city forest in Prague. Our contribution provides an insight into the unexplored relationships between gut microbiota, health and environmental pollution in wild birds.

Abstract ID: 1521
Poster board number:
P542

Secondary endosymbionts in aphid field populations

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The occurrence and effects of secondary endosymbionts has been studied in many laboratory experiments, and mainly on commercially important pest aphids. However, it is also important to study their occurrence and effects in more aphid species and in field populations. Secondary endosymbionts could strongly affect the community dynamics of aphids and their surrounding trophic levels. The objective of this study was to gain an overview of the occurrence of aphid secondary endosymbionts in the Netherlands, and study correlations between secondary endosymbiont presence, host plant genera, and ant tending. We sampled aphid colonies belonging to 104 aphid species and screened for the eight most common secondary endosymbionts with species-specific primer sets. We found that secondary endosymbionts are common in field populations and could affect community dynamics to a previously overlooked extent. However, since it is still unknown how many of these endosymbionts affect their hosts, more studies are needed to test the importance of secondary endosymbionts to community dynamics. Our screen for the occurrence of secondary endosymbionts is, to our knowledge, the first in the Netherlands, and provides a basis for future research in this field.

Abstract ID: 1549
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P543

Response of the gut microbiota and its host to warmer climate and habitat fragmentation.

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Climate warming and landscape fragmentation are both known to have direct negative impacts on biodiversity. While there are many researches on species phenotypical responses and adaptation to these two human-induced global change factors, their combined effects are more rarely studied, especially when it comes to the microbiota colonizing animals gut. The gut microbiota indeed ensures essentials function for its host, and its plasticity and adaptation to climate change and habitat fragmentation should hence mediate, at least partly, the response of the host. Here, we investigated the interplay between climate warming and habitat fragmentation on the gut bacterial communities of *Zootoca vivipara*, as well as their underlying drivers amongst host survival, dispersal and microbiota plasticity. To this end, we conducted a three year-long study in a semi-natural experimental set-up composed of connected or unconnected mesocosms subjected to present-day climate and a ~2°C warmer climate (IPCC's projections for year 2100). We found that a 2°C warmer climate leads to a decrease of the gut microbiota diversity over time and to gut microbiota compositional differences in

isolated habitats. The plasticity of the gut microbiota partly explains these modifications, while we found no evidence of differential selection on microbial diversity between climates. Habitat connectivity cancels the effects of warmer climate on lizard gut microbiota diversity and composition, and this canceling effect appears to be mediated by thermal habitat choices related to individual microbial diversity. Our study suggests that global changes factors may trigger host response by disrupting their microbiota.

Abstract ID: 1550
Poster board number:
P544

Altitudinal effect on gut microbiome composition of Anatolian Blind Mole Rat (Nannospalax xanthodon)

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While the ecological importance of the gut microbiome is undisputed, most research has been performed on a few laboratory animal models, leaving the wild species understudied. Thus, our knowledge of the intricate details of the interactions among the host, the microbiome, and the environment is still very limited. The altitude gradient offers one of the most powerful natural experimental settings to study the ecological role of the microbiome.
Using four populations of the obligate subterranean rodent, the blind mole rat (BMR - Nannospalax xanthodon), sampled across the elevational gradient in southern Anatolia, we tested two hypotheses: (i) altitude is a major factor shaping the difference in microbiome composition among the host populations, and (ii) the microbiome diversity increases with altitude. We collected ~10 caecum samples from each altitude category (two populations from 1100 m, one from 1800 m, and one from 2700 m. asl).
Using Illumina sequencing of bacterial 16S rRNA amplicons, we found that Firmicutes, Bacteroidetes, Proteobacteria, and Verrucomicrobia are the most dominant phyla in BMR. While the abundance of Firmicutes, Proteobacteria, and Verrucomicrobia phyla decreased with altitude, Bacteroidetes increased. Altitude, as opposed to geographic distance, was found to be a major factor affecting the microbiome composition, with an increasing trend in bacterial diversity at higher altitude. We are currently investigating additional populations to increase the statistical support for our results.

Abstract ID: 1764
Poster board number:
P545

Volatiles of bacterial origin associate ecto-parasitism and fledging success of hoopoes

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Bacterial symbionts are partly responsible of animal odors and, thus, they are likely involved in chemical communication of their hosts. Predators and parasites use animal odors as cues to detect their victims and, therefore, volatile profiles of symbiotic bacterial origin could affect the outcomes of interactions with these kinds of enemies. Here, we explore this relationship by experimental manipulation of the nest microbiota of hoopoes (*Upupa epops*) before reproduction started and quantifying ecto-parasitism of females and nestlings and characterizing microbial communities and volatile profiles of their uropygial secretion, the bacterial community of nest materials and the odors of hoopoe nests during the nestling stage. Our experiment affected the bacterial community of nest materials, volatiles found in the nest environment during reproduction, intensity of ecto-parasitism and fledging success. Moreover, microbial and volatile profiles of uropygial secretions resulted related to each other and explained the nest odor. Finally, some of the volatiles and bacteria detected in nest materials and uropygial secretions associated with intensity of ectoparasitism suffered by female and nestlings, as well as with reproductive success. All these results further support a link between microbial communities and animal odors and strongly suggest that the associations of symbiotic bacteria with ectoparasitism and reproductive success are, at least, partially, mediated by volatiles from bacterial metabolism.

Abstract ID: 1779
Poster board number:
P546

Effect of gut microbiota on male reproducitve traits in *Drosophila melanogaster* populations

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Phenotypes are shaped by their underlying genes, their environment and, as is becoming increasingly clear, by the microbes associated with them. Particularly the gut microbiota has emerged as an influential contributor to nearly any aspect of its host's life. However, little is known, about the influence of commensal microbes on their host's reproductive health, and, if sexually transmitted, how they interact with the microbiota of their host's sexual partners. Changes in the reproductive performance could be particularly consequential for males in species where females mate multiply and thus cause sperm from different males to compete for fertilization. Considering the importance of genetic variation, condition (especially nutrient) dependent expression of reproductive traits or male-female interactions in sexual selection theory, it may be time to begin incorporating microbiota into sexual selection research. Additionally, with a growing interest in targeting the microbiome of pest insects to address agricultural losses, starting to understand how microbes affect reproduction in both target and non-target species seems crucial and urgent.
Therefore, this project aims to study the consequences of commensal bacteria on male reproductive investments and fitness. Using wild-caught and lab-reared *Drosophila*

melanogaster as a study system and high-throughput long-read sequencing, we will study the extent of sexual transmission of bacteria and manipulate the microbial composition to study the effect of representative strains on various male reproductive traits, from sperm quality or composition of the seminal fluid to competitive fertilization success.

Abstract ID: 1789
Poster board number:
P547

Human encroachment into wildlife gut microbiomes

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In the Anthropocene, humans, wildlife, and their environments are interconnected, especially as humans advance further into wildlife habitats. Wildlife gut microbiomes play a vital role in host health, but anthropogenic disturbances can disrupt gut microbiota homeostasis, making animals vulnerable to infections with zoonotic potential. However, it remains unclear whether the disruption to wildlife gut microbiomes is caused by habitat fragmentation *per se* or the combination of habitat fragmentation with additional anthropogenic disturbances (such as contact with humans, domesticated animals, invasive species, and their pathogens). To test this, we 16S rRNA gene sequenced the gut microbiome of a generalist rodent species, *Proechimys semispinosus*, in central Panama in three landscapes differing in their degree of anthropogenic disturbance: (1) undisturbed continuous tropical forests; (2) undisturbed forested islands, allowing us to study the effects of fragmentation alone; and (3) forest fragments embedded in an agricultural matrix that are subjected to anthropogenic disturbances in addition to fragmentation. We found that habitat fragmentation alone did not impact gut microbiomes, but habitat fragmentation in combination with additional anthropogenic disturbances did by reducing alpha diversity and causing a shifted and more dispersed microbial composition with more taxa associated with domesticated animals and their potential pathogens. This indicates that adaptation via metagenomic plasticity might not occur fast enough in the face of rapid global change, even in generalist species, carrying potentially harmful consequences to both wildlife and human health. Funding provided by DFG Priority Program SPP 1596/2 Ecology and Species Barriers in Emerging Infectious Diseases (DFG SO 428/9-1, 9-2).

Abstract ID: 1812
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P548

Co-evolution between leaf beetles and their gut microbiome

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Gut microbes are important “biochemical brokers” that enable insects to exploit plants. Previous studies suggest that host-microbial systems can form long-term associations over evolutionary time and the dynamic changes of the intestinal system may represent major driving forces of contribute to insect dietary diversification and speciation during the long process of evolution. Our study system includes a set of closely related leaf beetle species (*Galerucella* spp.) and our study aim to separate the role of host phylogeny and ecology in determining the gut microbial community to identify eventual coevolution. We selected beetle species from different host plants in different regions, and analyzed them using 16S rRNA sequencing to detect the bacterial community. In combination of standard clustering tools and phylogenetically-controlled analyses of the microbial based on host diet and geographic distance, such data can be used for getting indications on difference in functional characteristics of the microbial community between host beetle species. Specifically, we address three main questions: (i) Do gut bacteria in *Galerucella* vary according to beetle species or sites? (ii) How much variation of the microbiome community can be explained by host phylogeny? (iii) Does each beetle specie have a unique bacteria composition compared to other beetle species, and are these inherited or transferred between the generation of leaf beetles? Our preliminary results showed that the beetle species shared a low proportion of operational taxonomic units. Beta-diversity indicators suggested that significant differences in gut bacterial composition among beetle species and among sites.

Abstract ID: 1839
Poster board number:
P549

The nature and the role of gut microbiome in terrestrial and aquatic isopods

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Symbiotic associations are ubiquitous in nature and can have profound effect on diversity and evolution. Most animal-associated microbes are harbored in the digestive tract with a majority cannot yet be cultured. It has become apparent that gut microbiome can strongly affect host phenotypes including nutrition, protection against pathogens, behaviour and development. Some animals harbour transient gut microbial communities that are dispensable for their growth and survival, while others cannot live in their absence. The gut microbial community composition and function have been found to vary substantially between species and are affected by multiple factors, including host genetics and environment. In our research, we study the nature and the role of gut microbiome in wild populations of terrestrial and freshwater isopod species using culture dependent and independent methods. Isopods have digestive tract of a simple structure and they prefer to feed on decayed plant material colonized by diverse microorganisms. Our results show high diversity and large between-individual variation in gut bacterial communities with a majority derived from isopod environment. We also identified several typical isopod-associated bacteria, but their function is unknown. The members of *Actinobacteria* (Streptomyces sp.) and *Bacteroidetes* are potentially involved in defence and cellulose digestion. These findings demonstrate transient gut microbial communities acquired through feeding on environmental sources. The ingested microbiota represents important source of nutrients, but also contributes to defence against pathogens. I advocate that only studies that integrate the host physiology,

ecology, and life-history with microbiome data, can understand the nature and role of gut microbiome.

Abstract ID: 1979
Poster board number:
P550

How do herbivory-induced changes in plant microbiota shape plant evolution?

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Plant microbiota, which is often altered by biotic stresses such as herbivory, plays a critical role in shaping plant ecology and evolution. Currently, to which extent the interactions between plant microbiota and biotic stresses jointly determine evolutionary trajectory of host plants remain unclear. Here, using aquatic macrophyte, *Spirodela polyrhiza* as a model system, we performed a long-term outdoor experimental evolution experiment, in which half of the plant populations were subject to snail herbivory. Our preliminary results showed that 12 weeks of herbivory, which is equivalent to ~20 generation of *S. polyrhiza*, altered plant microbiota and increased the levels of resistance in plant populations. To further understand how herbivory-mediated microbiota changes contribute to the evolution of plants, we will inoculate the evolved microbiota to microbe-free plants and quantify plant fitness landscape of plants under control and herbivory conditions. Together, these results will provide novel insights into the eco-evolutionary dynamics among herbivores, host plants and plant microbiota.

Abstract ID: 2114
Poster board number:
P551

Divergent gut microbiota and role of sociality in two closely related house mouse subspecies

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The gastrointestinal microbiota (GM) is considered an important component of the vertebrate holobiont, affecting its fitness and represent therefore an integral part of evolution. GM can be transmitted horizontally through social contacts and/or vertically from parents to offspring over multitudes of generations, resulting in host-GM codivergence and possibly also in mutual coadaptations. Although the house mouse (*Mus musculus*) is a prominent model for study of speciation and other microevolutionary processes, the role of GM in house mouse evolution remains poorly understood.This

knowledge gap is related to the fact that studying GM codivergence with different host lineages and horizontal or vertical GM transfer in spatially separated, free-living populations exposed to multiple sources of GM variation, is extremely challenging. We therefore studied GM in wild-derived populations of the two house mouse subspecies (*M. m. musculus* and *M. m. domesticus*) maintained under semi-natural, common-garden conditions, using 16S rRNA GM profiling of three gut sections (ileum, caecum and colon). Despite unrestricted contact between the the two subspecies during the experiment, we found a clear intersubspecific differences in their GM. This was mainly driven by several members of genus *Helicobacter*, where two of them showed a signal of co-divergence with their hosts. We also assessed relative importance of vertical and horizontal GM transfer on GM composition in each of the two subspecies. Our results show that the GM is affected mainly by horizontal transfer. However, the relative role of horizontal vs. vertical GM transmission also differs between individual gut sections.

Abstract ID: 2286
Poster board number:
P552

Effect of urbanization on microbiome composition of the garden spider *Araneus diadematus*

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Most organisms harbour a microbiome, and microbial symbionts can sustain essential functions to the host. Host-symbiont associations can be tightly associated as indicated by a core microbiome, or they can vary among host populations and be shaped by the host's environment. The microbiomes of various taxa have been shown to be affected by anthropogenic perturbations such as exposure to pesticides and heavy metals, climate change, and habitat fragmentation. As urbanization integrates several of these environmental perturbations, it can be predicted to affect host-symbiont interactions. Microbiome variation induced by urbanization may influence host phenotypic variation and thereby contribute to shape adaptive responses of the host to the urban environment. A few studies have investigated urbanised bird populations compared to rural populations, and found that the impact of urbanization on host microbiome varies according species, season and spatial scale. The garden spider *Araneus diadematus* (Araneae) is one of the most common species in both urban and non-urban orb web spider communities in Western Europe, making it a suitable model to study the effect of urbanization on the spider's microbiome. Using 16S RNA gene amplicon sequencing, I found that microbiome composition differs between urban and rural spider populations sampled in Denmark, Sweden, Germany and Belgium. Furthermore, using metabarcoding techniques, we found that both local urban/rural insect composition and the insects ingested by spiders differ among rural and urban habitats, suggesting a possible role of prey insect diet in shaping host microbiome.

Symposium: S38. Molecular evolution and trade-offs in host-pathogen interactions and host immunity (id: 968)

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Poster board number:
P553

Effects of gut microbiota manipulation on *Blattabacterium* abundance in *Blattella germanica*

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The German cockroach *Blattella germanica* harbours an obligate endosymbiont, *Blattabacterium,* as well as a rich gut microbiota. The endosymbionts are located within the bacteriocytes in the proximities of the urocytes, and are involved in uric acid degradation, nitrogen assimilation and nutrient provisioning. In this study, we aimed to investigate interactions between the gut microbiota, the *Blattabacterium* endosymbiont and host phenotype. To achieve this, we experimentally manipulated the gut microbiota and recorded the effects of treatment on *Blattabacterium* abundance as well as different host phenotypic traits. In addition to a conventionally reared control group, we reared cockroaches under three different sterile treatments: i) sterilization followed by life-long antibiotic treatment; ii) sterilization followed by two weeks of antibiotic treatment; iii) sterilization followed by 2 weeks of antibiotic treatment, and then re-inoculation with a conventional gut suspension. *Blattabacterium* abundances are analysed by qPCR and correlated with gut microbiota diversity, host development, size at maturity and immune gene expression. Our study aims to offer new insights into the multi-level host-microbiota interactions of this important hemimetabolous pest insect species.

Abstract ID: 1107
Poster board number:
P554

Trade-offs and the evolution of age-specific resistance to infectious disease

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Many species experience changes in their level of disease resistance as they age, for example due to prior exposure, senescence or evolutionary trade-offs. Although one might typically expect juvenile resistance to exceed adult resistance (because infection at a young age may lead to death or sterility before reproduction), empirical observations suggest that this is not always the case, with juveniles sometimes less resistant than adults even after accounting for prior exposure. Here, we use mathematical modelling to explore how trade-offs with other life-history traits affect whether adults evolve higher resistance than juveniles, or vice versa. We investigate how juvenile and adult resistance coevolve when trade-offs affect maturation (slower growth), mortality (autoimmunity, or resources diverted from other defences) and reproduction (fewer offspring). We explore how these trade-offs with resistance at different life-stages combine to affect the evolution of resistance across the lifespan of the host. Our key finding is that, all else being equal, trade-offs between juvenile resistance and adult reproduction consistently

select for higher resistance among adults than juveniles. This suggests that hosts may be predisposed to lower juvenile resistance when trade-offs exist with adult reproduction.

Abstract ID: 1324
Poster board number:
P555

MHC evolution and expression patterns in the Neotropical Midas cichlid species complex

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Host-parasite interactions drive immunogenetic divergence of host populations across environments, fuelling diversification. MHC genes are key to the immune response in vertebrates and their great polymorphism is driven by parasite-mediated selection. MHC diversity varies among populations inhabiting contrasting environments and exposed to contrasting parasite communities. Differential expression of specific alleles could be a determinant factor for responding to parasites. We studied MHC class IIB divergence in the Nicaraguan Midas cichlid species complex, and associated expression patterns. The Midas cichlid repeatedly colonized crater lakes in which it has independently radiated to form parallel species flocks associated with contrasting habitats. Populations within and among lakes host parasite communities that differ in infection intensities, providing a setting for divergent selection to act.We found stable MHC IIB allelic divergence over years among Midas cichlid species inhabiting different lakes and habitats. However, allele pools fluctuated considerably within populations, providing evidence for ongoing selection dynamics. Additionally, we determined allele-specific MHC IIB expression among populations of the Midas cichlid. Identifying expression patterns of MHC alleles further elucidates the mechanisms underlying the host response to parasites and its role in shaping biodiversity.

Abstract ID: 1334
Poster board number:
P556

MHC-based mate choice in bluethroats

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Parasites and pathogens are ubiquitous in nature and the ability to mount an immune response against foreign attacks is therefore crucial for survival in all organisms across the tree of life. In vertebrates, the major histocompatibility complex (MHC) plays an important role in fighting intra- and extra-cellular parasites and pathogens. There is evidence for mate preferences based on similarity of MHC genotypes from many species including humans. Passerine birds are characterized by unusually variable MHC, but the consequences of MHC-variation for mate choice are poorly understood. Furthermore, passerines are known for the common occurrence of multiple mating, yet the adaptive significance for females of this behavior remains controversial. Recent results from the bluethroat (*Luscinia svecica*) strongly suggest female MHC-preferences for optimally dissimilar genetic sires, resulting in extra-pair offspring with an intermediate MHC variability. Here we expand on these results, asking whether females without extra-pair offspring are able to obtain MHC-optimal mates as social mates and hence not in need to

adjust initial choice by engaging in extra-pair copulations. Preliminary analyses provide support for this scenario, with an intriguing difference between pairs involving young and older males. We also investigate possible fitness-consequences of intermediate MHC variability, finding evidence that offspring with intermediate variability mount a larger immune response to phytohemagglutinin-injection. We discuss the possible generality of our findings and their implications for the understanding of extra-pair mating systems in birds.

Abstract ID: 1379
Poster board number:
P557

Different evolutionary patterns in TLR7 and TLR8 in lagomorphs due to host-pathogen co-evolution

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The innate immune system lies at the forefront of the host defence against invading pathogens, with recognition dependent on pattern-recognition receptors (PRR). Toll-like receptors (TLRs) are one of the most ancient PRRs and have the ability to differently detect pathogenic bacteria, viruses, fungi and protozoan parasites. Among TLRs, TLR7 and TLR8 are intracellular receptors that sense and recognize internalized single-stranded (ss) RNAs. In vertebrates, these genes are arranged in tandem with conserved synteny, but present a highly dynamic evolutionary history, being randomly present/absent in the different groups. Indeed, in birds, TLR8 was lost in all species, but TLR7 was duplicated. In reptiles, TLR8 suffered duplication events, while TLR7 was maintained as a single copy. In mammals, TLR7 and TLR8 are overall present and highly conserved, except in the European rabbit, in which TLR7 is absent and TLR8 presents low activity. In this study, we conducted an evolutionary analysis of TLR7 and TLR8 in the Order Lagomorpha. We found that synteny was not maintained, with genes being relocated to a non-sexual chromosome and flanked by distinct genes. TLR8 was absent in hares, but widely expressed in rabbit tissues and present in pikas. TLR7 was present and expressed in hares and, in one pika species, it was duplicated, but disrupted. Our results further suggested a faster evolution of TLR7 and TLR8 in lagomorphs, particularly in the leporids lineage. We hypothesize that the long co-evolutionary history of

lagomorphs and (ssRNA) viruses shaped the TLR7 and TLR8 evolutionary rates and repertoire.

Abstract ID: 1389
Poster board number:
P558

Determinants of variation in natural selection on immune function

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Immune defence is an important determinant of organismal fitness. While theoretical models based on trade-offs in resource allocation predict quantitative immune traits to be subject to stabilizing selection due to associated energetic costs and self-harm, empirical studies report mainly positive directional selection. This discrepancy may arise from variation in ecological factors that influence the expression of immune traits and/or their cost-benefit ratio, thus altering selection. We examined if selection on immune activity varies depending on immune challenge/infection risk, between immune traits, and among populations in the freshwater snail *Lymnaea stagnalis*. We assessed selection on the phenoloxidase-like and antibacterial activity of snail haemolymph while manipulating the level of immune challenge imposed by environmental microbes. We did this using snails from multiple populations. We found that the infection risk and the examined immune trait determined selection on the snails' immune function. These factors may thus be important in determining selection on immune activity in nature.

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Poster board number:
P559

Adaptive evolution of inflammasome-related genes in amniotic vertebrates

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Inflammasomes are cytoplasmic multiprotein complexes comprising a sensor protein, inflammatory caspases, and in some (but not all) cases an adapter protein connecting the two. They form part of the innate immune system that triggers the activation of inflammatory cytokines, such as interleukin (IL)-1β and IL-18, in response to infectious microbes and host-derived danger signals. To understand the adaptive evolution of animal inflammasome genes, we analyzed all gene families involved in inflammasome formation, including RIG-I-like receptors, NOD-like receptors, and caspases. The sequence data set covers all major clades of mammals, birds, and reptiles. In total, we detected 86 positively selected sites based on a consensus of three detection methods (MEME, FUBAR, and PAML). Aiming at these sites, we preliminarily describe the patterns of molecular convergent evolution acting in inflammasome-related genes between birds and mammals, as well as the relationships between phylogeny and molecular phenotype clustering. Our result provides the first prediction of interspecific differences and similarities in inflammasome activation potential. It will contribute to further research on the factors that shape the evolution of an optimal immune response.

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Poster board number:
P560

Investigating associations between immunity and infectivity genes: vole MHC vs. *Borrelia* ospC

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Parasite molecules targeted by host immunity are expected to evolve to escape recognition by the most common host genotypes, thus selecting for rare/novel host immune response genes. Such Red Queen dynamics constitute a leading hypothesis explaining extreme polymorphism of major histocompatibility complex (MHC) genes which elicit adaptive immune responses by binding antigens of parasites. However, the evolution of the antigens themselves has rarely been characterized. We investigated associations between MHC class II functional clusters (supertypes) in bank voles *(Myodes glareolus)* and infection with Lyme disease agent *Borrelia afzelii* strains carrying specific variants of polymorphic outer surface proteins C (OspC). The OspC protein is a highly immunogenic antigen recognized by the host adaptive immune system, and its polymorphism is thought to be maintained by balancing selection of poorly understood origin. In the set of three sub-populations of voles from the northeastern Poland screened in 2002, 2006 and 2010, we detected five OspC variants, two of which were dominant (92,17% of all cases). The two dominant variants co-occurred in similar proportions through time and across populations. The Tajima test supported balancing selection acting on OspC in our population. However, redundancy analysis controlling for host age, sex, site and year revealed no significant association between MHC and OspC genotypes. Thus, our results do not support the role of MHC in driving balancing selection on OspC genes.

Abstract ID: 1538
Poster board number:
P561

The effects of host age at exposure on *Daphnia* species infected by a yeast

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A major challenge of infectious disease epidemiology and evolutionary ecology is to predict disease outbreaks and how rapidly may spread in a population. It is widely accepted that host and parasite genetics, host susceptibility, parasite virulence, resource availability, and variation at the environmental and spatiotemporal levels play a vital role in the establishment of an epidemic. Nonetheless, factors related to host demography are often overlooked in epidemiological analysis, even though host's age is a key factor to take into consideration when determining the outcome of a parasite infection. Previous

studies using the *Daphnia magna-Pasteuria ramosa* system have shown that juvenile *Daphnia* are more susceptible to infection than older ones. In this study, we investigated how general age effects are and whether they can be detected in different *Daphnia* hosts. By using three species of *Daphnia*: *D. magna, D. similis* and *D. curvirostris*, and their yeast pathogen *Metschnikowia bicuspidata*, we investigated the impact of host age on parasite-induced host mortality and on the relationship between pathogen virulence and transmission in different hosts. Age effects have been observed in all three *Daphnia* species. In general, in *D. magna* and *D. similis* the susceptibility to infection decreased with age while in *D. curvirostris* the opposite pattern has been observed. These results enhance our knowledge on the relationship between pathogen virulence and transmission in different hosts, reinforces the epidemiological predictions behind it, and improves our response to an epidemic.

Abstract ID: 1541
Poster board number:
P562

Immune gene diversity as driver of tuberculosis susceptibility and resistance in wild meerkats

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Pathogens of the *Mycobacterium Tuberculosis* complex, causing tuberculosis (TB), are highly transmissible and have a high capacity for between species transmission, making them a major global threat to a wide variety of mammal species. While the drivers of TB transmission and mortality are intensely studied in a small number of host systems, they remain generally poorly understood. TB infections caused by *M. suricattae* are characterized by prolonged latent periods, followed by rapid progression to terminal stages in meerkats (*Suricata suricatta*), and contribute significantly to mortality. Exposure to TB is high, but only a fraction of exposed individuals develop clinical TB, and the factors determining individual susceptibility, i.e. infection risk upon contact, and resistance, i.e. mortality risk upon infection, are not yet well understood. In this project, we leverage the exceptional long-term dataset the Kalahari-Meerkat-Project, which provides detailed behavioral, life history and health data for a wild meerkat population affected by TB, to investigate effect of Major Histocompatibility Complex genes on TB susceptibility and progression. We genotyped 1289 individuals, alive between 1993 and 2020, at the MHC-DRB-exon 2 locus to test whether functional MHC diversity and/or specific alleles impact whether individuals develop clinical TB and how fast infections progress. This project will significantly add to our understanding of the genetic drivers of TB epidemiology, which can potentially be used to extrapolate the findings to other, less well studied mammal species affected by TB.
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Poster board number:
P563

The potential for glasshouse whitefly to evolve resistance to biological control agent

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Pathogens and parasites can exert strong selection pressures on host populations in natural ecosystems and drive rapid evolutionary change. However, some of the most dramatic examples of evolutionary change come from ecosystems managed by humans. One example is pesticide resistance, where chemical pesticides have repeatedly driven rapid resistance evolution in crop pests. Environmental impacts of chemical pesticides are motivating a shift towards sustainable pest control using biocontrol agents. Whilst risks of resistance evolution to chemical pesticides are well understood, threats of pest resistance evolution to the pathogens and parasites used as agricultural biocontrol agents are underappreciated. One serious pest of protected horticulture is glasshouse whitefly (*Trialeurodes vaporariorum*). In European horticulture, this species is most commonly controlled using fungal biopesticides and parasitoid wasps. This study aimed to assess the potential for whitefly to evolve resistance to a fungal biopesticide and a parasitoid wasp. We did this by quantifying variation in susceptibility across 35 whitefly matrilines to the fungal biopesticide Botanigard (*Beauveria bassiana*) and the parasitoid wasp *Encarsia formosa* under laboratory conditions. We also assessed the potential for cross resistance. For both biocontrol agents, survival following exposure varied greatly between matrilines (0% - 70%). Furthermore, matriline survival tended to be positively correlated between the fungus and the wasp. This suggests that there is standing genetic variation in whitefly populations for resistance to both parasites. Our findings highlight the potential that consistent use of these agricultural biocontrol agents could select for greater resistance, resulting in impaired crop protection.

Abstract ID: 1572
Poster board number:
P564

The effects of infection intensity on the gene expression on tapeworm infected ants

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The effects of parasite load on host phenotype manipulation are understudied. Here we looked at the cestode *Anomotaenia brevis* and its ant host *Temnothorax nylanderi.* For the ant, an infection leads to an extension in lifespan and changes in behaviour. We analysed how gene expression changes contribute to this phenotype and specifically focused on the effect of infection intensity on both an individual and colony level, as well as the effects on the cestode itself.
We analysed differential gene expression on 3 datasets: individual infection load with highly, lowly and uninfected ants, colony level where we looked at infection rate (1% to 70% infected ants) and cestode gene expression with crowded and lone cestodes.
For the individual infection load dataset, 122 differentially expressed genes (DEGs) were found with, among others, functions in immunity, eye development and fecundity. In the colony infection rate dataset, we found 301 DEGs, with notable functions in the regulation of stress. And in the cestode dataset we found 377 DEGs, 11 of which function in bypassing the host immune system.
Based on the DEG analysis, we could conclude that high infection intensity causes a higher degree of stress on the colony level as well as a lower availability of resources for the parasites in individual ants. Furthermore we found a possibility that high infection

causes blindness in ants which may further decrease their ability to avoid predators, which is advantageous for the cestode.

Abstract ID: 1579
Poster board number:
P565

Parasites inducing differential immune gene expression in sexuals and asexuals of gibel carp

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Gibel carp (*Carassius gibelio*) is an invasive cyprinid species exhibiting a unique mixed reproductive strategy i.e., combining gynogenesis (asexual reproduction) and sexual reproduction. This fish species is parasitized by a wide range of metazoan parasites, and some differences in immunity were already documented between the two forms with different reproduction strategies. Differences in the effectiveness of the immune system and contrasting susceptibility to parasite infection may represent a potential mechanism facilitating the coexistence of asexual and sexual forms of gibel carp, thereby contributing to its invasive ability. In this study, the differential expression of genes related to immunity, activated by digenean species, was evaluated among three experimental groups: gynogenetic females, sexual females, and sexual males along with respective control groups. The sexual and asexual forms of gibel carp were infected by the larval stages (cercariae) of *Diplostomum spathaceum* (Digenea). Gynogenetic females were more infected than sexual specimens. Spleen was used as the target immune organ playing a role in innate and adaptive immune processes in fish. Based on the transcriptome profile analyses and extensive literature review, immune-related genes were selected, and their expression was quantified using RT-qPCR. We revealed, for the first time, the changes in immune gene expression profile involved in digenean infections in cyprinid fish. The contribution of different immune genes expression was highlighted as a potential mechanism contributing to the coexistence of sexual and asexual forms in nature.

Abstract ID: 1583
Poster board number:
P566

Intraspecific variation in how a specialist herbivore affects plant defences

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Manipulation of host immune defences is a strategy used by herbivores to maximize their fitness by reducing plant defences. This seems to be ubiquitous for the specialist spider mite *Tetranychus evansi* – a model herbivore for host defence manipulation. Although the magnitude of induced tomato defences in response to feeding differs between different mite populations, it is not clear whether this variation is linked to fitness. To

better understand this, we used four field populations and one laboratory outbred population created from controlled crosses of all four field populations, thus capturing natural, and assessed (i) their fecundity in the presence and absence of jasmonic acid (JA) plant defences, and (ii) induction of plant defences after mite feeding. We found that these populations varied in their fecundity in the presence of JA-defences and induced plant defences differently. We then investigated, using 59 inbred lines created from the outbred population, how much of this variability was due to genetic factors and whether it could be attributed to manipulation of JA-defences. We found that variation in fecundity among the *T. evansi* inbred lines has a genetic basis and is not influenced by JA-defences, indicating that factors other than these defences, influence fecundity. Indeed, JA-defences have a minimal impact on *T. evansi* performance most likely because all lines can adequately suppress them.

Abstract ID: 1613
Poster board number:
P567

Influenza A virus infection induces differential expression of the duck TRIM gene repertoire

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Tripartite motif (TRIM) genes are an ancient family of genes which has expanded throughout vertebrate evolution. Several TRIM proteins have demonstrated antiviral functions, including restricting viruses such as influenza A virus (IAV). Ducks are the natural host and reservoir of IAV and likely have evolved many strategies to control the virus. It is currently unknown which genes are present in the duck TRIM repertoire, and how many are involved in IAV resistance or restriction. To determine how many TRIM proteins were annotated in the duck we mined the NCBI protein database. We also assembled and interrogated a *de novo* duck transcriptome to search for any unannotated TRIM genes. We found 52 TRIM genes in the duck genome and transcriptome. To determine which TRIM genes responded to IAV infection, we examined the expression patterns of TRIM genes in ducks infected with a highly pathogenic H5N1 strain of IAV (VN1203) or a low pathogenic H5N2 strain (BC500). VN1203 replicates in lungs of infected birds while BC500 replicates in intestines. We determined that ducks infected with VN1203 differentially regulated 37 TRIM genes in lungs (20 upregulated and 17 downregulated). Ducks infected with BC500 had only 9 TRIM genes differentially expressed in lungs and 13 in intestines. Our analysis suggests several candidate TRIM proteins to test for antiviral function against influenza viruses.

Abstract ID: 1615
Poster board number:
P568

The genetic complexity of resistance to mycoinsecticides

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When selection is strong and the genetic basis of adaptation involves a small number of genes, selective sweeps of beneficial alleles are common. However, most traits are complex, requiring the additive effect of multiple, even numerous, alleles. There is a long history of pest control in agriculture that exerts intense selection pressures on herbivorous insects. Despite concerted efforts to manage resistance evolution in pests, such strong selection has repeatedly brought about resistance. In many cases, resistance has been fast and straightforward to evolve, involving only one or two genes. Fungal entomopathogens, used in mycoinsecticides, provide arguably the most complex challenge widely available as a biopesticide. Although resistance to mycoinsecticides could involve numerous loci, this does not necessarily equate to resistance evolution being complex. The potential for resistance to evolve has already been shown; however, it is unclear how many loci are involved or whether there are gene-environment interactions that could affect resistance evolution. We use next-generation sequencing to identify genomic regions containing variants associated with resistance on an important axis of environmental variation - the crop plant on which the insect feeds. We pay special attention to the consistency with which such alleles reflect high fitness across environment. We also assess differential gene expression between susceptible and resistant genotypes. This work reveals the complexity and context specificity of the genetic architecture of fungal infection resistance in a globally invasive crop pest with an impressive, difficult to manage, track record of resistance evolution: the cotton bollworm, Helicoverpa armigera (Lepidoptera: Noctuidae).

Abstract ID: 1622
Poster board number:
P569

Evolution of divergent infection responses against single vs coinfecting pathogens

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In nature, hosts can face multiple pathogens simultaneously. While this might warrant activation of different immune mechanisms to counter mixed infections, an expansion of diverse immune arms together can collectively increase the costs of immunity, reducing the rate of adaptation against pathogens. However, a comparative experimental framework is missing. Here, we used several *Tribolium castaneum* beetle lines evolving against either a single or a combination of pathogens with divergent within-host growth dynamics— Fast-growing *Bacillus thuringiensis* (Bt); Slow-growing *Pseudomonas entomophila* (Pe); A combination of both (M). Although we began by imposing an equivalent selection pressure (~60% mortality in all lines), resistance could evolve most rapidly against Pe by overexpressing antimicrobial peptides and lysozyme (within 12-generations), whereas resistance against fast-growing Bt did not evolve yet, possibly because beetles could not invest more in fast-acting immunity relevant to Bt-clearance such as cytotoxic phenoloxidase. Expectedly, resistance evolution against M was delayed (~17-generations), perhaps due to increased costs of an extended immune repertoire. We did not find any reproductive costs in these lines, thereby suggesting the lack of immunity-reproduction trade-off.

Abstract ID: 1682
Poster board number:
P570

Natural selection on gene expression across invertebrate immune system

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A strong immune defence should evolve as a response to parasitism, which, however, can be constrained by associated trade-offs with other fitness-related traits. The form and strength of natural selection on immune activity are generally poorly understood. This is because of difficulties in examining which traits of a complex immune system are subject to selection under exposure to natural parasite communities. Here, we investigated natural selection on the gene expression of several components of the immune system of the freshwater snail *Lymnaea stagnalis* in a field experiment. We individually caged more than 200 snails in a pond for six weeks. We quantified snail fitness (i.e., total reproductive output) and immune activity at the gene expression level. We show that multiple components of the snail immune system were subject to natural selection. Positive directional selection predominated, especially for the components of non-self-recognition. However, also stabilizing selection on a few components of defence was observed. Interestingly, selection on the expression of some genes with similar functions varied (e.g., fibrinogen-related proteins). Our findings highlight the variation in natural selection on different components of the complex immune system and the power of multi-gene expression analysis to examine it.

Abstract ID: 1713
Poster board number:
P571

High MHCIIβ divergence associated with survival and parasite resistance in sticklebacks

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The genes of the immunologically important major histocompatibility complex (MHC) in vertebrates are a prime candidate to understand how natural selection mediates adaptation to pathogens. Several non-mutually exclusive selection mechanisms are proposed to explain the exceptional sequence diversity typically exhibited by MHC genes, yet identifying the relative contribution of those remains challenging. One of them, the “divergent allele advantage” (i.e. individuals combining highly divergent MHC alleles can fight a wider range of pathogens), is conceptually well established, but empirical evidence is still limited and awaits thorough experimental testing. Here, we performed a semi-natural experiment exposing lab-bred three-spined sticklebacks in cages to their natural parasites in their native lake habitat. Sticklebacks were selected to harbor different levels of MHCIIβ sequence divergence to test whether high MHC divergence confers parasite resistance and other fitness advantages. An unusually warm season led

to a high mortality during the field exposure. However, mortality was non-random with regard to MHC and highest among individuals with low MHCIIβ divergence. Among the surviving fish we observed significant variation in parasite infection, in both prevalence and abundance. Fish harboring high MHCIIβ divergence were less infected, but the strength of the association varied according to parasite taxa. Overall, this study provides strong experimental evidence for the “divergent allele advantage” hypothesis in playing an important role in the evolution of MHC diversity.

Abstract ID: 1873
Poster board number:
P572

Contemporary selection on MHC genes in a free-living ruminant population

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Genes within the major histocompatibility complex (MHC) are the most variable identified in vertebrates. Pathogen-mediated selection is believed to be the main force maintaining MHC diversity. However, relatively few studies have demonstrated contemporary selection on MHC genes. Here, we examine associations between MHC variation and several fitness measurements including total fitness and five fitness components, in 3400 wild Soay sheep *(Ovis aries*) monitored between 1989 and 2012. In terms of total fitness, measured as lifetime breeding success of all individuals born, we found haplotypes named C and D were associated with decreased and increased male total fitness respectively. In terms of fitness components, juvenile survival was associated with haplotype divergence while individual haplotypes (C, D and F) were associated with adult fitness components. Consistent with the increased male total fitness, the rarest haplotype D has increased in frequency throughout the study period more than expected under neutral expectations. Our results demonstrate that contemporary natural selection is acting on MHC class II genes in Soay sheep and that the mode of selection on specific fitness components can be different mode from selection on total fitness.

Abstract ID: 1875
Poster board number:
P573

Trans-species polymorphism and convergent functionality at MHC IIB across cichlid radiations

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Genetic diversity is crucial for responding to environmental pressures. The adaptive immune response in vertebrates is largely driven by the diverse and polymorphic genes of the major histocompatibility complex (MHC). An intriguing evolutionary feature of MHC genes is the generalized sharing of alleles across species (trans-species polymorphism, TSP), likely the result of parasite-mediated balancing selection. However, convergent evolution could also explain this shared polymorphism. Here, we investigated the evolution of MHC class IIB genes across the radiations of cichlid fish worldwide, one of the most species-rich vertebrate clade. Cichlid fish present some of the largest diversity at MHC. We analyzed available MHC IIB DNA sequence data to explore allele

similarities among cichlid radiations, and the role of TSP versus convergence. We found that TSP best explains MHC allele similarity between cichlid species from different continents. Also, MHC alleles clustered into few functional groups, or supertypes, which were largely shared and convergent across continents. The maintenance of similar MHC alleles with equivalent functionality for long evolutionary times may imply that certain alleles are essential for immune adaptation, even in species that diverged around 60 million years ago and occupy an array of different environments.

Abstract ID: 1899
Poster board number:
P574

Balancing selection on the complement system of a wild rodent

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Genes of the immune system interact with pathogens in numerous ways to recognise and eliminate them, enabling evolutionary conflict necessary for pathogen-mediated selection to prevail. The complement system is a component of innate immunity, critical to pathogen clearance. Many of the complement proteins interact directly with pathogens, either when sensing pathogenic components (pathogen recognition) or when exploited by pathogens to escape host immunity (targets of immune evasion). While considerable positive selection has been documented in genes of the complement system across mammals, the extent of balancing selection has largely been unexplored, barring a few candidate gene studies. We elucidate the level of genetic diversity and balancing selection across multiple complement genes (n=44) using whole-genome resequencing data from wild bank voles. We found four complement genes (*A2M*, *FCNA*, *CFI* and *CLU*) to be under balancing selection. All of these encode proteins that are known to interact directly with pathogens (pathogen recognition or targets of immune evasion). Localised signatures of balancing selection were mainly found in intronic regions, but extensive linkage disequilibrium makes it difficult to infer what region is the target of selection. This study is among few that systematically characterises genetic diversity and balancing selection in the complement system of a mammalian species.

Abstract ID: 1926
Poster board number:
P575

Lineage-specific influence of Haemosporidian parasites on European Robin's autumn migration

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Though Haemosporidian blood parasites might strongly affect the different life-history traits of the birds, their role in migration is less studied. Here we tested whether a

relationship exists between *Haemoproteus* or *Plasmodium* infection and body condition or the timing of autumn migration of European Robins (*Erithacus rubecula*). We found that infection status had no effect on the body mass and fat scores of the individuals, however infected juveniles arrived later than parasite free individuals from the same age group. When we analysed the effects of the three most common parasite lineages separately, we found that the direction of the relationship between parasite prevalence and body condition or timing of autumn migration differed between the different lineages. Juveniles infected with P-Turdus1 had a higher probability, while adult birds infected with the lineage H-Robin1 had a lower probability of having a visible fat. Prevalence of both P-Turdus1 and H-Robin1 infections correlated with the arrival time of the birds: individuals infected with any of these lineages arrived significantly later at the study site. Our results therefore emphasize that lineage-specific effects of parasites during migration may exist.

Abstract ID: 1966
Poster board number:
P576

Infection increases activity via Toll dependent and independent mechanisms

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Host behavioural changes are among the most apparent effects of infection**.** **'**Sickness behaviour' can involve a variety of symptoms, including anorexia, depression, and changed activity levels. Here we use a real-time tracking and behavioural profiling platform to show that, in *Drosophila melanogaster*, many systemic bacterial infections cause significant increases in physical activity. Using various bacteria and *D. melanogaster* immune and activity mutants, we show that increased activity is driven by at least two different mechanisms. Increased activity after infection with *Micrococcus luteus*, a Gram-positive bacterium rapidly cleared by the immune response, requires the *Toll* ligand ***spätzle***. In contrast, increased activity after infection with *Francisella novicida*, a Gram-negative bacterium that cannot be cleared by the immune response, is independent of both *Toll* and the parallel IMD pathway. The existence of multiple signalling mechanisms by which bacterial infections drive increases in physical activity implies that this effect may be an important aspect of the host response.

Abstract ID: 2010
Poster board number:
P577

Mechanisms supporting haplotype groups in mammalian TLRs

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The haplotype structure of anti-bacterial Toll-like receptor genes (TLR1, -2, -4, -5 and -6) in Czech Red Pied cattle was explored. Initially, single nucleotide polymorphisms were detected by hybrid resequencing that combined PacBio RSII and WGS with HiSeq X Ten. 15 haplotypes were directly revealed in TLR2 by amplicon sequences and two distinct holotype groups were detected using the Network program. Clustering in TLR2 was independently confirmed for statistically reconstructed haplotypes. The bimodal distribution was also detectable in the haplotypes of TLR5 and -6, while only a trend was seen in TLR4 and -1. The pattern is consistent with the previously reported clustering of TLR haplotypes in other cattle breeds. Fluctuating selection due to the prevalence of pathogens, although considered as a reason earlier, should lead to the loss of diversity due to the stochastic processes. Similarly, three clusters of TLR2 haplotypes observed in bank vole (Myodes glareolus) were ascribed to the positive selection by Borrelia afzelii (Tschirren et al., Proc. R. Soc. B 280:20130364, 2013). The balancing selection in bovine TLR2 might originate from two different functions of heterodimers formed with the TLR1 and TLR6 products, although this view was not previously supported by protein modelling (ibid.). However, functional bifurcation corresponds not only to different interactions with bacterial lipopolysaccharides, but also with the endogenous vs. exogenous ligands (Song et al., Crit. Rev. Eukaryot. Gene. Expr. 29:37, 2019). The TLR haplotype role will be further interpreted in the frame of the newly designed large amplicons.

Abstract ID: 2060
Poster board number:
P578

Evolution of immune responsiveness to mycoplasmal conjunctivitis in house finch populations

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Understanding mechanisms of host pathogen coevolutionary dynamics is a vital goal in evolutionary immunology. Yet, vertebrate model systems to investigate shifts in regulating host immune responses to pathogens are rare. In North America, a poultry pathogen *Mycoplasma gallisepticum* (MG) jumped in early 1990s to a new host, the house finch (*Haemorhous mexicanus*), causing millions of bird deaths due to severe conjunctivitis, a driving selective pressure across host populations. Here we report results of a common garden experiment using four different house finch populations (15 individuals per population) differing in their coevolutionary history with MG: a gradient from Virginia, where populations have interacted with MG for >20 years, to Hawaii, where populations are still naïve to MG. Birds were inoculated in conjunctiva with either control media or one of two MG isolates: the earliest known finch isolate (1994) or a more recently derived one (2013). We performed 3'-end transcriptomic sequencing on conjunctival tissues 3-days post-infection to reveal which genes are differentially expressed during infection and how populations differ in their interaction with

differentially evolved MGs. In response to MG, we found upregulation of the IL17 pathway and downregulation of the IL12/IL23 pathway, suggesting significant role of γδ T cells and innate lymphoid cells in activating IL17-driven inflammation in conjunctiva. The same pathways were also differentially expressed between the host populations. We used RT-qPCR to confirm expression patterns of selected genes. Our results reveal a mechanism of house finch immunological interaction with MG that differs between host populations.

Abstract ID: 2083
Poster board number:
P579

Evolutionary responses to transmissible cancers

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Transmissible cancers, where the pathogens are clonal malignant cell lines that spread horizontally as allografts and/or xenografts, have most likely existed since the evolution of multicellularity. Transitioning from unicellularity to multicellularity required shifting the Darwinian unit of selection from individual cells to the multicellular community. Forgoing the reproductive interest of individual cells, division of labour and specialization by differentiated cells in multicellular organisms also accrued the risk of these tissues being colonized by fproliferating cheater cells. Cells that sabotaged multicellularity and entered a selfish lifestyle could, by acquiring the ability to spread between hosts, also acquire higher fitness. Transmissible cancers and their hosts indeed present as unique host-pathogen systems where the pathogen is evolving on the landscape of the genome it has originated from.
Although rare, there are currently ten transmissible cancer lineages known in nine host species from both terrestrial (two vertebrate species) and marine environments (7 invertebrate species). The last 20 years have seen an avalanche of research investigating these peculiar host-pathogens systems, and thus provide an ideal platform to review and discuss the evolution of host responses to transmissible cancers. Thus, we aim to review the defence mechanisms multicellular organisms have evolved to prevent colonization by horizontally spreading selfish cells. We discuss how hosts adapted to recognize cells that spread as allografts/xenografts, prevent their establishment, suppress their growth and inhibit intra- and inter-individual transmission. Finally, we propose that sexual reproduction and the development of the immune system may have limited the emergence of transmissible cancers.

Abstract ID: 2126
Poster board number:
P580

T-cell repertoire diversity during infection in a natural model system for adaptive immunity

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The vertebrate adaptive immune system is based on lymphocyte recognition of pathogen-derived antigens presented by Major Histocompatibility Complex (MHC) molecules. As the engagement of a peptide-MHC complex with a suitable T-cell receptor (TCR) is the critical first step in the initiation of adaptive immune responses, the availability of a diverse T-cell repertoire, constituted by a pool of broad TCR specificities, is crucial. However, surprisingly little is known regarding the degree of natural variation in the inter-individual diversity and dynamics of the T-cell repertoire, especially during infection. Our research thus examines the qualitative and quantitative variation and dynamics of TCRβ repertoires within and among individuals of the three-spined stickleback, an eco-evolutionary model species. Here we analyze T-cell repertoires of lab-bred sticklebacks that were experimentally exposed to the cestode parasite *Schistocephalus solidus*, known to trigger adaptive immunity. Using NGS sequencing and advanced bioinformatics tools, we investigate TCRβ repertoire size and diversity in relation to infection treatment, family background, and individual MHC diversity. Preliminary analyses indicate a substantial variation of TCRβ repertoires among individuals and across infection status, as expected for a species with a natural level of genetic diversity. Interestingly, infected individuals appear to exhibit higher inter-repertoire overlap than control ones. The existence of public, expanded clonotypes shared by all infected individuals further hints at convergent antigen-specific T-cell responses. Yet -surprisingly- most of the top public clonotypes are shared across experimental groups. Lastly, we show significant biases and a family effect on the usage of V-J gene segments.

Abstract ID: 2227
Poster board number:
P581

Hyper-divergent haplotypes in nematode parasites contain genes involved in host-parasite interaction

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Nematodes are the most abundant animal on our planet and many have evolved to parasitise other organisms, including humans. Despite a long history of studying host genetics within the context of host-parasite interactions, parasite genetics are often neglected. Recent studies have shown that the genomes of free-living nematodes contain ancient, hyper-divergent haplotypes containing genes that allow the nematode to sense and respond to its environment. Although similar haplotypes likely exist in parasite populations, sequencing their genomes has previously been hindered by their small size and high genetic diversity, which prevents sequencing pools of individuals. Here, we

apply a novel low-input sequencing approach to sequence the genomes of several individual males of two parasitic nematode species: *Heligmosomoides bakeri*, a parasite of laboratory mice and a widely used model for gastrointestinal nematode infection, and *Heligmosomoides polygyrus*, a related parasite of wood mice. Despite a long-standing debate over whether these two taxa belong to a single species, we show that their genomes show levels of divergence consistent with millions of years of independent evolution. Consistent with findings in free-living nematodes, we show that the genomes of both species, including the purportedly inbred *H. bakeri,* contain hyper-divergent haplotypes. Importantly, we find that these haplotypes often contain genes that are known to interact with the host immune system, including a homolog of H11, a secreted antigen that has been proposed as a vaccine candidate against gastrointestinal parasites of sheep. Our findings highlight the importance of considering parasite genetics when studying host-parasite interactions.

Abstract ID: 2228
Poster board number:
P582

Peptidome-wide analysis of lineage specific peptides of Mycobacterium tuberculosis strains

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Tuberculosis (TB) still remains a serious infectious disease killing millions of people every year and is caused by strains belonging to the *Myobacterium tuberculosis* (Mtb) complex. Although the genomes of the Mtb complex strains are highly conserved, the different strains present distinct differences in virulence, transmissibility and geographic dominance. Thus, new insights into the genomic features of the Mtb complex strains are required for development of novel vaccines and for control of Mtb infection, but also for a better understanding of host-pathogen coevolution. We present here a peptidome-wide analysis of the human-adapted Mtb complex lineages providing insights into their lineage-specific evolutionary characteristics. Our findings reveal substantial peptide sharing, but also lineage-specific peptides with several human-like peptides that could indicate molecular mimicry. This study suggests that careful consideration of shared and strain/lineage-specific characteristics must guide our attempts to decipher what determines the pathological potential and thus the outcomes of infection with Mtb complex in different human populations.

Abstract ID: 2240
Poster board number:
P583

Susceptibility to trypanosomatid parasites in Drosophila melanogaster

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Trypanosomatids are an extremely diverse group of single cell eukaryotic parasites infecting a wide range of animals and plants. Relatively recently, they have been discovered to be common parasites of insects in the wild, including different species

of *Drosophila*. While *Drosophila melanogaster* has become an important model for evolution of innate immunity and host-parasite interaction, remarkably little is known about its genetic susceptibility to trypanosomatid infection. In the current study we investigate monoxenous trypanosomatids in several distantly related *Drosophila* species and demonstrate their genetic diversity. Further, we performed infection trials in fly strains from *Drosophila melanogaster* genetic reference panel to study variation in the host response to the infection and its effect on the flies fitness, assessed as survival, longevity and fecundity. We perform GWAS to unveil the genetic underpinnings of parasite susceptibility and plan to use RNAseq to complement our results with gene expression data.

Abstract ID: 2313
Poster board number:
P584

Imprints of past and present-day processes on the beaver MHC genes variability

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MHC genes form essential part of adaptive immunity and as the most polymorphic genes have attracted interest of evolutionary biologists during the last decades. MHC studies in wild organisms pose a challenge due to extreme numbers of alleles and frequent loci duplications, and hence the low diversity and non-duplicated nature of the Eurasian beaver (*Castor fiber*) MHC seem to provide a useful unique model. The Eurasian beaver undergone dramatic bottleneck culminating at the end of the 19th century, when only 1200 individuals were surviving, with these scattered in several different locations. Subsequently it was followed by a phenomenal re-expansion supported by multiple reintroductions. As a result, beavers of various origin meet in newly-established populations. We aim to demonstrate how the different periods influenced MHC variability in beavers using sequences of DRB and DQA loci. While the allele sequences show signs of both positive and balancing selection in the past pre-bottleneck times, the reduced variability illustrates the effect of drift during the bottleneck. Moreover, the signal of divergent allele advantage suggests the importance of re-established selection in the present-day populations.

Abstract ID: 2334
Poster board number:
P585

High variability in MHC gene evolution among the adaptive radiations of cichlid fishes

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The adaptive radiations of cichlids are the result of the interplay between natural and sexual selection. This interplay is also reflected in their immune system. Among the immunity genes, the ones of the major histocompatibility complex (MHC) stand out for

their high diversity. These pleiotropic genes play a central role in recognizing the antigens of parasites and (directly or indirectly) also in mate choice. They evolve following a birth and death process whereby new loci appear by duplication followed by gene loss at other loci. This process has led to high copy number variation of MHC class IIB genes in cichlids. The post-genomic era with the availability of hundreds of genomes has enabled the study of such complex gene families to unprecedented detail. In this study, I screened the genomes of more than 500 cichlid species for MHC class IIB genes. High levels of shared polymorphisms among different cichlid lineages indicate that most loci predate the contemporary adaptive radiations. Some lineages have a reduced MHC diversity and possibly even lost loci with classical MHC function, while others have a drastically expanded MHC locus repertoire. It remains unclear how trans-species polymorphisms are retained throughout the process of adaptive radiation. We may assume that selection for copy number variation is strong in many, but not in all cichlid lineages. This new exhaustive view on the evolution of MHC class IIB genes offers new opportunities to test hypotheses about the role of the MHC in parasite defense and mate choice in cichlids.

Abstract ID: 2345
Poster board number:
P586

Climate warming triggers the emergence of native viruses in Iberian amphibians

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Emerging infectious diseases are important drivers of amphibian population declines and species extinctions worldwide. One of the high-profile pathogens associated with these declines are viruses of the genus *Ranavirus*, casual agents of ranavirosis. Despite the increasing number of multihost epizootics, the origin of ranaviruses and the factors triggering their emergence remain generally undiscovered. We sequenced samples from amphibian carcasses collected in 15 never before studied incidents that occurred between 1988 and 2020 inclusive. We confirmed that two phylogenetically related viruses, the common midwife toad virus (CMTV) and *Frog virus 3* (FV3) are responsible for mass mortalities in a wide range of amphibian taxa in Iberia. Our findings reveal that

the highly virulent CMTV could be a European clade, with the Iberian Peninsula being the hotspot for CMTV diversity. The pattern of diversity found among CMTVs in Europe is consistent with spread by natural dispersal and we hypothesize that the Iberian Peninsula might contain the ancestral population of CMTVs that could have spread into the rest of Europe following the last ice age. Additionally, we find that climate warming could be triggering some of the ranavirosis outbreaks described here, supporting the endemic status of CMTVs in the Iberian Peninsula. Our study provides valuable new insight into the origin and emergence of the CMTV lineage and its spread throughout Europe.

Abstract ID: 2348
Poster board number:
P587

Sexual selection and disease resistance: a case study in amphibians

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Sexual selection is known to target disease resistance. This is seen in many vertebrate taxa where individuals tend to select mates based on traits related to disease resistance (e.g. MHC genotype). However, very little known about this mechanism in amphibians; this is particularly surprising as it is well established that there is strong sexual selection in many amphibian species. Currently, amphibians are experiencing massive population declines worldwide, with many of these declines being related to the emerging infectious disease chytridiomycosis. This disease is the result of an infection with fungi of the genus Batrachochytrium and has been associated with population declines of 501 amphibian species, out of which 90 went extinct and another 124 decreased in abundance by least 90%. Surprisingly, some populations thought to be driven to extinction by chytridiomycosis may be recovering, suggesting the evolution of resistance or tolerance. Hence, sexual selection for disease resistance could theoretically play a major role in population survival or recovery. We explore the potential role of sexual selection in such recovery.

Abstract ID: 2428
Poster board number:
P588

Cryptic pseudogenization in penguin *TLR15*: an adaptive change or a ratchet to poor immune function?

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Pathogen-facing immune genes occupy a changing adaptive landscape; one in which pathogens continually evolve to evade recognition. Single-nucleotide polymorphisms and other small-scale variants are often the focus of investigations into host immune adaptation. At the other extreme, pseudogenization represents a rare but high-

consequence means of honing the immune response and potentially avoiding immune-mediated pathology. However, our understanding of the mechanism of gene function erosion and eventual pseudogenization is poor, since the vast majority of pseudogenizations are fixed in the population. In this presentation, I will describe an instance of catching this process in action. In a large population study of *Eudyptes* (crested) penguins, we found several pseudogenized haplotypes of Toll-like receptor 15 (TLR15) – a TLR that recognizes fungal pathogens. Pseudogenized haplotypes were very common (>70%), but not universal, and there were infrequent intact haplotypes. However, functional analysis in an *in vitro* system revealed that the apparently 'intact' haplotypes were, in fact, non-functional. This contrasts to TLR15 from the closely related Emperor penguin and Northern fulmar, which were both fully functional. The apparently 'intact' *Eudyptes* TLR15 haplotypes – devoid of premature stop codons – are therefore likely to be cryptic pseudogenes (genes which are capable of producing a non-functional protein product). TLR15 pseudogenization in penguins will be discussed in relation to immune function in a changing world; one in which the incidence of fungal pathogens, such as *Aspergillus* spp., will increase along with global temperatures. Will the ratchet of pseudogenization mean penguins are ill-prepared for future pathogen threats?

Abstract ID: 2435
Poster board number:
P589

48 hours of solitude

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Reproduction and Immunity are two traits which affect the fitness of an organism and are expected to tradeoff with each other since both of them are resource intensive. Both immunity and reproduction are highly plastic, being affected by environmental and physiological factors. Adult densities have been suggested to influence both immunity and reproductive investment. The theory of *Density Dependent Prophylaxis* (DDP) proposes an overall increase in immune function under condition of conspecific crowding. Also, *Sperm Competition theory* predicts that males should alter their reproductive investment depending on the number of potential rivals in their environment. In this experiment, I tried to investigate the composite effect of density and reproduction on the immunity of male *Drosophila melanogaster*. I subjected males to a fully factorial treatment of two different adult densities (high and low) and two mating conditions (mated vs virgin). The flies were then infected with the pathogen *Pseudomonas entomophila* and their post infection survivorship was recorded. I found that overall males survived better when held at higher densities but that mating had a negative effect on survivorship. However, there was a significant interaction between the adult density and the mating treatment, where the positive effect of increasing density on immunocompetence was greatly reduced in the mated treatment, relative to the virgin treatment.
These results suggests that density dependent effects on immunity predicted by DDP, potentially, interacts with the effects of mating in complicated ways. Therefore, investigating these two phenomena in isolation may not be prudent

Symposium: S39. Mechanisms of host-symbiont coevolution: from genotype to phenotype (id: 967)

Abstract ID: 1140
Poster board number:
P590

Phenotypic plasticity of both partners in the giant ciliate Zoothamnium niveum thiotrophic mutualism

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The giant colonial ciliate *Zoothamnium niveum* is covered by a monolayer of sulfide-oxidizing bacterial ectosymbionts that show two different morphologies depending on their differential access to oxygen and sulfide for primary production. Bacteria close to the cilia beating oral part of the ciliate cells show larger sizes and are coccoid-shaped, while the ones observed in the aboral parts are smaller and rod-shaped. A suite of experiments under sulfide starvation in oxic seawater show diminishing populations of rod-shaped symbionts after 48 hours, and complete disappearance of the symbionts after 72h. In contrast, all symbionts are coccoid-shaped in sulfide supplemented oxic cultivations. Ciliate host colonies reproduction is through release of swarmers into the pelagial. Swarmers are covered by symbionts, ensuring the vertical transmission of the mutualism. Exposed to lack of sulfide dispersing swarmers completely lose the symbionts between 24 and 48h. Aposymbiotic swarmers fund aposymbiotic colonies with smaller size and short but wide shape due to higher number of zooids on each branch compared to symbiotic colonies. Because this morphology resembles the shape of the other, closely related *Zoothamnium* species, we interpret this profound change as the ancestral form. Conventional and well-established techniques such as fluorescence in situ hybridization and scanning electron microscopy already revealed aspects from both sides of this binary partnership. Easy access to *Zoothamnium niveum* in shallow marine waters and feasible manipulation in controlled experiments make this system a good candidate to employ additional approaches in order to enlighten mechanisms and processes from molecular to ecological and evolutionary levels.

Abstract ID: 1151
Poster board number:
P591

Programmed cell death in endosymbiotic *Chlorella* affects the fitness of its host

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We have been investigating the role of programmed cell death (PCD) in the evolution of endosymbiosis using a chlorophyte *Chlorella* (endosymbiont) and a ciliate *Paramecium* (host) as model organisms. We observed that heat shock induces PCD-like cell death in *C. variabilis* where heat-shocked cells show caspase-like proteases activity, chromatin condensations, and activation of ROS; ultrastructural

changes using transmission electron microscopy further confirm the nature of cell death. To check the effect of endosymbiont PCD on the host, we collected cell-free supernatants from heat-shocked (PCD) and controlled Chlorella cultures, and applied them to *Paramecium* cells. The PCD supernatants from the endosymbiont *Chlorella* specifically stimulated the growth of its symbiotic host *P. bursaria* and inhibited the non-symbiotic predatory *P. duboscqui*. These results suggest that PCD in *Chlorella* explicitly improves the fitness of its endosymbiotic host. The inhibitory effects of PCD supernatants on predatory *Paramecium* suggest that the endosymbiont PCD also plays a role in the host's inter-species competition.

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P592

Cross-species statistics to infer host-parasite interactions using genome-wide polymorphism data

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Coevolution is driven by genotype x genotype (GxG) interactions between hosts and their symbionts. While identifying the genes underpinning these interactions can be undertaken using host-parasite genome co-GWAs, deciphering the sign and magnitude of these interactions is so far only possible using experiment approaches. To tackle this limitation, we develop a new theoretical framework and set of statistical indices based on genome data of infected and non-infected hosts sampled from a wild population, along with the pathogen strains extracted from each infected host. We compare the value of each index with neutral expectations in order to 1) assess how many GxG interactions are biologically relevant, and 2) infer the sign and direction of the underlying model of interaction between host and parasite alleles. As a proof of principle, we apply our method to a set of previously published data of 451 human European individuals and the matching infecting parasites strains of the HCV virus, as well as 503 genomes of uninfected European individuals. We demonstrate that 50 host SNP x parasite amino acid associations are relevant GxG interactions, and those, even at the MHC genes, do not follow a matching-allele but gene-for-gene or parasite infectivity models of interactions. In the light of the recent history of HCV infections in Europe, we show that 1) hosts do not possess any resistant allele, and 2) the parasite evolves to match the host allele frequencies with only 5 to 17 parasite amino acids being key for infection and exhibit significant GxG interactions.

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Poster board number:
P593

Impact of host selection and social environment on gut microbiome varies with development in finches

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The assembly of gut microbiota during early development is an important process influencing the development and fitness of vertebrates. The major forces shaping the assembly process are transmission from the early social environment and host selection. However, we still don't know how the strength of these different forces changes over ontogeny, particularly in avian species. To fill this gap, we conducted heterospecific and conspecific fostering experiments in Zebra finches (*Taeniopygia guttata*) and Bengalese finches (*Lonchura striata domestica*) under controlled conditions and repeatedly sampled the faecal microbiota of individual birds over the first three months of life. We documented the gut microbiota development and characterised the relative impacts of the early social environment and host selection across different ontogenetic stages, employing 16S ribosomal RNA gene sequencing. The microbial taxonomic composition and community structure changed across ontogenetic stages. Furthermore, in the early developmental stages, the microbial communities of chicks raised by conspecific and heterospecific foster parents resembled those of foster families, underpinning the importance of the social environment. In later stages, the social environment still influenced the microbiota, albeit with the increased impact of host selection. Our study revealed for the first time in avian species that the relative strengths of host selection increase with development, advancing our understanding of the processes that influence host-symbiont interactions. Our findings open new perspectives to studying the mechanistic basis of host-microbial symbiont coevolution.

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Poster board number:
P594

Genotype-genotype interactions revealed in alga-virus coevolution

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When microbial hosts and viruses coevolve, they often transition from arms race dynamics (escalating resistance and host range evolution) to fluctuating selection dynamics (stable coexistence of susceptible and resistant hosts caused by a growth-defense trade-off). However, this interpretation is commonly based on time shift experiments that use population-level samples for the virus partner. Consequently, it is uncertain whether the expanding host range of the population - i.e. the supposed arms race dynamics - actually occurred at the virus genotype level. We investigated this in the algal model *Chlorella variabilis* and its virus PBCV-1. The arms-race-to-fluctuating-selection pattern has been observed multiple times in this system, but always on the virus population level. We revealed the genotype level in two replicate communities from a *Chlorella*-virus coevolution experiment. For each community, we isolated ~40 virus genotypes (from 6 time points) and tested their ability to infect ~12 algal clones (from ~6 time points). We found that host range does expand at the virus genotype level, confirming 'gene for gene'-like GxG interactions and arms race dynamics. Interestingly, broad host range genotypes emerged and were maintained in one replicate community, but repeatedly appeared and disappeared in the other. We consider the mechanisms that could cause this difference, including population-dependent trade-offs and drift.

Abstract ID: 1856
Poster board number:
P595

Different immune genes show variation in strength of positive selection: genomic approach in birds

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Theory predicts that during host-symbiont co-evolution, arms races diversify immune genes. However, it remains unclear if this holds true equally for all immune genes. Specifically, little is currently known about the frequency and strength of positive selection among different immune gene sets. Does the pattern of positive selection differ based on the gene´s molecular function? Do membrane-bound proteins experience stronger selection than cytosolic ones? To answer these questions, we performed a comparative analysis of positive selection across immune genes in 50 avian genomes (ENSEMBL) and transcriptomes (sequenced by Illumina NextSeq after systemic LPS treatment). First, we compiled the list of immune genes based on human-chicken orthologs overlapping between databases AmiGO (GO: Immune system process) and Reactome (Immune system) enriched about chicken genes without clear human-chicken orthology. Then using three dN/dS-based methods (CODEML, FUBAR, MEME), we revealed positive selection in 340 protein-coding immune genes (≥ 1 positively selected site, PSS) and 240 (≥ 10 PSS) genes out of the total of 436 genes assessed. According to the Gene set enrichment analysis, strong effect of positive selection was revealed in cytokine receptor signalling, TLR signalling, NOD-like receptor signalling or RIG-I-like receptor signalling pathway but weak selection was found in genes involved in enzymatic activities. Our preliminary results also show that membrane-bound and extracellularly secreted immune genes are under stronger positive selection than those expressed in cytosol or nucleus. These findings support the hypothesis that immune genes whose products physically interact with pathogen structures are under stronger positive selection.

Abstract ID: 1858
Poster board number:
P596

Population genomics of disease transmissibility by apple psyllids and their coevolving endosymbionts

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Apple proliferation (AP) is a chronic disease of apple trees caused by the bacteria *Candidatus Phytoplasma mali*, which is primarily transmitted by two phloem feeding psyllid vectors, *Cacopsylla picta* and *C. melanoneura*. The extent of AP transmission arises from a complex interaction between *Ca. P. mali*, the psyllid insects, their primary and secondary endosymbionts, and the apple tree. Our research focuses especially on genetic variation in the psyllids and their endosymbionts associated with psyllid transmission efficiency and regional disease prevalence, based on field collections, field-laboratory experiments, and next- and third-generation sequencing. Populations of *C. picta*, the primary vector of *Ca. P. mali* across most of Europe, and *C. melanoneura*, an emerging vector in areas of North-Western Italy, were collected from North-Western and North-Eastern Italy. Isolines were established via single crossing with virgin females, and offspring sibling families were raised on experimental apple trees infected with *Ca. P. mali*. Quantitative PCR was used to determine disease uptake in individuals in each sibling family and, after high quality nuclear and mitochondrial psyllid and endosymbiont genomes were assembled, long- and short-read genomic sequencing of the sibling families was conducted. The resultant dataset allowed us to examine genetic differences associated with disease uptake after psyllids had fed on infected apple trees and with regions where co-evolution between *Ca. P. mali* and the psyllid vector was recent versus long established. Results provide insight into the coevolutionary population genomics of psyllids and their endosymbionts with respect to their effects on spreading an agriculturally important disease.

Abstract ID: 1868
Poster board number:
P597

Population genomics of horizontal Wolbachia transfers between native and invasive cherry fruit flies

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Symbiosis forms the basis of many beneficial interactions between species, despite the continuous appearance of antagonistic traits. Environmental alteration can disrupt this balance of forces. *Wolbachia* is a maternally inherited obligate endosymbiont that can induce a broad range of effects in its host, ranging from mutualism to reproductive parasitism. Mounting evidence shows that horizontal *Wolbachia* transmission might be commonplace. Once acquired by a new host, *Wolbachia* can spread through the new host population by manipulating its reproduction or providing some level of benefits. However, the early stages of *Wolbachia* spread in new hosts are still poorly understood, particularly in natural settings. Here we investigate the early invasion stages of the

Eastern cherry fruit fly, *Rhagoletis cingulata*, that acquired a *Wolbachia* strain from a native congener after its invasion in Europe. Taking advantage of the univoltine life cycle of our model, we are now able to track the invasion in slow motion. Given the continent-wide distribution of the fly, we assessed whether horizontal *Wolbachia* transfers between the two species are single or recurrent events using a broad comparative whole-genome sequencing approach of natural populations from across Europe. This work constitutes the first in-depth study of the early stage of ongoing *Wolbachia* spread in a new host using whole genome sequencing at the population level, with potential applications to develop new pest biocontrol approaches where *Wolbachia* are already successfully used.

Abstract ID: 1892
Poster board number:
P598

Diversity of symbionts in psyllids of the genus *Cacopsylla* and their co-divergence with its host

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Cacopsylla spp. are phloem-feeding insects (Hemiptera; Psylloidea). They feed on a wide range of plants and some species are considered important agricultural pests by spreading plant pathogens such as phytoplasma. As other sap feeding insects, they harbor symbionts, that help overcome nutritional deficiencies caused by a diet low in amino acids and vitamins. The primary endosymbiont '*Candidatus* Carsonella ruddii' plays an essential role in the supplying of these nutrients. It has a very reduced genome with around 170 kb and a low GC content. Since the genome reduction process involved also some genes for amino acid biosynthesis, *Cacopsylla* species often harbor a second symbiont, which can complement these essential functions. For instance, our previous study on *Cacopsylla* spp. from apple trees confirmed the presence of a second endosymbiont (*Enterobacteriaceae* family, proposed name '*Candidatus* Psyllophila symbiotica') with a likewise small genome, but able to provide the necessary nutrients for the host. In this work, we explore the metabolic potential of other symbionts of European *Cacopsylla* spp. applying a whole-genome sequencing approach. Preliminary results show that some *Cacopsylla* species harbor a different second endosymbiont, which might complement the missing genes in the primary symbiont '*Candidatus* Carsonella ruddii'. Here, we will present a comparative genome analysis of the different *Carsonella* as well as the co-primary symbionts in various *Cacopsylla* species in order to describe their metabolic potential and the co-divergence with the host.

Abstract ID: 1917
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P599

Defensive symbionts and the evolution of parasitoid host spezialization

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Insect host–parasitoid interactions exhibit a high degree of host specialization. In addition to overcoming their hosts' behavioral and immunological defenses, parasitoids are often faced with heritable microbial endosymbionts protecting their hosts. Work on aphids of the genus *Aphis* and their parasitoid *Lysiphlebus fabarum* has shown that resistance conferred by the toxin-producing bacterial endosymbiont *Hamiltonella defensa* acts more specifically than the host's own immune defenses. This suggests that heritable defensive symbionts may be a source of diversifying selection promoting parasitoid specialization, which has been demonstrated using experimental evolution in the laboratory. We looked for evidence of this process in the field by characterizing the strain diversity of *H. defensa* in four *Aphis* species exploited by populations of *L. fabarum* showing host-associated genetic differentiation, indicative of host specialization. Then we tested whether these parasitoids show signs of adaptation to their hosts' endosymbionts, a form of local adaptation. Each aphid species carried its own strains of *H. defensa*, making them a potential target of adaptation for host-associated parasitoids. However, there was only partial support for parasitoid local adaptation to symbionts. Strongly protective strains of *H. defensa* were restricted to just two aphid species, *A. fabae* and *A. hederae*. While parasitoids collected from *A. hederae* were indeed more likely to overcome resistance conferred by symbiont strains from the same species, the same was not true for parasitoids from *A. fabae*. We discuss the ecological factors likely to modulate the opportunity for local adaptation of parasitoids to defensive symbionts in the field.

Abstract ID: 1975
Poster board number:
P600

Exposing symbiosis: how selecting symbionts when free-living influences endo-symbiotic interactions

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Theory dictates that stable symbioses emerge if adaptation to a symbiotic niche trades off against free-living fitness, resulting in the alignment of host-symbiont fitness without the requirement for complex stabilising mechanisms. Consequently, for endosymbiotic species, the external selective environments have an important role in shaping their evolution. The highly tractable microbial protist-algal symbiosis study system *Paramecium bursaria* and *Chlorella spp.* offers a unique model to experimentally test how selection on a symbiont in the external environment affects later interactions with its host. Several members of the Chlorellaceae family that form this symbiosis can also, at least to some degree, survive independently from the host and, therefore, can be exposed to external environments, as well as be horizontally

exchanged between hosts. Our study combines the experimental evolution of algae to different external environments with data on field collected samples. As part of this study, we experimentally evolved symbiont strains of *Chlorella variabilis* and *Micractinium conductrix,* isolated from different *P. bursaria* hosts, to different sources of nitrogen. We then combine whole genome sequencing and metabolic profiling to explore how traits at the interface of host-symbiont interactions, such as cell wall chemistry and nutritional compound exchange, are impacted when algal symbionts experience different environments in their free-living state and how this consequently affects the efficiency of their relationship with hosts.

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P601

Comparative genomics of *Wolbachia*

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Wolbachia are maternally inherited endosymbiotic bacteria that manifests reproductive parasitism and mutualism. *V*arious strategies of reproductive manipulation and mutualistic interactions of bacteria have been described in arthropods and nematodes. The most common reproductive manipulation is cytoplasmic incompatibility (CI), which is sometimes observed along with fitness advantages such as nutrition provision, fecundity increase, viral protection, temperature resistance, etc. However, they are not well understood from a genomic perspective. Both parasitic and beneficial traits can be found in distinct phylogenetic groups of bacteria, so it is often hard to identify particular genetic factors by characterizing closely related strains. Here we attempted to search key features of *Wolbachia* genomics that may explain manifestations of certain phenotypes: reproductive parasitism (CI, male-killing, parthenogenesis, feminization); obligate symbiosis; no detectable effect on the reproductive system. We constructed the *Wolbachia* pangenome based on the set of 1178 high-quality genomes and performed detailed functional annotation. Parasitic phenotypes dominating in A and B supergroups of *Wolbachia* showed a high content of phage genes and mobile elements, with the highest number in *Wolbachia* with the feminization phenotype. Bacteria with fitness advantages were distinguished by having more than two thousand unique genes. They contain a set of genes responsible for interactions with the host organism similar to the CI phenotype. These findings gave means to differentiate endosymbiont phenotypes based on genomic features as well as highlight the importance of the mobilome in the evolution of parasitic *Wolbachia.*

Abstract ID: 2388
Poster board number:
P602

Ecological speciation via co-evolution? Population genomic differentiation in a freshwater parasite

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Ligula intestinalis is a tapeworm parasite found in freshwater ecosystems worldwide. It has a complex life cycle involving a planktonic copepod as the first intermediate host, planktivorous fish as a second intermediate host, and a fish-eating bird as the final host. The most conspicuous stage within the life cycle is the plerocercoid, which develops in the abdominal cavity of the fish host and has a substantial effect on its health, fecundity, and behaviour. Several evolutionary lineages of *L. intestinalis* were found to occur, some parasitising multiple host species. To better understand the evolution of *L. intestinalis* host-parasite interactions, we performed both a genomic and transcriptomic analysis of a lineage common in Europe. We investigated genomic diversity on 60 tapeworms from 3 fish host species (freshwater bream, white bream, and roach) through ddRAD sequencing. Population genomic analyses revealed that the parasite population in roach diverged from sympatric populations in freshwater bream and white bream. The transcriptomic dataset composed of 16 *Ligula* individuals from roach and freshwater bream hosts showed differences in gene expression of *Ligula* individuals between different fish hosts. Based on GO enrichment and HHpred analysis, we identified multiple up- and down-regulated genes that were significantly overrepresented between the two groups. Among the most regulated genes belonged serin proteases (inhibitors) and other genes involved in immune response and regulation of gene expression. Even though further analyses (qPCR) are required to confirm the revealed patterns, *Ligula* host-parasite system is a promising candidate to study the processes of ecological speciation in parasites.

Abstract ID: 2451
Poster board number:
P603

Effects of parasites on human cognitive performance and personality: Manipulation or side effects?

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Many parasitic organisms specifically affect the behavior of their hosts, including humans. Protozoan *Toxoplasma gondii* is known to affect human behavior, personality profile, simple reaction times, and intelligence. These changes are often interpreted in the theoretical framework of the manipulation hypothesis. However, recent studies show that “asymptomatic” latent toxoplasmosis is characterized by many adverse effects on physical and mental health. Therefore, the observed behavioral changes could be just side effects of the impaired health of infected individuals. To study this problem, we compared the effects of two ubiquitous pathogens, *Toxoplasma* (transmitted by predation) and bacteria *Borrelia* (transmitted by ticks’ infestation). Using an internet questionnaire, we collected data on the cognitive performance of about 2,500 subjects who knew their *Toxoplasma* or *Borrelia* serostatus. The differences between seropositive and seronegative individuals were analyzed with nonparametric partial Kendall tests controlled for age and sex. We found that self-declared seropositive subjects (22% in toxoplasmosis, 38% in borreliosis) scored higher than seronegative in intelligence

(Cattel's B) and identically in the memory (Meili test) and reaction time tests, including the Stroop test. Individuals seropositive for either *Toxoplasma* or *Borrelia* expressed lower Big Five-factor Conscientiousness, whereas seropositive individuals scored lower in Dark Triad traits Machiavellianism and Narcissism (the former was significant for toxoplasmosis, the latter for borreliosis). *Toxoplasma* seropositive subjects had worse physical and mental health, whereas *Borrelia* seropositive subjects had worse physical health than corresponding controls. However, nearly all effects of infections on performance and personality remained unchanged when the subjects' health was controlled. Our results are more compatible with the parasite-manipulation hypothesis than the side-effect hypothesis.

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P604

Role of gene flow in dictating the adaptive response, and reproductive barriers in yeast.

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Gene flow between populations is known to enhance the adaptive response of a population. On the other hand, gene flow homogenizes populations and hence, hinders the evolution of reproductive isolation between participating groups. While considerable evidence towards these phenomenon exist from studies of ecological systems, limited laboratory experiments exist to test the precise role in which gene flow influences adaptive response and reproductive barrier evolution. In this work, using the yeast *Saccharomyces cerevisiae*, we evolve populations in several environments, and control the frequency of gene flow between the two populations. The evolved lines were then tested pairwise, for pre- (mating efficiency) and post-zygotic (mitotic growth rate, and meiotic efficiency) barriers. In addition, we test the evolved lines for their fitness, as proxy for adaptation. Our results demonstrate that depending on the environmental context, gene flow can aid or hinder the adaptive response of the participating populations. On the other hand, gene flow was found to hinder establishment of pre-zygotic barriers between the two populations. However, depending on the environmental context, post-zygotic barriers can evolve between two populations, despite extensive gene flow. Overall, our work highlights the significance of the environment in dictating the relationship between gene flow and adaptation/speciation.

Abstract ID: 1003
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P605

Heliconius-Passiflora Coevolution: evidence from its geographic distribution and species richness

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The adaptive diversification of plants and their herbivorous insects is potentially influenced by coevolutionary processes. The morphological, physiological, and behavioural aspects of the biotic relationship between *Heliconius* butterflies and their host plants *Passiflora* is well documented. However, whether the degree of geographic correlation between their distributions and richness is informative regarding their coevolution is poorly known. To explore this, we modelled the richness and distribution of 165 *Passiflora* and 34 *Heliconius* species in Colombia using four different algorithms. Isothermality and seasonality of precipitation were the environmental variables that best explained the observed distribution patterns of *Passiflora* and *Heliconius*, respectively. Furthermore, we found a low degree of geographic overlap between both genera. In addition, we compared the distributions of a monophagous (*H. eleuchia*) and an oligophagous (*H. cydno*) species with each of their host plants. *H. eleuchia* had a higher correlation with its host plants than *H. cydno*, which is consistent with their larval dietary preferences. Other ecological factors such as toxicity of plants deserve more attention as potential drivers of coevolution. On ageographical scale, it can be concluded that the pattern of diversification of both genera is likely to be different. Furthermore, since they do not share species richness hotspots, our results are not compatible with a strict coevolution scenario.

Abstract ID: 1011
Poster board number:
P606

Evolution is shown to be a function of species culture and evolutionary freedom, not selection

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The theory of (cultural and) evolutionary freedom shows evolution is a function of species culture and evolutionary freedom. Evidence includes: **1** species with exceptional evolutionary freedom evolving in characteristic ways, **2** characteristics not crucial to survival (termed species' culture), including elaborate characteristics (evolve from being desirable), relief characteristics (desirable from providing relief, do not improve fitness), alternate characteristics (describe characteristics with the same function as a characteristic of another species, but structurally are different), and (simple and complex) safety characteristics (not crucial to survival, which improve fitness), **3** evidence that evolutionary processes occur without selection, including the evolution of complex characteristics, characteristics crucial to survival, speciation, higher intelligence and an ability to reason and **4** evidence for **the freedom to intellectualize theory**, as to how higher cognition evolves. I provide evidence for heritable animal behavioural culture. Hardships in a species' life history can restrict evolutionary freedom but can stimulate evolution. Restrictions of evolutionary freedom include heavy predatory impact. The ability to reason evolves in vertebrates as a function of sexual preferences, reduced aggressive interactions between conspecifics, and a friendship-favourable group composition. These two important theories best explain how the common bottlenose dolphin evolved, which has unique exceptional evolutionary freedom and show that the innate response of improvements in effectiveness of behaviour from a friendly greeting is of importance to evolution and society. A new psychology, and a new leaning-

instructional theory are derived from the theorem that humans are loving, non-competitive, and non-aggressive, derived from these two new theories of evolution.

Abstract ID: 1029
Poster board number:
P607

The transformability of genotype-phenotype landscapes

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The mapping from genotype to phenotype to fitness typically involves multiple nonlinearities that can transform the individual and combined effects of mutations. For example, mutations may contribute additively to a phenotype, but their effects on fitness may combine non-additively because selection favors a low or intermediate value of that phenotype. Here, we study transformability of genotype-phenotype landscapes under a non-linear phenotype-to-fitness map. We do so by comparing the topographical properties of genotype-phenotype landscapes, constructed using a diversity of theoretical models and empirical data on transcription factor-DNA interactions, to the topographical properties of fitness landscapes when selection favors a low or intermediate phenotypic value. Using the theoretical models, we prove a number of fundamental results. For example, selection for low or intermediate phenotypic values cannot transform simple sign epistasis into reciprocal sign epistasis, yet it transforms reciprocal sign epistasis into simple sign epistasis and no sign epistasis with equal probability. More broadly, we show that such selection tends to create fitness landscapes that are more rugged than the underlying genotype-phenotype landscape, but surprisingly this increased ruggedness typically does not frustrate adaptive evolution, because the local adaptive peaks in the fitness landscape tend to be nearly as tall as the global peak. Many of these results carry forward to the empirical genotype-phenotype landscapes, which may help to explain why low- and intermediate-affinity transcription factor-DNA interactions are so prevalent in eukaryotic gene regulation.

Abstract ID: 1052
Poster board number:
P608

Impact of population density on sexual selection in the red flour beetle

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The strength, form and direction of sexual selection have often been found to vary substantially within and among species. Theory predicts that demographic factors may play a critical role for understanding this intra- and inter-specific differences. One key demographic factor that often varies largely in space and time is population density, but we still know surprisingly little about its effect on mating behaviour and the strength of sexual selection. Therefore, we tested experimentally the effect of population density on mating behaviour in terms of the number of mating partners, mating duration and copulation attempts of males and females using the red flour beetle *Tribolium*

castaneum as a model system. Specifically, we examined the effect of density by manipulating its two key parameters independently: group size and enclosure area. Hence, we were able to separate potential effects of the number of partners and competitors from effects of habitat area. Importantly, we contrasted the strength and direction of sexual selection across different densities using standardised metrics such as the opportunity for selection, the Bateman gradient and the Jones' index. We predicted that density affects mating rate, which in turn may translate into changes of sperm competition intensity and female harassment by males. Moreover, we partitioned the variance in reproductive success to examine a potential shift from pre- to post-copulatory sexual selection under increasing density. Overall, our study aims at broadening our understanding of environment-dependent sexual selection by providing an experimental test allowing to infer a causal relationship between density and sexual selection.

Abstract ID: 1063
Poster board number:
P609

A global phylogeny of black and pied oystercatcher reveals two new species

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Oystercatchers (order Charadriiformes, family Haematopodidae) are a genus of globally distributed shorebirds with eleven currently recognised extant species. Phylogenetic reconstruction and species delimitation of this group has been a longstanding challenge due to their morphological similarity and inconsistent sampling. The purpose of this study was a complete reconstruction of the evolutionary history of taxa inclusive of all recognised oystercatcher species. Nuclear and mitochondrial DNA were isolated from feathers and toepads of specimens and sequenced for phylogenetic reconstruction. Based on a combined alignment of mitochondrial and nuclear markers, a robust time-calibrated phylogeny was constructed, resulting in an improved understanding of the evolutionary history of the genus. It was found that oystercatchers separated into two ancient clades approximately 24.13 mya (CI: 19.86-28.24 mya) representing the New and Old Worlds. Within the New World, the endemic Galapagos Oystercatcher (*Haematopus galapagensis*), previously treated as a subspecies of the American Oystercatcher (*Haematopus palliatus*) likely represents a valid new species. Likewise, in the Old World clade, the Pacific Oystercatcher (*Haematopus osculans*), previously a subspecies of the widespread Eurasian Oystercatcher (*Haematopus ostralegus*), should be treated as a separate species. We subsequently recommend several changes to be made to oystercatcher taxonomy.

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Poster board number:
P610

Holey niche! A novel method to find holes in niche hypervolumes using persistence homology

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Animals are limited in the range of ecological gradients they can explore. This defines where animals exist (or could exist) and forms an ecological fingerprint that explains species' distribution at global scales
A concept known as Hutchinson's niche hypervolume represent this, and has enabled signifiant progress in our understanding of species' ecological needs and distributions across environmental gradients. Nevertheless, the properties of Hutchinson's n-dimensional hypervolumes can be challenging to calculate and several methods have been proposed to extract meaningful measurements of hypervolumes' properties (e.g., volume).
One key property of hypervolumes are holes, which provide important information about the ecological occupancy of species. However, to date, current methods rely on volume estimates and set operations to identify holes in hypervolumes. Yet, this approach can be problematic because in high-dimensions, the volume of region enclosing a hole tends to zero.
We the use of the topological concept of persistence homology (PH) to identify holes in hypervolumes and in ecological datasets more generally. PH allows for the estimates of topological properties in n-dimensional niche hypervolumes and is independent of the volume estimates of the hypervolume. We demonstrate the application of PH to canonical datasets and to the identification of holes in the hypervolumes of five vertebrate species with diverse niches, highlighting the potential benefits of this approach to gain further insights into animal ecology.
Overall, our approach enables the study of an yet unexplored property of Hutchinson's hypervolumes (i.e., holes), and thus, have important implications to our understanding of animal ecology

Abstract ID: 1087
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P611

Heterogeneous introgression at late stages of species formation in a grasshopper hybrid zone

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The process of species formation is characterized by the accumulation of multiple reproductive barriers. The evolution of hybrid male sterility, or Haldane's rule, typically characterizes later stages of species formation, when reproductive isolation is strongest. Yet, understanding how quickly reproductive barriers evolve and their consequences for maintaining genetic boundaries between emerging species remains a challenging task because it requires studying taxa that hybridize in nature. Here, we address these questions using the meadow grasshopper *Pseudochorthippus parallelus*, where populations that show multiple reproductive barriers, including hybrid male sterility, form natural hybrid zones. Using mitochondrial data, we infer that such populations diverged

some 100,000 years ago, at the beginning of the last glacial cycle in Europe. Nuclear data show that contractions at multiple glacial refugia, and post-glacial expansions have facilitated genetic differentiation between lineages that today interact in hybrid zones. We find extensive introgression throughout the sampled species range, irrespective of the current strength of reproductive isolation. Although hybrid zones are narrow, we find heterogenous introgression throughout the genome, consistent with differential selection at the gene level. Together, our results suggest that reproductive barriers that characterize late stages of species formation can evolve relatively quickly, particularly when associated with strong demographic changes. Moreover, we show that such barriers persist in the face of extensive gene flow, allowing future studies to identify associated genomic regions.

Abstract ID: 1112
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P612

Mutation bias shapes the spectrum of adaptive substitutions

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Evolutionary adaptation often occurs by the fixation of beneficial mutations. This mode of adaptation can be characterized quantitatively by a spectrum of adaptive substitutions, i.e., a distribution for types of changes fixed in adaptation. Recent work establishes that the changes involved in adaptation reflect common types of mutations, raising the question of how strongly the mutation spectrum shapes the spectrum of adaptive substitutions. We address this question with a codon-based model for the spectrum of adaptive amino acid substitutions, applied to three large data sets covering thousands of amino acid changes identified in natural and experimental adaptation in *S. cerevisiae*, *E. coli*, and *M. tuberculosis*. Using species-specific mutation spectra based on prior knowledge, we find that the mutation spectrum has a proportional influence on the spectrum of adaptive substitutions in all three species. Indeed, we find that by inferring the mutation rates that best explain the spectrum of adaptive substitutions, we can accurately recover the species-specific mutation spectra. However, we also find that the predictive power of the model differs substantially between the three species. To better understand these differences, we use population simulations to explore the factors that influence how closely the spectrum of adaptive substitutions mirrors the mutation spectrum. The results show that the influence of the mutation spectrum decreases with increasing mutational supply Nμ, and that predictive power is strongly affected by the number and diversity of beneficial mutations.

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P613

Putting life history theory to the test - the estimation of reproductive values from field data

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Quantifying fitness is important to understand adaptive evolution. Reproductive values are useful for making fitness comparisons involving different categories of individuals, like males and females. By definition, the reproductive value of a category is the expected per capita contribution of the members of that category to the gene pool of future generations. Life history theory reveals how reproductive values can be determined from life-history parameters, but this requires matrix algebra. Recently, a more intuitive, pedigree-based method has become popular. It estimates genetic contributions of individuals to future generations by tracking their descendants down through the pedigree. We compare both methods. We implement various life-history scenarios (for which the "true" reproductive values can be calculated) in individual-based simulations, use this data to estimate reproductive values with both methods, and compare the results with the true reproductive values. We show that the pedigree-based estimation of reproductive values is either systematically biased (and hence inaccurate), or very imprecise. This holds even for simple life histories and under idealized conditions (such as complete knowledge of the pedigree). The traditional algebraic method estimates reproductive values with accuracy, and the precision of estimates can be determined by sensitivity analyses. However, these estimates can be biased as well when they are based on inadequate life-history models.

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P614

Sexual conflict over mating frequency in a sexually cannibalistic mantis

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Sexually cannibalistic behaviour is often considered a manifestation of sexual conflict whereby females avoid costs of sexual interaction. We hypothesised that sexual conflict over mating number—where increased matings enhance male fitness but reduce female fitness—could favour precopulatory cannibalism if it allows females to control the number of times they mate. Using the highly cannibalistic Springbok mantis, *Miomantis caffra*, we took an experimental approach to assess female responses to mating number. We predicted that females would incur more injuries, have higher mortality, and produce fewer offspring the more times they mated, and that cannibalism would help females avoid these costs. We found that the highest rates of injury and premature death occurred in twice mated females, but a single mating was not optimal: net fitness peaked at the third mating and declined thereafter, indicating direct benefits of an intermediate mating rate. Despite these benefits, many females were reluctant to mate more than once and took longer to remate a second and third time, suggesting male-induced nonreceptivity to remating. Cannibalism reduced the incidence of mating as predicted, but the reduction was suboptimal, possibly reflecting a trade-off between early-life and lifetime performance. Taken together, our results show that *M. caffra* females experience sexual conflict over mating number and use precopulatory cannibalism to avoid mating too frequently, but males appear to have hijacked female mating reluctance for their own ends. We suggest that sexual conflict over mating number could be a widespread selective force in many taxa where cannibalism is precopulatory.

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P615

Evolutionary ecology of resistance to sexually transmitted mites: The *Drosophila-Gamasodes* system

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Genetic variation for parasite resistance is commonly observed in nature, despite strong directional selection imposed by parasites on their hosts. Fitness costs of resistance are a general factor expected to maintain polymorphisms at resistance-conferring loci. Here, we examine the mechanisms, genetic basis, and costs of ectoparasite resistance in the host, *Drosophila melanogaster* Meigen. The ectoparasite is a sexually transmitted mite, *Gamasodes queenslandicus* Halliday and Walter, that co-occurs with its host in nature. Very little is known about both the genetics and costs of ectoparasite resistance, even though ectoparasites are ubiquitous and of enormous ecological, medical and veterinary significance. Flies deploy well-defined defensive behaviors to resist parasite attack, including brisk grooming behaviors and burst of flight. Artificial selection for increased behavioral defenses in replicate selection experiments resulted in significant evolutionary responses, demonstrating heritable genetic variation for behavioral resistance in the original field population. Resistant flies in the absence of parasites exhibited increased nutrient reserve depletion relative to controls, and compromised starvation resistance and female fecundity. This increased nutrient reserve depletion was reflected in altered metabolic gene activity revealed by RNA-seq analyses, and increased nighttime activity levels and oxygen consumption. Thus, resistance is conferred though increased behavioral activity, and costs emerge as a result of shifts in nutrient metabolism and body reserve depletion. Our integrative research provides unique knowledge about the functional components of resistance and of associated trade-offs, contributing to a refined ability to predict the evolutionary dynamics of host-parasite interactions.

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P616

Domestication of the fungi *Penicillium roqueforti* to make blue cheeses

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Domestication is an excellent model for studying adaptation because it involves strong and recent selection for known traits. Easy to manipulate and long used in fermentation, microorganisms are good models for studying domestication. *Penicillium roqueforti* is the mould used in the production of all blue cheeses and has four genetically and phenotypically differentiated populations *in vitro*, one of which is used in the Roquefort PDO and another in the production of all other blue cheeses, the other two populations moulding silage or feed. Manufactures of Roquefort-type cheeses with all four populations of *P. roqueforti* revealed that the cheese populations produced cheeses with more blue surface on the slices and higher amounts of positive volatile compounds. The Roquefort population, in particular, produced higher amounts of positive aroma compounds in the cheeses, linked to more efficient proteolysis and lipolysis. An association genetics study on a progeny between a Roquefort strain and a non-Roquefort strain identified a genomic region potentially responsible for lipolysis efficiency. Heterozygous genotypes in the offspring of this haploid species grew faster and were due to a chromosomal rearrangement between the parental strains. Finally, an analysis of 200 genomes revealed a fifth population, specific to Termignon blue cheese, a cheese spontaneously colonised by *P. roqueforti*. These results allow us to understand the influence of *P. roqueforti* populations on different important aspects of cheeses as well as to explore the relationships between genotype and phenotype, and thus contribute to our understanding of domestication and adaptation processes.

Abstract ID: 1234
Poster board number:
P617

The effect of mutagenic drugs on influenza A virus populations: bridging experiments and simulations

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The search for effective therapeutics for viral infections remains a crucial challenge in medicine. Mutagenic drugs, such as favipiravir and molnupiravir, promise successful treatment of RNA virus infections such as influenza and SARs-Cov-2. These drugs act by increasing the mutation rate, which eventually leads to the extinction of the viral population due to extensive deleterious mutation load. This evolutionary process has been studied theoretically and experimentally under the names of mutational meltdown and lethal mutagenesis. Here, we set out to confirm whether and how a previously described resistance mutation and four other genetic backgrounds affect the evolutionary dynamics and the time to the mutational meltdown of influenza A virus in the presence of Favipiravir. We used a laboratory evolution approach to passage the five virus strains under a constant drug concentration. Interestingly, extinction occurred within less than ten experimental passages, with little time variation between replicates in almost all strains, including some strains that carried resistance mutations. However, a single replicate of one population survived longer than all others, and the reasons are so far unclear. Here, we further explore the evolutionary mechanisms allowing viruses to escape mutational meltdown. We implement simulation-based modelling to explain possible population scenarios, showing the effects of de novo mutations that change mutation rates and fitness effects in viral populations under treatment. We discuss our results in the light of proposed adaptation mechanisms, predicted extinction times, and

future steps to decipher the genomics underlying extinction versus survival of a virus population.

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P618

Cheating triggers tragedy of the commons, group size attenuates it

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Cooperative societies frequently contain cheats that reap the rewards provided by others without contributing anything. Cheating is predicted to lead to the demise of cooperative groups, and yet cooperation is widespread in animals. Under what conditions does cheating occur without causing the breakdown of cooperation? Here we test the idea that in complex social groups cheating is more likely to occur because cheats are harder to detect and the costs of cheating are shared among more cooperators. We investigated this by experimentally manipulating group size in a species renowned for having reproductive cheats, the cooperatively breeding ostrich, *Struthio camelus*. Ostrich groups nurture a common nest where multiple individuals contribute offspring, but not all individuals contribute to parental care (incubation). We found that while the opportunities for cheating are greater in larger groups with more cooperators, cheats maximize their reproductive success in small groups. However, in small groups cooperators react strongly to cheats by reducing incubation effort, leading to a collapse of reproduction. In contrast, in large groups, individuals appeared buffered from the reproductive costs of cheating by the presence of many cooperators. Our results suggest that the emergence of cheats in social groups contributes to group complexity. Small groups are destabilized by cheating while the impact on individuals in large groups is offset by the presence of more cooperators.

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P619

Worker task specialization in ants linked to differential expression of odor receptors in antennae

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Social insects dominate arthropod communities worldwide due to their efficient division of labor. Not only do queens and workers divide their tasks, but workers also specialize in tasks such as nursing or foraging. In ants, worker task specialization depends on age, experience, colony needs and is thought to be regulated via variation in response thresholds to task-related stimuli, which are determined by differential gene expression. Workers of ant *Temnothorax longispinosus* show division of labor, the molecular regulation of which interests us. In a previous study, RNAi downregulation of gene *vitellogenin-like A*, which is overexpressed in the fat bodies of T. longispinosus nurses, led to a reduction in brood care behavior and sensitivity to brood-related stimuli,

suggesting a change in odor perception and olfactory-driven decision-making in the ant brain. Here, we examined gene expression in brain and antenna of nurses and foragers of *T. longispinosus*. While the expression of 333 genes or 4% changed in workers specializing on different tasks, more than 2000 genes or 25% changed in the antennae, suggesting more pronounced transcriptome shifts in the peripheral nervous system than in the central nervous system during behavioral specialization. In addition, approximately half of all olfactory receptors were differentially expressed in the antennae of nurses and foragers, suggesting that workers focusing on different tasks perceive their chemical environment differently. Our results support the response threshold model of division of labor, and future studies will examine to which extend changes in odorant perception with tasks are causes or consequences of behavioral switches.

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P620

Isolation in glacial refugia and extreme habitats drive lineage diversification in Arabian mangroves

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Biological systems occurring in ecologically heterogeneous and spatially discontinuous habitats provide an ideal opportunity to investigate the relative roles of neutral and selective factors in driving lineage diversification. The gray mangroves (*Avicennia marina*) of Arabia occur at the northern edge of the species' range and are subject to variable, often extreme, environmental conditions, and to historic large fluctuations in habitat availability and connectivity resulting from Quaternary glacial cycles. We analyzed 200 resequenced genomes sampled from 20 locations across the Red Sea, the Arabian Sea and the Persian/Arabian Gulf to reconstruct the evolutionary history of the species in the region, and to identify environmental drivers of lineage diversification. Population structure and phylogenetic analyses revealed marked genetic structure and highly supported clades among and within the seas surrounding the Arabian Peninsula. Demographic modelling revealed times of divergence consistent with periods of geographic isolation and low marine connectivity in (cryptic) marine glacial refugia. Limited to no migration was detected among Red Sea populations, in contrast to significant gene flow within the Persian/Arabian Gulf and across the Strait of Hormuz to the Arabian Sea. Genetic-environment association analyses identified signs of multi-loci local adaptation driven by temperature extremes, annual precipitation and hypersalinity. Divergent association patterns between mangrove populations of the Red Sea were also recovered, suggesting incipient reproductive isolation resulting from adaptive differentiation. These results support a process of lineage diversification driven by the combined factors of historical isolation and environmental selection, and reveal peripheral mangrove populations as relevant sites for speciation.

Abstract ID: 1330
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P621

Eligibility and criteria for scientific awards in ecology and evolution – biases and opportunities

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Individual awards recognize achievements of researchers and influence career progression in academia. Such awards may also propagate existing biases and reinforce traditional career trajectories. Therefore, these awards can have significant downstream effects on promotion and retention of underrepresented minorities in science by discriminating against researchers with less conventional careers and these with less access to opportunities. To assess the equity of individual awards, we collected data on eligibility rules and assessment criteria of international awards available to early and mid-career researchers in evolutionary biology and ecology. We also quantified gender biases and historical trends in the lists of past awardees in relation to the award policies. Overall, we evaluated 14 “best researcher” awards and X “best paper” awards from over 30 journals and 18 societies that fulfilled our inclusion criteria. Our results reveal which awards foster equitable access and assessment. We highlight instances of desirable practices, such as accommodating non-traditional careers, assessing achievements relatively to opportunity, and rewarding Open Research practices. We hope this work will nudge award committees to shift from simple but non-equitable award policies towards strategies promoting inclusivity and diversity – benefiting whole research community, but especially these at early and mid-career stages.
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P622

Genomics of insecticide resistance in bed bug

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In the last few years, the common bed bug *Cimex lectularius* step out the shadow as an increasing problem world-wide. Globalization, together with the development of insecticide resistance, are the main reasons underlying its re-emergence. Although the massive use of insecticides in the twentieth century has helped regulate bed bug populations, a phenomenon of resurgence of this species has started in the early 1990s. Insecticide exposure exerts a strong selective pressure, which can facilitate the rapid spread of advantageous mutations in insect populations. In order to achieve effective interventions, these mutations and their diversity must be described. This study aims to identify the genetic determinants involved in *Cimex lectularius* insecticide resistance. To this end, we carried out a genome-wide population genomic analysis, by comparing the genomic composition of two ancient susceptible strains with two recent resistant strains. By performing a genome scan, we identified single nucleotide polymorphism outliers

delineating genomic regions associated with insecticide resistance. Additionally, variation in gene copy number was analyzed.We confirmed the involvement of some expected loci together with new candidates for insecticide resistance, which should be further explored.

Abstract ID: 1399
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P623

Early divergence of Metallura tyrianthina in the Colombian Andes

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The highly variable topography, the climatic history and the great variety of niches of the Andes Mountain range have had major contributions to the formation and maintenance of the genetic and morphological diversity of tropical birds. The main causes of divergence promoted by the Andes are attributed to the accumulation of mutations by genetic drift in populations that are reproductively isolated by geographic accidents, and other have also described rapid divergence events mediated by adaptation to ecological niches. Studying early evolutive patterns of diversification has shown promise for understanding the role of the Andes Mountain behind speciation. Therefore, I propose to study the evolution of the *Metallura tyrianthina* subspecies which had a rapid diversification in the Andes that resulted in 7 subspecies with variable coloration. Here, we corroborate and extend previous studies on the evolution of the Tyrian Metaltail hummingbird in Colombia, using reduced genome (NextRAD) and quantitative coloration assessments for finding phyllogenetic, genetic, demographic and morphologic evidence of two early divergence with gene flow processes in the same species. First, evidence showed that Quaternary glacial cycles played a major role in the recent foundation and poterior rapid divergence of the Sierra Nevada Mountain populations of *Metallura tyrianthina districta,* and also found evidence of a subtle divergence between eastern and western populations of *Metallura tyrianthina tyrianthina* that was not explained by the topography nor isolation by distance.

Abstract ID: 1400
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P624

A supermatrix phylogeny of the world's bees (Anthophila): A tool for macroevolutionary analyses

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Large phylogenies are necessary to tackle macroecological and macroevolutionary questions. The increasing availability of large phylogenies has provided new opportunities to study the evolution of species traits, their origins and diversification, and biogeography; yet taxonomically well-curated phylogenies are currently lacking for major insect groups. Bees are a large group of insect pollinators that have a worldwide distribution, and a wide variation in ecology, morphology, and life-history traits, including sociality. For these reasons, as well as their major economic importance as pollinators, numerous molecular phylogenetic studies of relationships between and/or within families

or genera for this group have been published. By using sequence data available from NCBI, we constructed a supermatrix phylogeny that includes data for nearly 4,000 (~20%) of the currently recognised bee species (~77% of genera that contain 96% species), and includes between 14% and 39% of the species in each of the 7 families that comprise the Anthophila. This supermatrix phylogeny may enable new insights into long standing questions about evolutionary drivers in bees, and potentially insects more generally. As an example, we use this phylogeny to examine the evolution of structural colouration in bees, a functionally important trait that has long fascinated biologists.

Abstract ID: 1416
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P625

Male-biased sex ratios increase sexual selection against a mutant in *Drosophila melanogaster*

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Sexual selection explains the enormous diversity of exaggerated and seemingly cumbersome display and weapons. The strength of sexual relative to nonsexual selection is often quantified to explain variation in the degree of investment in sexual traits, but experimental analyses of factors that affect the strength of sexual selection are scarce. In this study, we investigate how operational sex ratio influences the strength of selection on a mendelian trait in *Drosophila melanogaster*. To this end, we measure competitive paternity success of two genotypes, one with a homozygous mutation in the ebony gene and the wild type, under different sex ratio treatments. We further estimate how ecologically relevant covariates such as density and spatial complexity interact with sex ratio to yield differential sexual selection on this genetic polymorphism. We find that not only does the strength of sexual selection increase through the continuum of female to male biased sex ratios, but it also wanes temporally through the experiment. With this approach, we directly measure the totality of sexual selection (pre-and post-copulatory components) in different ecologically relevant scenarios and strengthening the evidence for the role of sex ratio on the strength of sexual selection.

Abstract ID: 1437
Poster board number:
P626

More than just density: fitness-functions in crowded *Drosophila* cultures

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Density-dependent selection is an important interface between evolution and ecology, and posits that fitness-functions will be altered by density. Long-term selection experiments using *Drosophila* have been central to advancing our understanding of evolutionary trajectories under high or low density rearing. An important recent finding in such studies has been that differing combinations of egg number and food amount per rearing vial, that yield similar overall larval density, can nevertheless result in different

distributions of major fitness components like pre-adult survivorship and development time. Similarly, differences in the specific combination of egg number and food amount per rearing vial experienced during selection for adaptation to crowding can affect which traits mediate the evolution of greater competitive ability. The picture emerging from these studies suggests that the combination of egg number and the height of the food column in rearing vials plays a major role in determining the specific ecological and evolutionary responses to larval crowding. The present study expands upon this work by examining pre-adult survivorship and development time in different density treatments varying egg number, food column height, and horizontal cross-section area, in a fully factorial design. Our results show that different combinations of food height, surface area and egg number yielding the same overall density can affect fitness components differently. We also find that the density of larvae within the 'feeding band' – a restricted volume of food, near the surface, where the larvae feed – better explains variation in fitness components under larval crowding than the overall eggs/food density.

Abstract ID: 1439
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P627

Aposematic colouration in mammals

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Some of the most notable species of mammals are black and white, colouration classically thought of as aposematic to advertise noxious anal secretions as exemplified by skunks. The original formulation of aposematism, however, encompassed a broader range of morphological, physiological, and behavioural defences, and there are many mammal species with black and white contrasting patterns that do not have noxious adaptations. Using Bayesian phylogenetic models and data from 1,726 terrestrial non-volant mammals, we find that two aspects of conspicuous colouration, black and white colour patterns on the head and body, advertise defences that are morphological (spines, large body size), behavioural (pugnacity), and physiological (anal secretions), as well as being involved with sexual signalling and environmental factors linked to crypsis. Black and white colouration in mammals appears to be multifunctional; it serves to warn predators of several defences other than noxious anal secretions, and aposematism is not restricted to carnivores.

Abstract ID: 1450
Poster board number:
P628

A potentially new insecticide-resistant aphid sweeps through the Dutch greenhouses

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The green peach aphid (*Myzus persicae*) (Hemiptera: Aphididae), is the economically most important aphid crop pest worldwide, and is notorious for its ability to develop resistance against many different groups of insecticides. One crop in which *M. persicae* causes great economical damage is sweet pepper. We followed the population structure of *M. persicae* in both conventional (chemical pesticides are used) and organic (no chemical pesticides are used) Dutch sweet pepper greenhouses from 2019 till 2022 with the use of microsatellites. We found strong signals for insecticide-driven selection in conventional greenhouses. Hitherto, no resistance has been reported for the insecticides used to control *M. persicae* in these greenhouses, which was pymetrozine until 2020 and is flonicamid since 2020. To confirm that pesticide resistance was driving clonal selection, the sensitivity of ten clonal lines of *M. persicae*, collected from sweet pepper greenhouses, was tested against both pymetrozine and flonicamid in leaf dip bioassays. The results reveal that the aphid lines most abundant in the conventional greenhouses displayed the lowest sensitivity against the used insecticides. Future research will have to elucidate which mechanisms underlie the decreased sensitivity against both groups of insecticides. Our results suggest that *M. persicae* has rapidly developed (partial) resistance against the novel insecticides pymetrozine and flonicamid, and emphasize the need for alternative, non-chemical, aphid control strategies such as biological control.

Abstract ID: 1455
Poster board number:
P629

Lokiretroviruses are still alive and in good health in at least two species of lamprey

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Lokiretroviruses are a recently discovered lineage of retrotransposons within the genomes of fishes, amphibians and reptiles, which is sister to all the other retroviruses so far known. Being one of the most basal living vertebrates, lampreys (Petromyzontiformes) constitute an excellent material to study the evolution of these retrotransposons. Through exhaustive blast searches using reverse transcriptase (RT) and ribonuclease-H (RH) queries, we have retrieved the sequences of lokiretroviral insertions from the assembled genomes of four lamprey species, namely *Petromyzon marinus*, *Entosphenus tridentatus*, *Lethenteron reissneri* and *Lethenteron camtschaticum*. The abundance of these insertions differs strikingly among the four genomes, from just one or at most two, very much fragmented copies, in *E. tridentatus*, to nearly 100 intact copies in *L. reissneri*. Both the phylogenetic analyses and the % identity of the LTRs of specific insertions indicate that lokiretroviruses are actively transposing in both *Lethenteron* species, and perhaps also, but with a much lower intensity, in *P. marinus*. The discordance between the species tree and the phylogeny of lokiretroviral insertions is a clear indication of recent events of horizontal transmission of

these elements. In addition, the comparison of RT and RH phylogenies supports the hypothesis of their mosaic evolution through recombination.

Abstract ID: 1468
Poster board number:
P630

Inferring speciation histories for species pairs across *Drosophila*.

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The allopatric model of speciation, with potential reinforcement following secondary contact, is considered an uncontroversial null model of speciation. Since the late 1980s, broad comparative surveys of reproductive isolation in *Drosophila* have supported this, with faster evolution of premating isolation seen between species which have become sympatric. However, very few studies have explicitly inferred speciation histories and, critically, quantified gene flow between species pairs at scale. Here, we use publicly-available whole-genome data for 96 pairs of *Drosophila* species, alongside data on reproductive isolation and range overlap, to (a) reconstruct the demographic histories of speciation events across *Drosophila*, (b) measure the duration and amount of gene flow between species pairs and (c) understand the effect of geography on reproductive isolation and gene flow. We find that the majority of *Drosophila* species pairs, including pairs historically considered allopatric, show strong evidence of recent gene flow and are almost as likely to have speciated with gene flow as sympatric pairs. We find little evidence for stronger pre-mating isolation in sympatric pairs compared to allopatric pairs when historical demography is taken into account. Additionally, we find no difference in the time-to-speciation between allopatric and sympatry species pairs, suggesting little evidence for reinforcement. Altogether, our results suggest speciation-with-gene-flow is the dominant model of speciation across *Drosophila* and current ranges do not accurately reflect speciation histories.

Abstract ID: 1502
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P631

Fitness landscapes reveal context-dependent benefits of oviposition choice

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Resource choice behaviour has enormous fitness consequences and can drive niche expansion. However, individual behavioural choices are often mediated by context, determined by past experience. Do such context-dependent behaviours reflect maladaptive variation, or are they locally adaptive? Using *Tribolium castaneum* (the red flour beetle), we demonstrate that context-dependent oviposition behaviour reflects distinct, context-specific local fitness peaks. We measured offspring fitness to generate fitness landscapes as a function of all possible oviposition behaviours (i.e., combinations of fecundity and resource preference) in a habitat containing optimal and suboptimal resource patches. We did this by experimentally manipulating female egg allocation

across patches, which allowed us to assess behaviours not typically observed in the laboratory. We found that females from different age and competition contexts exhibit distinct behaviours which optimize different fitness components, linked in a tradeoff. With prior exposure to strong competition and increasing age, females produce few but fast-developing offspring that are advantageous under high resource competition. In contrast, young naïve females produce significantly more (but slower-developing) offspring, which is beneficial under weak competition. Systematically mapping complete context-dependent fitness landscapes is thus critical to infer behavioural optimality, to understand the evolution of behaviour, and may offer predictive power in novel contexts.

Abstract ID: 1505
Poster board number:
P632

The role of micro and macro-evolutionary processes in determining insect communities on forest trees

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The community of insect herbivores on individual host trees can be driven by processes ranging from ongoing leaf development via recent microevolution to ancient phylogeny represented in the neighbourhood. To elucidate the relative importance of these processes, we sampled spring caterpillars from oaks (*Quercus petraea)* that varied in budburst phenology, trunk diameter, genotype, genome size, and phylogenetic neighbourhood. We found that free-living caterpillar abundance decreased with leaf age. Larger trees tended to show higher parasitism rates of herbivores. Casebearers were less abundant on more heterozygous oaks, but we detected no other effects of genotype or genome size on caterpillar abundance. In contrast to most previous studies, oaks growing among phylogenetic distant tree species had higher abundances of all three caterpillar guilds. Lower parasitism was associated with higher abundances of co-dominant caterpillar species. Neighbourhoods and traits of trees were also related to community composition and diversity, but not to the average wingspans or specialization of species, consistent with the assembly of herbivore communities being driven by leaf traits and parasitism pressure on trees rather than by insect movement among trees. Overall, we suggest that the assembly of insects on a tree is mostly driven by trophic interactions controlled by a mosaic of processes playing out over very different time scales. The overall dominating effect of phylogenetically distant neighbourhoods increasing caterpillar abundance suggests that the consequences of growing amongst distantly related tree species may depend on factors such as geographic region and tree age. Grant 2018/29/B/NZ8/00112 National Science Centre (Poland).

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P633

Molecular evolution of Na^+,K^+ -ATPase and its role in cardenolide resistance in avian predators

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The Na^+,K^+-ATPases are heterodimeric transmembrane proteins consisting of a catalytic α- subunit and a structural β-subunit. It uses ATP hydrolysis to maintain a concentration gradient of Na^+ and K^+ ions across the membrane and is thus vital for physiological homeostasis. Cardiac glycosides are a group of plant (cardenolide) and animal derived (bufadienolide) steroid compounds which exert their effects by binding to and inhibiting the Na^+,K^+-ATPases. Many predators that feed on chemically defended prey share a striking pattern of convergence in molecular resistance via the substitutions in the cardiac glycoside binding pocket αM1-2 loop of the Na^+,K^+-ATPase. We have identified a series of recurrent substitutions predicted to confer target site insensitivity (TSI) in diverse avian predators. Using a protein engineering approach we have measured the phenotypic effects of these substitutions and quantified the additive function of each. Our functional analysis of recombinant proteins suggest that substitution at position 111 is critical in conferring resistance in some species, but its effects varies between taxa, and substitutions at other positions within the gene can have pleiotropic effects in protein activity.

Abstract ID: 1526
Poster board number:
P634

Eco-evolutionary extinction/recolonization dynamics reduce genetic load in highly inbred populations

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Understanding how genetic and ecological effects can interact to shape genetic loads within and across local populations is key to understanding the ongoing persistence of systems that should otherwise be susceptible to extinction through mutational meltdown. Classic theory predicts short persistence times for metapopulations comprising small local populations with low connectivity, due to accumulation of deleterious mutations. Yet, some such systems have persisted over evolutionary time, implying the existence of mechanisms that allow metapopulations to avoid mutational meltdown. We first hypothesize a mechanism by which the combination of stochasticity in the numbers and types of mutations arising locally (genetic stochasticity), resulting local extinction, and rapid recolonisation through evolving dispersal, facilitates metapopulation persistence. We then test this mechanism using a spatially and genetically explicit individual-based model. We show that genetic stochasticity in highly structured metapopulations can result in local extinctions, which can favour increased dispersal, thus allowing recolonization of empty habitat patches. This causes fluctuations in metapopulation size and transient gene flow, which reduces genetic load and increases metapopulation persistence time. Our suggested mechanism and simulation results provide an explanation for the conundrum presented by the continued persistence of highly structured populations with inbreeding mating systems which occur in diverse taxa.

Abstract ID: 1535
Poster board number:
P635

Toward proper nomenclature: reassessing honeybee (*Apis mellifera*) mtDNA nomenclature using phylogeny

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The western honey bee (*Apis mellifera*) is one of natures' most important pollinators and domesticated species. Through human management, it has spread all around the world becoming a cosmopolitan species, and its genetic diversity has been shaped over millennia by anthropogenic influence. Six main mtDNA lineages (M, C, O, Y, A and S) with a large number of existing sublineages are recognized, usually associated with appropriate subspecies. Current nomenclature is inconsistent and the naming of newly identified haplotypes is not standardized. Here we reassessed the nomenclature of C lineage using sequences of the *tRNA^{leu}-cox2* intergenic region and complete mitogenomes. Most of the available honey bees' mtDNA haplotypes are based on the sequence variability of this region while available complete mitogenomes are still few. The first complete mitogenome of *Apis mellifera* (NC_001566) was used as the reference genome for haplotype determination. We propose that the naming of the mtDNA haplotypes should be performed based on the differences to the reference mitogenome and according to the phylogenetic relationship between detected haplotypes. Our analyses showed that the current nomenclature of C sublineages is not consistent with the phylogenetic relationships between existing haplotypes and that the reassessment followed by the proper naming of haplotypes is needed. We propose to keep the names of the main lineages but correct the names of sublineages using the same approach as in the identification of human mtDNA lineages. This newly standardized nomenclature will bring more order to the studies of honey bees' genetic diversity.

Abstract ID: 1581
Poster board number:
P636

The dynamic ontogenetic shape patterns of adaptive divergence and sexual dimorphism

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The interplay between ecological diversification and sexual dimorphism has been largely overlooked in the literature. Sexually dimorphic species which are also undergoing adaptive radiations are ideal for filling this knowledge gap. The Arctic charr in lake Thingvallavatn is one such system: it is a sexually dimorphic species which has recently diverged along the benthic-limnetic ecological axis. In a long-running common-garden experiment we studied the shape variation throughout ontogeny of intra- and inter-morph crosses of a benthic (small benthic SB) and a limnetic (planktivorous, PL) ecomorphs from the lake. We found that shape differences between the ecomorphs had a genetic component. The differences were attributable to adaptations to benthic and limnetic niches, i.e., shorter lower jaws and rounder snouts in the benthic and evenly protruding snouts and pointier snouts in the limnetic. Prior to the onset of sexual

maturation reciprocal hybrids showed intermediate, transgressive and/or maternal morphologies. After the onset sexual maturation however larger morphological differences occurred between sexes than among cross types. Taken together, our results demonstrate that the interplay between ecological diversification and sexual dimorphism is complex and dynamic throughout ontogeny, and that long-term common garden experiments are immensely valuable for studying shape dynamics in different evolutionary scenarios.

Abstract ID: 1590
Poster board number:
P637

Demographic history of the South African Coloured population

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The South Africa Coloured people (SAC) are the most prominent self-denominated admixed population in the country. They are descendants of Khoe-San, and Bantu-speaking populations, European settlers, and enslaved people from the East Coast of Africa, South and East Asia brought during the slave trade period. This study aimed to investigate the remnant Khoe-San ancestry within the Coloured population by doing an admixture analysis employing whole-genome sequence data. Newly generated genotypes and data from previously published studies were used to assess the ancestry of 222 SAC individuals from 17 different locations. Thus, this study has gathered the most extensive dataset of SAC individuals sampled from the largest number of sites to date. In 14 places, the Khoe-San/Rainforest Hunter-gatherers group had the most significant contribution of genetic material. Meanwhile, the East African contribution was the smallest one overall. The West African, East Asian, South Asian, and European groups present diverse shared ancestry levels that vary depending on the sampling location and the social policies that governed the country. This research highlights the importance of studying the South Africa Coloured population to comprehend the impact of complex migration patterns and systems of racial segregation in the oldest human lineage.

Abstract ID: 1594
Poster board number:
P638

Implications of ancestor-descendent relationships on catarrhine phylogeny

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The extant and extinct catarrhine primates that span the Old World are a highly diverse clade, yet there are few comprehensive catarrhine time calibrated phylogenies with sampled fossil species. Further, none directly test ancestor-descendant relationships. An accurate phylogeny is fundamental to providing context for understanding the evolutionary biology of catarrhine primates. Morphological studies allow the placement of both living and fossil taxa on a phylogenetic tree, but for many decades there have been significant gaps within the catarrhine fossil record. Now, a new generation of models for phylogenetic inference provides us with the opportunity to revisit the catarrhine tree of

life. Here, using Bayesian inference with the fossilized birth-death range process model, we provide a revised time-calibrated phylogeny for the evolution of non-hominin catarrhines. Our findings suggest new and updated phylogenetic placements for *Saadanius hijazensis, Rukwapithecus fleaglei*, and *Oreopithecus bambolii*, and the putative stem catarrhine clade Pliopithecoidea. We propose updated divergence date estimates for the crown anthropoid, crown catarrhine and crown hominoid clades, which support prior estimates based on morphological evidence. The new method indicates direct ancestor-descendant relationships within the catarrhine primates for the first time, and our results strongly suggest that nine species, including *Victoriapithecus macinnesi, Morotopithecus bishopi*, and the recently published *Kapi ramnagarensis*, are ancestral, rather than falling as independent species. These ancestral species are not confined to any particular time frame, but are scattered throughout the tree. Our findings have implications for how researchers think about and study speciation and diversification of catarrhines, and primates more generally.

Abstract ID: 1608
Poster board number:
P639

Genome resequencing reveals hybrid zone dynamics of secondary contact in darters (Percidae)

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Speciation does not always lead to complete reproductive isolation which can result in hybrid zones with gene flow. Freshwater fish are an ideal study system; although different stream populations are geographically isolated favoring allopatric speciation, secondary contact and hybridization can arise when river courses shift. Natural freshwater fish dispersal proceeds upstream and downstream within river basins, but physical and ecological dispersal barriers can lead to fragmented species distributions within the same stream system. In this study, we examine a secondary contact hybrid zone in western New York (USA) between the Tessellated Darter (*Etheostoma olmstedi*) and the Johnny Darter (*E. nigrum*) in the Genesee River system. *Etheostoma olmstedi* and *E. nigrum* populations have been colonizing this area only for about 20 000 years following the retreat of Pleistocene glaciation. We investigated *E. olmstedi* and *E. nigrum* species interaction within this hybrid zone and aimed to determine whether there is broad-scale collapse into a single hybrid swarm or maintenance of distinct species identity. Low coverage whole genome sequencing (lcWGS) from 314 individuals show patterns of genomic divergence between the two species. Genotype likelihoods reveal hybrid zone dynamics and structure, as well as species distributions and genomic ancestry with stream habitats. We observe active and stable states of hybridization with habitat partitioning maintaining species identity without broad-scale collapse of species boundaries.

Abstract ID: 1638
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P640

Evolutionary stasis: the missing fraction problem in a wild population of Soay sheep (Ovis aries)

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Quantitative genetics methods have allowed us to predict changes in traits in domestic settings. However, the same methods have had limited success in predicting evolutionary change in wild populations -- a phenomenon known as the paradox of stasis. Amongst the explanations for this phenomenon, the missing fraction problem has received little attention. Partly, this is because the missing fraction refers to the phenotypic information of any trait (often measured later-in-life) that cannot be measured due to individuals dying before that trait was expressed, leading to the question: How can we know the phenotypes of individuals that never expressed them? Here we layout several methods to mitigate against the missing fraction and improve our estimates of selection in wild populations, which could improve our ability to estimate evolutionary change. Empirical data from a Soay sheep population that lives in the St Kilda archipelago is used as a case study.

Abstract ID: 1643
Poster board number:
P641

The morphological basis of social immunity in ants

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Ants form a hyperdiverse and ecologically successful insect family. In their early evolution, they went through extensive morphological and ecological changes from a wasp-like solitary ancestor, to the ground-dwelling social ants we know today. Reshaping their genetic, morphological, and behavioural life history traits, this complex transition allowed the worldwide ecological domination they have reached today. There are no solitary ant species, and their social organisation into colonies with cooperating members is key to their success. They counteract the risk of disease that their lifestyle of densely-living closely-interacting individuals would bring, by cooperative disease defence, which acts in addition to the physiological immune systems of colony members and protects the whole colony by “social immunity". While many studies on ant evolutionary ecology focus on the behavioural features and their underlying genetics, the functional morphology of the organs they acquired early in their evolution is often overlooked. This is despite the fact that they evolved unique structures that combine morphological tools and antibiotic-producing glands that help them reach individual and collective hygiene in the colony. I present these morphological features of the ants and their contribution to social immunity.

Abstract ID: 1647
Poster board number:
P642

Should trees escape their relatives or invest in leaf defense to avoid leaf miners?

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The community of leaf miners on a tree may be affected by leaf quality and the rate of movements among trees. Leaf quality results from gene-by environement interactions, including responses to herbivory and intercations with neighbouring trees. Insect movements among trees in a forest may be limited by distantly related neighbours. We recorded leaf mines in the crowns of mature oaks (*Quercus petraea*) in a forest in western Poland in July and October of three years. We evaluated the effects of budburst phenology, tree size, microsatellite traits, genome size, physical and chemical traits of leaves, leaf damage by other insect herbivores, and the phylogenetic distance to neighbours as predictors of leaf miner density, diversity, and community composition. We found that leaf miner abundance was higher on trees that appeared less nutritious (low nitrogen content) and more defended (high polyphenol content). The phylogenetic neighbourhood of the tree affected community composition, but did not affect leaf miner abundance or diversity. These results suggest that trees cannot escape leaf miners by investing more in leaf defense or by adapting to different niches to avoid growing among closely related species.
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P643

Rapid radiation in the wild allopolyploid tobaccos (Nicotiana sect. Suaveolentes)

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Nicotiana sect. *Suaveolentes* originated through hybridization between ancestors of widely divergent diploid species and dispersed widely following formation, producing a few species each in Africa, Australia, French Polynesia and New Caledonia. In Australia, after first being confined to wetter areas in the north and east, this clade colonized the arid interior (also called Eremaean Zone), radiating to produce the currently observed plethora of species (i.e., *ca* 60). Two main alternatives exist regarding the timing of the radiation in *N.* sect. *Suaveolentes*: The first one hypothesizing that most groups inhabiting this region were already present and had to adapt in parallel to the gradual aridification of the area that started six Mya. However, the alternative scenario suggests that *N.* sect. *Suaveolentes* started to radiate only in the last two Mya, extending its distribution into the more extreme habitats that already existed at the time. In this study, we were able to test these hypotheses and estimate the timing of the radiation in *N.* sect. *Suaveolentes* using multispecies coalescent methods on genome-wide single nuclear polymorphisms (SNPs). We found three radiations during *N.* sect. *Suaveolentes*evolution, one in the clade comprising species related to *N.*

occidentalis, another in the *N. gascoynica* clade, and a more recent one comprising the species from the drier parts of southern Australia. The estimation of divergence times supports most species diverging in the last two Mya, when the interior of Australia was already arid as today.

Abstract ID: 1668
Poster board number:
P644

Impacts of human land use on genetic diversity in a set of generalist and specialist butterfies

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Human-induced land use changes can differentially affect species depending on factors such as habitat preference, dispersal affinity, and specialization. While census size and distribution are important measures of a species response to land use change, these measures do not capture the impacts on genetic diversity and their long-term evolutionary implications. Here, we examine the genomic effects of agricultural intensification on a pair of blue-winged butterfly species that vary in habitat specialization and mobility. Populations come from sites featuring either a predominance of cropland, production forest, or suitable grassland habitat in the surrounding landscape. When possible, we have sequenced museum specimens collected in the early 20th century from nearby localities to establish historical measures of diversity. We measure nucleotide diversity, heterozygosity, and runs of homozygosity, as well as reconstruct past effective population size changes in these populations to examine how diversity is being impacted by land use changes. We examine population structure to determine if habitat fragmentation is a barrier to gene flow and if it has resulted in increased inbreeding within populations. Combining these results, we aim to determine the differing evolutionary effects land use may have on species with varying life histories and their implications for conservation practice.

Abstract ID: 1669
Poster board number:
P645

Persistence of Lambda prophages coevolving with Escherichia coli during frequent prophage induction

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Temperate bacteriophages are important sources of genetic diversity in bacteria. They act as mobile genetic elements, altering the evolutionary trajectory of their bacterial hosts. Bacteriophages are critical to spreading beneficial genes involved in antibiotic resistance and novel pathogenesis. However, prophage carriage is not always beneficial for bacteria as induction occurs stochastically and under stress lysing the bacteria. It remains unclear how prophages and their host bacteria co-evolve in environments that frequently induce the lytic cycle, and how this effect changes when prophages encode beneficial genes, such as antibiotic resistance genes. By experimentally evolving *E. coli* lysogenized by phage lambda, we could see how repeated prophage induction

affects prophage persistence. When prophages are subjected to induction, we observed fast selection against prophages, driven by loss of prophages from the bacterial genome. In contrast, prophages subject to counteracting selective pressures from antibiotics and an inducing agent remain persistent in their bacterial host through two different mechanisms. Prophages that provided a selective advantage with antibiotic resistance that acts as a public good facilitate the emergence of phage free bacteria. Therefore, prophage containing bacteria persist at an equilibrium frequency with phage free bacteria to counteract the antibiotics. Lysogens without this beneficial resistance gene also maintain their prophage by going through successive rounds of beneficial mutations against the presence of antibiotics and inducing agent. Our study suggests that prophage persistence and the frequency of carriage within populations is environmentally dependent, and the pressure of induction can lead to rapid loss of prophages from a population.

Abstract ID: 1684
Poster board number:
P646

Temperature shapes chromosome inversion polymorphism of *Drosophila subobscura* through generations

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Drosophila subobscura is a wide spread Palearctic species, which possesses very rich inversion polymorphism in all of the five acrocentric chromosomes. As populations rapid response to fast changes of environmental conditions can be seen through changes in inversions frequency, this polymorphism is good candidate to measure the effect of temperature on the genetic structure of population. Frequencies of particular chromosomal arrangements are correlated with temperature, with standard arrangements increasing in frequency at lower temperatures, and more complex arrangements like J_1, U_{1+2}, U_{1+2+6}, $E_{1+2+9,}$ and O_{3+4} increasing in frequency at higher temperatures. In order to explore the effect of optimal and suboptimal temperatures on the arrangements frequencies, samples of *D. subobscura* population from a high altitude were reared in laboratory at suboptimal (16°C) and optimal (19°C). Chromosome arrangements frequencies were analyzed and compared through generations (F_0, $F_{5,}$ and F_{16}). The increasing frequency of complex chromosome arrangements and the decreasing frequency of standard chromosomal arrangements were observed. There are significant differences in some of the chromosome arrangements between suboptimal and optimal conditions and also between generations, indicating laboratory adaptation through generations.

Abstract ID: 1722
Poster board number:
P647

Context- and sex- dependent links between father's sexual success and offspring pathogen resistance

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"Good Genes" hypotheses stipulate that positive genetic correlation exists between sire's sexual success and offspring's non-sexual fitness. However, previous studies testing "Good Genes" have provided mixed results. Part of this is because context of where sexual selection happens, though an important component in the framework of testing "Good Genes" hypotheses, is often overlooked. Changes of environment may violate the additive genetic correlation between father's sexual success and offspring fitness as the effects of the selected genes also reply on their interactions with the environments. Meanwhile, offspring sex represents another unique environment for expression of "good genes" and it should be included in "Good Genes" studies. Surrounded by numerous pathogens and parasites, one fitness component is of great interest: pathogen resistance and the occurrence of pathogens generate changes in the environment. In this study, we used the fruit fly *Drosophila melanogaster* and the fungal pathogen *Metarhizium brunneum* as our experiment system to investigate the relationship between father's sexual success and offspring pathogen resistance in different epidemiological context (when father is or is not exposed to pathogens before competing for mates). The sire-offspring relationship was analyzed separately for female offspring and male offspring. We found that the relationship between father's sexual success and offspring pathogen resistance is dependent on the epidemiological context at which sexual selection operated and on the sex of the offspring.

Abstract ID: 1752
Poster board number:
P648

Shady Christmas beetles? Reflecting sunlight reduces heating but does not correlate with hot climate

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Christmas beetles (Scarabidae: Rutelinae) are known for their shiny, beautiful elytra, a product of the interaction between light and cuticle nanostructures. Species within this subfamily are extraordinarily diverse in their ability to reflect sunlight - in both the colour spectrum (visible) and near-infrared (NIR) wavelengths. What are the evolutionary reasons for this diversity? We tested whether selection for thermoregulation could explain some of this variation. We first showed that across 26 species, the amount of solar energy absorbed by elytra is strongly correlated with heating rate and final steady state temperature in a biologically significant range (3 to 5°C). Using a larger dataset of 60 species, we tested whether reflectance of elytra could be predicted by environmental variables, such as temperature, solar radiation, and aridity. We found no correlation between high reflectance and species' occurrence in hotter environments. The lack of correlation was consistent for both visible and NIR light, indicating that despite the thermal benefits of high reflectance, selection for thermoregulation is not a strong driver of among-species variation in the reflectance of Christmas beetles. Nevertheless, the

extraordinarily high NIR reflectance observed in some species could aid passive thermoregulation in those species. Microhabitat data combined with behavioural experiments are needed to further understand the biological relevance of high reflectance in Christmas beetles.

Abstract ID: 1765
Poster board number:
P649

Packing of transcription factor binding sites

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Much of gene regulation is carried out at the level of transcription by regulatory proteins called transcription factors that bind short DNA sequences to activate or repress the expression of target genes. These ranscription factors often evolve via gene duplication. Upon duplication, the daughter transcription factor will have the same (or a highly similar) binding specificity as its parent. We do not fully understand how transcription factors evolve new binding specificities after duplication. This problem can be thought of in terms of “sequence space packing”, where sequence space comprises all 4^L transcription factor binding sites of length L, and a transcription factor’s binding specificity defines a volume in this space. How are new binding specificities incorporated in this space upon duplication? Is this a local optimization problem, involving the adjustment of binding specificities for only the parent and daughter transcription factors, or a global optimization problem, involving the adjustment of binding specificities for many transcription factors? To answer these questions, we build a model which combines a biophysical description of gene regulation with evolutionary modeling of transcription factor specialization following gene duplication.

Abstract ID: 1782
Poster board number:
P650

Perception of dead conspecifics increases reproductive investment in *Drosophila melanogaster.*

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Adaptive plasticity in life-history traits is often critical to maximize fitness in the face of environmental heterogeneity. For example, many organisms respond to a threat to their survival (and hence residual reproductive value) by adaptively increasing investment into current reproduction (i.e. terminal investment). A key to successful terminal investment is the use of adequate environmental cues to extrinsic mortality sources. In species that live at high population densities, the presence of dead conspecifics could potentially act as a reliable cue to extrinsic mortality. We experimentally tested this idea using the model organism *Drosophila melanogaster*, a pest species that experiences high population demography shifts. We monitored the reproductive output of young mated females during repeated bouts of egg-laying in the presence (i.e. dead-exposed) or absence (i.e. controls) of dead conspecifics, interspersed by mating periods where dead conspecifics were always absent. Dead-exposed females produced more offspring than

controls when in the presence of dead conspecifics, but less offspring than controls when dead conspecifics were subsequently removed. These changes were repeatable across time, and are thus indicative of high plasticity in reproductive behaviour. Additionally, we found that dead-exposed females produced heavier daughters (but not sons) than controls. Given that in this species body size correlates more strongly with fitness in females than in males, higher investment in daughters is congruent with terminal investment. Altogether, our results show that perception of dead conspecifics leads to highly plastic life-history adjustments in the form of higher investment in both the quantity and the quality of offspring.

Abstract ID: 1813
Poster board number:
P651

Heterozygous male lions live longer than homozygous males. A creatine-mediated effect?

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In this communication we use 125 African lions and a total of 64 Namibian lions (*Panthera leo*), from both sexes, to show that more heterozygous male lions are larger, heavier and present higher creatine levels than more homozygous counterparts. We also show that while young male lions have a wider range of heterozygosity measures, only older males present high heterozygosity (0.8), strongly suggesting increased survival of larger more heterozygous males. We find that the association between heterozygosity and creatine holds for females, but we fail to detect a heterozygosity-fitness correlation (HFC) with female survival, suggesting that increases in body mass only generate fitness benefits in males. This is expected given the critical role of this phenotypic trait in male-to-male competition for territories and females. These results suggest that, either an increase in creatine-linked anabolic activity or in creatine-linked growth hormone levels, is responsible of the observed increase in weight and size that leads to longer lifespans in Etosha male lions.

Abstract ID: 1852
Poster board number:
P652

Co-variation between cortisol, behaviour, and immunity supports the pace-of-life syndrome hypothesis

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The biomedical literature has consistently highlighted that long-term elevation of glucocorticoids might impair immune functions. However, patterns are less clear in wild animals. Here, we re-explored the stress-immunity relationship considering the potential effects of behavioural profiles. Thirteen captive roe deer (*Capreolus capreolus*) were monitored over an eight-week period encompassing two capture events. We assessed how changes in baseline faecal cortisol metabolite (FCM) concentrations following a standardised capture protocol and an immune challenge using anti-rabies vaccination affected changes in thirteen immune parameters of innate and adaptive immunity, and whether these changes in baseline FCM levels and immune parameters related to behavioural profiles. We found that individuals with increased baseline FCM levels also exhibited increased immunity and were characterised by more reactive behavioural profiles (low activity levels, docility to manipulation and neophilia). Our results suggest that the immunity of large mammals may be influenced by glucocorticoids, but also behavioural profiles, as it is predicted by the pace-of-life syndrome hypothesis. Our results highlight the need to consider co-variations between behaviour, immunity and glucocorticoids in order to improve our understanding of the among-individual variability in the stress-immunity relationships observed in wildlife, as they may be underpinned by different life-history strategies.

Abstract ID: 1859
Poster board number:
P653

Partial support for the Trivers-Willard hypothesis in the contemporary Hungarian population

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According to the Trivers-Willard Hypothesis (TWH), when the mother's condition around conception influences the future reproductive success of male and female offspring differently, the adjustment of offspring sex ratio to maternal condition would increase the fitness of the parents. The TWH has been tested in several taxa, including humans. In human studies, socioeconomic status as an index of condition has been widely used, and the results are inconsistent, possibly because the preconditions of the TWH are not met in every population. To investigate the preconditions and prediction of the TWH in the contemporary Hungarian population, we collected data using an online survey. We asked respondents about their self-perceived childhood and adult socioeconomic status (the former can be used as a proxy of maternal status), their number of children, and the sex of the respondents' siblings. We found that childhood (or maternal) socioeconomic status predicted socioeconomic status and reproductive success of the offspring in adulthood. When the analysis was restricted to families not affected by induced abortion, the socioeconomic status in adulthood was also positively correlated with reproductive success, but only for people who were born and living in the capital. The effect of socioeconomic status on reproduction was not sex-dependent. Still, for people who were born and living in the capital the prediction of the TWH was supported, i.e. maternal

socioeconomic status correlated positively with the proportion of sons within the family. The TWH was not supported for people who were born or living in the countryside.

Abstract ID: 1869
Poster board number:
P654

Functional study on an uncharacterized gene in caste differentiation in Monomorium pharaonis

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The transition from solitary organisms to social life is one of the major transitions in evolution. Eusocial hymenopterans (ants, some bees, and some wasps) best exemplify the transition for their reproductive division of labor between queen caste and worker caste. However, the molecular mechanisms mediating caste differentiation during development is largely unknown. After analyzing >1400 whole-genome transcriptomes of two ant species, *M. pharaonis* and *A. echinatior,* we identify an uncharacterized gene (ID: 39887) with caste-differentiated expression in all post-embryonic developmental stages. Using *M. pharaonis* as a model organism, we find that 39887 gene is transcribed in larval fat body through HCR RNA-FISH. Immunostaining results suggest that 39887 protein is secreted to many organs including brain. Vivo-Morpholino-based knockdown of 39887 gene in the last stage of queen larvae results in several worker-biased traits when they developed into pupae, including smaller thorax, wings, compound eyes and ocelli. Treat worker larvae with juvenile hormone analog significantly increases the transcription level of 39887 gene. These results show that 39887 gene plays an important role in regulating development of queens and workers, in a way mediated by juvenile hormone.

Abstract ID: 1874
Poster board number:
P655

Sexual conflict in complex environments: temperature buffers male harm in wild *D. melanogaster*

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Sexual conflict is increasingly recognized as a fundamental evolutionary process by shaping organism phenotypes, generating diversity, and mediating population growth/viability. A particularly striking consequence of sexual conflict is male harm, whereby males increase their reproductive success at the expense of harming females and decreasing population productivity. Despite being widespread across the tree of life, we know little about what factors modulate male harm and how it operates in the wild. We studied male harm, its estimated impact on population growth, and its underlaying pre- and post- copulatory mechanisms across an optimal reproductive temperature range for a wild *Drosophila melanogaster* population. While females were equally productive across temperatures, male harm to females was extraordinarily plastic, peaking at moderate (24ºC), decreasing at colder (20ºC) and almost disappearing at warm

temperatures (28ºC). We thus show that the impact of male harm on female fitness and population growth drastically varies across the natural thermal range (with lower lower net effects than expected), and that, by hampering male harm, a warming climate may have unexpected positive consequences on population viability. Finally, we show that temperature effects on male harm mechanisms and female fitness components are asymmetric. At cold temperatures, male harassment decreased and male harm impacted female actuarial ageing. At warm temperatures, seminal fluid proteins (i.e. ejaculate toxicity) were severely affected, and male harm mainly impacted female reproductive senescence. This study underscores thermal ecology as a critical factor to understand how sexual conflict unfolds, and its population-level consequences in the wild.

Abstract ID: 1884
Poster board number:
P656

Predation risk regulates assortative mating in a desert isopod

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Animals exhibit size assortative mating (SAM), but how predation affects it remains largely unknown. We hypothesized that predation risk may turn prey less choosy, thereby disrupting SAM, or reduce the reproductive value of mates, maintaining SAM but with different size ratio between mates. We tested these hypotheses in desert isopods in the Negev desert. They are crustaceans that live in burrows and exhibit male mate choice. We conducted a manipulative field experiment by digging burrows and introducing live scorpions near half of them. We found that isopods under predation risk maintained SAM, but males were on average smaller for a given female size. Fewer isopod pairs were formed in risky sites but there were no differences in female sizes and progeny number, size, and age near and away from scorpion burrows. Therefore, we find that males anticipated future costs of predation leading to an equal fitness choice between high quality mates in risky sites and lower quality mates in safer sites. A complementary behavioural experiment revealed that bigger males prefer safe burrows and won more male-male contests indicating competition to be the driving mechanism. Finally, in a follow up field experiment we investigated whether isopods proactively choose habitats that match their own quality, thereby exhibiting 'prudent habitat choice'. Preliminary results suggest that indeed smaller individuals prefer risky habitats without first competing for safer habitats. Overall, our findings highlight that predation risk weakens SAM by affecting male-male competition, and this may be driven by habitat choice rather than mate choice.

Abstract ID: 1898
Poster board number:
P657

Ultra-fine population structure powered by SNPs and SINE insertions

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Using MobiSeq, a technique based on targetting insertions of a highly repetitive transposable element to analyze SNPs in adjacent single-copy regions dispersed all over the genome of a given species, we have been able to obtain several thousand loci immediately downstream the insertion sites of Squam1 in a population of the rock-lizard *Iberolacerta monticola.* Squam1 is a tRNA-derived SINE family, widely distributed among lepidosaurian genomes, usually in tens of thousands of copies. The studied population of *I. monticola*, an endemic species of the Iberian Peninsula, is located at a Specially Protected Area of the European Natura 2000 Network, threatened by the fragmentation of its natural habitat. The initial objective of the MobiSeq project was to produce a battery of SNPs to study the connectivity of the population. As shown in this communication, the project rendered very good results on that respect, confirming the impact on genetic variation of known barriers to gene flow within the protected area, and unveiling patterns of incipient differentiation among subpopulations that had escaped observation so far. But the results from MobiSeq did not restrict to the production of SNPs. They contained an added value, in allowing us to identify individuals bearing brand-new or very recent insertions of Squam1, i. e., either unique or shared by just a few closely related individuals. By paying attention to shared new insertions, we have obtained information regarding dispersal within a short temporal range, and refined the conclusions about the fine structure of the population obtained through SNPs.

Abstract ID: 1904
Poster board number:
P658

Museomics of the regionally extinct Black-veined White butterfly in Britain

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Current rates of climate change and additional anthropogenic effects on ecosystems are causing an extinction rate far above the expected 'background' rate of extinction. Many species will go extinct locally before global extinction, so understanding causes of local extinction may help prevent global extinctions through more informed conservation management practises. Archival or historical samples of regionally extinct species offer a unique opportunity to provide a genomic view of the extinction process.
The Black-veined White butterfly *Aporia crataegi* went extinct in Britain around 1925. This species is also extinct in the Netherlands, Czechia, and likely South Korea, and is declining in other European countries. There is no clear consensus on the reason(s) for this extinction in the British Isles, including whether this was a gradual decline or an abrupt extinction.
We extracted DNA and generated whole genome shotgun (WGS) sequencing libraries from 100-200 year old *A. crataegi* specimens from the British Isles and continental Europe. Average sequencing depth of libraries varied from 3-10x. We are currently exploring temporal patterns of genetic diversity and inbreeding within the species leading up to its disappearance in Britain. Using genomics to investigate the decline and extinction of this species in the UK may be directly informative of its decline in other parts of the world and may potentially aid in reintroduction programmes.

Abstract ID: 1910
Poster board number:
P659

Pedigree-based estimation of *de novo* mutation rate in the epaulette shark, *Hemiscyllium ocellatum*

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Sharks are considered 'living fossils' having undergone limited morphological change since their origin 450 MYA. This reduced rate of evolution is likely underpinned by: (1) their slow life histories – most sharks are long lived and slow to reproduce; and (2) a presumably low mutation rate based on unfounded low instances of cancer. A mitochondrial DNA sequence-based study previously indicated that sharks may be a "slow molecular clock lineage", which – if true – would have important consequences for our understanding of the evolution, ecology, genomics and cancer development in this basal vertebrate group. However, this has never been followed up and even more importantly, the nuclear mutation rate is unknown. Here, we provide the first direct estimate of the nuclear mutation rate in a shark – the epaulette shark (*Hemiscyllium ocellatum*). Using whole-genome sequencing of parents and nine full-sibs we identified putative *de novo* mutations and verified mutations by Sanger sequencing of parents and offspring. Using stringent filtering criteria, we estimate a mutation rate in the range of 5.6 x 10^{-10} mutations per base pair per generation. This represents the lowest directly estimated mutation rate for a vertebrate to date.

Abstract ID: 1911
Poster board number:
P660

Previous pathogen experience modulates sanitary brood care behaviour in ants

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Social insects often live in microbe-rich environments and show close physical contacts with colony members, which should increase their risk of colony-wide infection. Yet, disease outbreaks are rare, as social insects have evolved sophisticated behavioural defences in addition to their physiological immune systems that protect their colonies from disease. One important defence line is the performance of sanitary care behaviours such as allogrooming, where infectious particles are removed from the body surface of

contaminated individuals by their nest-mates. Whilst this caregiving greatly reduces the risk of infection for exposed individuals, the close interaction with contagious colony members can result in cross-contamination and subsequent infection of the caregiver. It is known that this interaction changes the caregiving behaviour of the insects, yet the underlying basis for this behavioural change is still unexplored. Using the invasive garden ant and its fungal pathogen *Metarhizium*, we test how very recent interaction with contagious colony members affects the immediate caregiving response, even before an infection could have established in the caregiving ant. In particular, we determine how healthy workers that cared for pathogen-contaminated brood subsequently alter their grooming behaviour towards unexposed brood. We find that workers indeed modulate their grooming of uncontaminated brood in a way that epidemiological modelling predicts to limit disease transmission through the colony. We try to understand, which pathogen cues may trigger this immediate behavioural change of the ants' brood care behaviour.

Abstract ID: 1918
Poster board number:
P661

Valley of free-riders between horizontally and vertically transmitted mutualism

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Distinct organisms can become integrated into a single evolutionary unit via mutualistic symbiosis with strictly vertical transmission, where a host inherits the symbionts from its parents. A possible way to establish such mutualism is the evolutionary transition from a looser relation, horizontally transmitted mutualism, where a host gathers symbionts from its surroundings. However, the transition between the two types of mutualism is still unclear because they differ in how to prevent free-riders from exploiting. In particular, horizontally transmitted mutualism requires "partner choice", a mechanism to associate with only cooperative symbionts, but as relying on vertical transmission the choosiness will no longer be favored because hosts tend to inherit limited partners. Here, I theoretically examined the coevolutionary dynamics of partner choice by hosts and cooperation by symbionts. My study shows that even with the loss of partner choice during the transition, mutualism usually persists by vertical transmission without a gap. In addition, depending on the manner of partner choice, mutualism can break down in the middle of the transition and the two types of mutualism are disconnected. Those provide new insights into how the evolutionary integrations via mutualism proceeds and why there are many types in symbiotic systems.

Abstract ID: 1924
Poster board number:
P662

MTaxi : A comparative tool for taxon identification of low coverage ancient genomes

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In zooarcheology, morphological identification of closely related species from skeletal remains is challenging, particularly when they are highly fragmented. If the candidate species have similar quality reference nuclear genomes, shotgun sequencing of ancient DNA (aDNA) extracted from the remains and comparative alignment to the references can be of use. However, this approach may not work when reference genomes of similar quality are lacking. Here, we propose an alternative tool, MTaxi, to identify closely related species pairs from aDNA sequences, using mitochondrial DNA (mtDNA) reference genomes, which is more frequently represented in databases than nuclear reference genomes. In order to determine the sample taxon, MTaxi assigns reads to either species by utilising mtDNA transversion-type substitutions between pairs of candidate species, then performs a binomial test. We tested MTaxi on sheep/goat and horse/donkey pairs, which are compelling to classify through zooarchaeological methods, in ways that exemplify our case. For the trials on simulated ancient genomes, MTaxi performed successfully on sheep/goat data with down to 2x, and horse/donkey data with down to 1x mitochondrial coverage, yielding no false positives. Ancient sheep/goat samples (n=15) and horse/donkey samples (n=10) of known species identity were also assigned correctly with 100% accuracy. Overall, MTaxi provides a simple approach to distinguish between closely related species, of which zooarcheological classification can be problematic, using low coverage aDNA data.

Abstract ID: 1943
Poster board number:
P663

Influence of food web complexity on genetic diversity in coral reef fishes from Moorea

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Genetic diversity is a consequence of demographic history and thus can be influenced by environmental changes or life history traits. While patterns of genetic diversity have often been linked to species traits, the relationship between genetic diversity and food web has never been studied despite its potential influence on demographic stability over time. Here, we investigated the relationship between genetic diversity and food web by sampling 576 reef-associated bony fishes from Moorea (French Polynesia) in 40 species. Intraspecific genetic diversity was estimated using thousands of single nucleotide polymorphisms obtained from genomic data sequenced by a Target Gene Capture protocol. Trophic groups and food web complexity, both derived from previous gut content metabarcoding and stable isotope results, were subsequently used to model genetic diversity in conjunction with other life history traits. Multi-species modeling of genetic diversity revealed ecosystem-wide features, as demographic stability over time is

expected to be related to food web complexity: species with a high number of interactions should exhibit greater demographic stability. This highlights food web complexity as a potential predictor of genetic diversity, and thus the species' ability to adapt to natural or anthropogenic pressures. Multi-species studies at other sites will be needed to characterize the behavior of genetic diversity when food web complexity varies, thereby providing insight into the future of genetic diversity in changing ecosystems.

Abstract ID: 1963
Poster board number:
P664

New form of sexual selection by threshold preference explains costly male ornaments without benefit

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In many sexually reproducing species, exaggerated ornaments in males have evolved due to females preferring them as partners for mating. It is commonly assumed that these preferences have been selected because it provides some benefit for the females to choose males with an ornament. However, a benefit may not be needed when female preferences resemble a threshold function, where she will only mate with males having an ornament either above or below a certain fixed standard. Here, we study how this threshold impacts the sexual selection process with an evolutionary model of haploid individuals. Each individual carries a gene for male type and one for female preference. The type determines if males have a costly ornament that increases their mortality. The preference determines which type the female mates with, resulting in two subpopulations where matings occur randomly within but never between them. Using agent-based and mathematical modelling, we show that the male type with the higher mortality is actually selected for. This is due to the presence of “mismatch” males carrying a gene for preference opposite of their own type, which can be inherited and then expressed by their daughters. The subpopulation with the higher male mortality filters out mismatch males faster, resulting in a net inflow of newborn females into this subpopulation which causes them to outcompete the other subpopulation. This new process, which we call “match selection”, implies that it cannot automatically be assumed that females preferring a costly ornament in their partner incur a fitness benefit.

Abstract ID: 1965
Poster board number:
P665

Investigating the Neolithic Transition along the Danube route through spatially explicit simulations

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The genetic diversity of modern Europeans has been greatly influenced by the transition of the way of life from hunting and gathering to farming, known as the Neolithic

Transition. According to genetic data, this was not just a phenomenon of cultural diffusion, but was facilitated by the arrival in Europe of Farmer populations from the Eastern Mediterranean. In our study we investigate this transition along the Danubian expansion axis, by using genomic data from 59 newly sequenced ancient genomes. We use spatially explicit simulations to simulate different models for the arrival of the first Farmers in Europe and their interactions with the local Hunter-Gatherers and identify the most probable one through an Approximate Bayesian Computation analysis. In addition, we infer demographic characteristics of the Neolithic Transition, such as the level of admixture between Farmers and Hunter-Gatherers, their effective population sizes, and the levels of competition between them. Our results suggest that Long Distance Dispersal events played an important role to the spread of Farmers along the Danubian route and that admixture and competition levels between Farmers and Hunter-Gatherers were not homogeneous across this dispersion axis. Our study presents a new angle of the Neolithic Transition in Europe and offers new estimations on the demographic characteristics of that era, helping elucidate European prehistory and understand modern European genetic diversity.

Abstract ID: 1982
Poster board number:
P666

Implications of differing measures of reproductive isolation in *Pseudochorthippus parallelus*

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Species formation is a process along which various reproductive isolation (RI) mechanisms restrict gene flow between incipient species. Tools used to identify RI vary in their underlying assumptions and thus in their implications. Commonly used methods include (i) fitness analysis of F1 hybrids, (ii) demographic inferences of gene flow, and (iii) geographic clines. These measures of RI are often incongruent and the relationship between them, as well as their implications about species formation are still unclear. Here, I compare these three methods in two populations pairs of the meadow grasshopper *Pseudochorthippus parallelus* hybridising in the Alps and Pyrenees. (i) F1 hybrids between each of the two population pairs show decreased fitness phenotypes, such as hybrid male sterility, implying strong RI between parental populations. (ii) Demographic modelling shows older divergence time and lower effective migration rate across the Pyrenees, implying stronger RI. Yet, (iii) geographic clines show greater spatial introgression across the Pyrenees, implying weaker RI. Despite the widespread view of a forward-in-time speciation process, the accumulation of reproductive barriers is neither linear nor irreversible, as numerous studies focusing on the admixing effects of hybridisation have found. Instead, the collective strength of reproductive barriers can fluctuate, for example in cycles of geographic isolation (blocking gene flow) and secondary contact (allowing gene flow). I suggest that the differing results for strength of RI in the same system may represent windows into different stages of species formation, which often evolve towards the breakdown of reproductive barriers and “reversal of speciation”.

Abstract ID: 1983
Poster board number:

P667

Overwinter users of nest cavities affect breeding birds via nest-dwelling ectoparasites

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Nest-dwelling ectoparasites should adjust their diapause period to their host breeding time, while both host and parasite phenology depends on environmental conditions. Nest cavities used for avian reproduction in spring often host other organisms for roosting during winter, which could affect cavity temperature and humidity. These environmental changes should then influence the emergence patterns of pupae of nest-dwelling ectoparasites within nest cavities and, ultimately, successful parasitism. To test this hypothesis, we experimentally blocked the entrance of half of nest-boxes previously used for reproduction by hoopoes (*Upupa epops*), while recording microclimatic conditions during the fall-winter period. Next spring, we estimated abundance and emergence patterns of ectoparasitic flies (*Carnus hemapterus)* and intensity of parasitism in hoopoe nestlings growing in control (open) and experimental (blocked) nest-boxes. Temperature and humidity of nest-boxes depended on experimental treatment and on occupancy of open nest-boxes by dormice (*Eliomys quercinus*). Experimental treatment or dormice occupancy did not predict onset or duration of *Carnus* emergence. However, *Carnus* flies were more abundant in open nest-boxes. Moreover, open nest-boxes occupied by dormice showed the lowest abundance of parasitic flies. These results suggest that the use of nest cavities by other vertebrates than rodents enhance emergence of *Carnus* flies. Finally, hoopoe nestlings developing in nest-boxes with their entrance blocked during winter experienced lower intensity of ectoparasitism than those developing in open nest-boxes. These results point to the existence of cryptic effects of overwinter occupants of nest cavities on subsequent emergence and viability of nest-dwelling ectoparasites, which may profoundly impact on ectoparasite-host interactions.

Abstract ID: 1989
Poster board number:
P668

Is brood sex ratio related to parental feeding rate? An experimental study on collared flycatchers

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Sex allocation theory predicts that parents can maximize their fitness by biasing offspring sex ratio to the sex that is less costly to rear, have better reproductive chances or higher survival prospects under the prevailing circumstances. While in several species, the sex ratio of the offspring is related to parental quality and environmental conditions, in most cases, information on the adaptive value of the observed pattern is missing. We aimed to investigate the relationship between brood sex ratio and the cost of chick rearing in a Hungarian collared flycatcher population by manipulating offspring sex ratio via cross-fostering and analysing parental feeding activity. As previous studies suggested larger

sensitivity of males to rearing conditions, we assumed that males have higher energy requirement. If so, a positive correlation between original sex ratio and feeding rate is expected (i.e. those parents should produce more of the less sensitive female offspring that are not able to pay the costs of intensive care). It is also expected that parents caring for male-biased foster broods would provide more food in response to the higher need of male nestlings. According to our results, neither female nor male feeding rate was affected by the sex ratio of the foster nestlings. In addition, only male feeding frequency was correlated with original sex ratio, but in contrast to our prediction, males with female-biased original brood sex ratio fed their foster chicks at a higher rate. Consequently, we found no evidence that sex ratio patterns are adaptive in this population.

Abstract ID: 1996
Poster board number:
P669

Copy number variation analysis of ancient human genomes by CONGA

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Copy number variations (CNVs) are structural variations that include deletions and duplications of >50 bp. Many CNVs can have phenotypic influences, and have been described to evolve under purifying selection, while some cases have also been associated with adaptation mechanisms. Investigation of CNV evolution, however, has yet been mainly limited to modern-day genomes, due to difficulties of genotyping CNVs from low coverage ancient DNA data. We recently developed a new algorithm, “Copy number variation genotyping in ancient genomes and low-coverage sequencing data (CONGA)”, and showed that it can successfully genotype >1 Kb deletions in ancient human genomes with coverages down to 0.5x. Using CONGA-called deletions on 56 ancient Eurasian genomes we further replicated the signal of stronger negative selection on deletions than SNPs. Here we will further present preliminary results on the contribution of deletions to overall mutation load in ancient genomes from Eurasia dated between 1000 BP to 50,000 BP.

Abstract ID: 2018
Poster board number:
P670

Birds line their nests with aromatic plants in response to ectoparasites: the missing experiment

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The addition of aromatic plants to the nests of birds has been mainly interpreted within functional frameworks of protection against parasites and microorganisms and of sexual signalling. However, whether birds carry aromatic plants to nests in response to ectoparasitism is still unknown. We experimentally tested this possibility in a spotless starling *Sturnus unicolor* population. In half of the nests, we increased the abundance of *Carnus hemapterus*, a common ectoparasite of incubating birds and nestlings. Given aromatic plants in nests of this species play a role in male's sexual signalling, we also explored the potential effect of female size in triggering the addition of aromatic plants to nests by males. As expected, the amount and number of plant species carried to nests by males increased in response to the experimental parasite infestation, but only in nests with females of large body size. These results suggest that aromatic plants are carried to nests by males in response to both ectoparasitism and female quality. Moreover, ectoparasite abundance during incubation and during the early nestling period were more strongly correlated in control than in experimentally infested nests, suggesting that the response of the birds to the ectoparasite infestation managed to break this relationship. This study adds to the still scant evidence of self-medication in animals and, for the first time, demonstrates an experimental link between the presence of parasites in avian nests and the use of plants with antiparasitic properties.

Abstract ID: 2023
Poster board number:
P671

Pleistocene divergence and population turnovers in Collared lemmings

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Collared lemmings (*Dicrostonyx* spp.) are key Arctic species present today in the tundra of Siberia and North America. Previous mitochondrial evidence suggests that the Eurasian collared lemming (*D. torquatus*) had multiple distinct lineages that went extinct during the Late Pleistocene, although the timings of these lineage turnovers remains unresolved. Here we sequenced genomes from 21 Eurasian collared lemmings, ranging in age from modern to 50 thousand years old. We aimed to further investigate lineage turnovers during the Late Pleistocene, and to evaluate whether there was any gene flow between these extinct lineages and the sole lineage persisting today. Additionally, we generated modern genomes from three North American *Dicrostonyx* species (*D. groenlandicus*, *D. hudsonius*, and *D. richardsonii*) and one 300 thousand year old Siberian *Dicrostonyx* to evaluate phylogenetic relationships between the collared lemming species, and to examine whether post-speciation gene flow occurred during the Late Pleistocene.

Abstract ID: 2031
Poster board number:
P672

Machine-learning facilitated pedigree-based mutation rate estimation in guppy (Poecilia reticulata)

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De novo mutations (variants that arose in-between generations, DNMs) are the primarily source of genetic variation, on which natural selection operates. Knowledge about DNMs rate allows calibrating species paste demography and population genetic studies. During our study we aimed to find the rate of nucleotide substitution in eco-evolutionary model species – guppy (Poecilia reticulata). We bred, resequenced and screened for DNMs in twenty four individuals (two families). We found almost 700 candidate DNMs and used a machine-learning tool to reduce the high false positive rate. Using a subset of the candidate variants, we prepared a training set based on Sanger sequencing. Then we filtered the rest of mutations and validated those likely to be true. Finally, we compared the number of true DNMs to the total number of effective sites (sites in which mutation could have been found according to our quality filters). Our estimated guppy MR is $3{,}44 \cdot 10^{-9}$ per site per generation and is similarly low to other fishes' MRs. Our study shows utility of machine-learning approaches for estimation of MR and demonstrating how effectively this approach reduces false positive calls.

Abstract ID: 2040
Poster board number:
P673

Can a novel predatory tactic invade to rodent populations with herbivore diet?

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In evolutionary history, predatory tactic has evolved many times in herbivorous animal populations. Here we mimic the evolution of predatory tactic and tested whether a novel predator tactic can invade to rodent populations with plant dominated diet. In the experiment, we used the selection lines of wild rodent, the bank vole Myodes glareolus, which were selected towards predatory behaviour and unselected control lines. Here we show that negative frequency-dependent (NFD) selection a benefit of a rare tactic, is a crucial evolutionary mechanism, which can promote the invasion of predatory tactic to the populations. The analyses of reproductive success of females with different tactics also predicts that NFD selection can maintain stable polymorphism of tactics in populations. Our results gives a novel evidence for the selections benefits of predatory behaviour, which will inspire field studies of the specific behavioural or physiological costs and benefits of this widespread diet strategy.

Abstract ID: 2041
Poster board number:
P674

Repeat proliferation and partial endoreplication jointly drive the genome size evolution of orchids

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The exceptional diversity and unique characteristics of orchids have always attracted a lot of attention. One such feature that remains little known is partial endoreplication (PE), a form of endopolyploidy that results in the propagation of only part of the genome during cell differentiation. Using repeatome analysis in a new evolutionary framework, we investigated the association between PE and genome size evolution in orchids of the tribe Pleurohtrallidinae. Our results show that PE likely facilitates the expansion of repetitive elements by excluding them from the endoreplicated part of the genome. This suggested that the orchid genome is somehow organized into two independent parts under different selection against the accumulation of repetitive content. While the endoreplicated part evolves slowly and remains the same at the genus level, the non-endoreplicated part of the genome changes rapidly and forms a major part of the evolution of genome size. This also implies that compared to orchids with conventional endoreplication, orchids with partial endoreplication allow greater genomic expansion. Surprisingly, genome size is hardly affected by variation in chromosome number.

Abstract ID: 2047
Poster board number:
P675

Fishing for reproductive senescence

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Origin, incidence and consequences of reproductive senescence vary greatly across the tree of life. In vertebrates, research has been mainly focused on mammals and birds, demonstrating that patterns of reproductive senescence are largely linked to critical life history traits such as growth mode, juvenile and adult mortality, and reproductive strategy. Fishes represent 50% of vertebrate taxonomic diversity and display remarkable variation in life history. Based on thorough literature review, we summarize current knowledge on reproductive senescence in ray-finned fishes. While survival and physiological senescence is acknowledged to occur in fish, their potential age-related reproductive decline has often been disregarded due to the prevalence of indeterminate growth. We review the effect of age on reproductive functions of male and female ray-finned fish and provide a broad overview of their reproductive senescence. This will help to link reproductive senescence and in/determinate growth, reproductive mode, phylogeny and ecology across the fish species.

Abstract ID: 2050
Poster board number:
P676

Variation and evolution of immunity with ageing

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Evolutionary theory predicts late-life decline in the force of natural selection. This might lead to late-life deregulation of immune pathways due to perturbation in evolutionarily conserved signaling pathways, causing their over-activation with increased immunopathology. We hypothesize that another outcome of such ageing-induced immune-deregulation is the inability to produce specific immune responses against target pathogens. Instead, non-specific responses with ageing would use an extended set of immune repertoires, increasing the fitness costs of general immune activation. We tested this possibility by infecting *Drosophila melanogaster* lines with an entomopathogen *Providencia rettgeri* across age-groups, where individual, as well as different combinations of antimicrobial peptides (AMPs) from Imd & Toll-pathways, were knocked out by the CRISPR/Cas9 gene-editing. *Drosophila* AMPs show a high degree of non-redundancy and pathogen-specificity in young flies such that only a single AMP *Diptericin* could confer complete resistance against *P. rettgeri*. In contrast, ageing leads to complete loss of such specificity, producing complex interactions between multiple AMPs across Toll and Imd pathways. Age-specific expansion of the AMP-pool was also associated with (a) reduced post-infection survival (b) downregulated negative regulators of the IMD-pathway (e.g., *caudal* & *pirk*) and (c) increased immunopathology, as features of poorly regulated ageing immune responses. Finally, we used experimental evolution lines with divergent reproductive schedules and ageing rates (e.g., early vs delayed) to show such features of ageing immunity might manifest earlier in populations evolving faster rate of reproduction and shorter lifespan, linking weaker selection strength after reproductive senescence as a plausible driver of age-specific immune system deregulation.

Abstract ID: 2070
Poster board number:
P677

Urban population genomics and adaptation of brown rats (Rattus norvegicus) in Paris

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Brown rat (*Rattus norvegicus*) is among the most abundant species living in urban environments, but it remains poorly studied in this ecological context. The lack of knowledge on their dispersal and adaptation is detrimental to a wise regulation of their populations in large urban centers. In this study, we whole genome sequenced 23 rats in Paris to investigate local population structure and putative signature of adaptation to urban environment. With a set of more than 3 millions single-nucleotide polymorphisms (SNPs), we show that Parisian rats present a weak structure globally, with the Seine river acting as a geographic barrier separating the populations, and bridges as corridors facilitating populations connections. In a second part, we will assess the genomic footprint of natural selection to this environment in these individuals, and the biological functions involved in this adaptation.
The high density of buildings and the complexity of the fine-scale geographic features of Paris makes this city a fascinating case to study the biogeography of such commensal

species. Finally, this work will help to improve the control of brown rat in Paris and articulate it to the eco-evolutionary dynamics of these populations in the future.

Abstract ID: 2102
Poster board number:
P678

Monogeneans and chubs: ancient host-parasite system under the looking glass

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Monogenea (ectoparasitic Platyhelminthes) and their fish hosts represent one of the best models for studying host-parasite evolutionary relationships using cophylogenetic approach. These parasites developed remarkably high host specificity, where each host species often serves as potential host for its own host-specific monogenean species. We investigated cophylogenetic relationships of monogenean *Dactylogyrus* and their *Squalius* hosts (Cypriniformes). Thirteen *Dactylogyrus* species were collected from 20 out of 29 investigated *Squalius* species. The phylogenetic relationships of both parasites and hosts were based on multilocus approach. Cophylogenetic analyses were based on dual approach: distance-based methods allowed to calculate patristic distances for parasite and host phylogenies to assess the significance of global fit and individual coevolutionary links; and event-based methods allowed to test importance of each coevolutionary event in the host-parasite phylogenies. Phylogenetic reconstruction revealed polyphyletic origin of *Dactylogyrus* species parasitizing *Squalius*. Although, the distance-based methods did not reveal statistically significant global cophylogenetic structure, several host-parasite links among Iberian endemic species were revealed to contribute significantly to the overall structure. The highest host range and associated genetic variability were recorded in *D. folkmanovae*, parasitizing nine *Squalius* species, and *D. vistulae*, parasitizing 13 *Squalius* species. Two different dispersion mechanisms and morphological adaptations to potential fish hosts were well reflected in contrasting cophylogenetic patterns for these two generalist species in our study. While cospeciation plays important role in diversification within *D. folkmanovae*, *D. vistulae* diversification is driven mainly by host switching. This study was supported by the Czech Science Foundation, project no. GA20-13539S.

Abstract ID: 2122
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P679

What drives the rapid buildup of sterility barriers in the Arctic crucifer *Draba nivalis*?

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We have shown that several taxonomically well-defined, diploid plant species in the Arctic produce more or less sterile offspring when populations from different geographic areas are crossed. These within-species sterility barriers seem to have evolved recently and are not accompanied by obvious morphological or ecological divergence. Why Arctic plants develop such hidden species diversity is still a mystery, but we hypothesize that a selfing mating system and/or colonization history might be involved. To gain a better understanding of the genetic basis and possible drivers of incipient speciation in the Arctic, we combined QTL and population genomic analyses of *Draba nivalis* (Brassicaceae) – a diploid and predominantly selfing species. We crossed Norwegian and Alaskan plants and produced an F_1 population. One semi-sterile F_1 plant was selfed to produce a large F_2 population for genetic linkage and QTL mapping. We identified six QTLs possibly tied to reproductive isolation: two with pollen sterility, and four with abnormal seed development. The recombination landscape was typical of a small Brassicaceae genome, suggesting no large-scale chromosomal rearrangements. However, we did find evidence for both micro-chromosomal divergence and BDM incompatibilities based on inheritance patterns. Based on whole genome resequencing data for populations sampled across the Arctic, we currently analyze genetic history, inbreeding levels, and genetic divergence to gain insight into the drivers of incipient speciation in the Arctic flora.

Abstract ID: 2139
Poster board number:
P680

Sexual-size dimorphism has evolved via sex-specific trait architecture

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The evolution of sexual dimorphism, the difference between the sexes in a trait, is a puzzle to researchers. The reason is that selection may favor different optima for the same trait in each sex, but that variation of this trait is based on the same genes in both sexes, generating intra-locus conflict. According to quantitative genetics theory, this conflict can be detected by a high and positive genetic correlation between the sexes, which limits sex-specific evolutionary change of the trait through sexually antagonistic

coevolution. The presence of a sexually dimorphic trait thus requires at least a partially resolved sexual conflict and this resolution has been suggested to involve, among others, sex-specific genetic and developmental control, including sex-specific maternal effects. Using a quantitative genetics approach, we examined the genetic architecture of body size in the recluse spider *Nephilingis cruentata* with extreme sexual size dimorphism (SSD), i.e., adult size of females exceeds that of males. Specifically, we estimated the sex-specific significance of genetic and maternal effects on size in laboratory-reared individuals across several generations. The model estimates suggest that size variation is predominantly determined by additive genetic effects in females, but by maternal effects in males, with low correlations in both components between the sexes. These results suggest a straightforward mechanism to avoid intra- locus conflict and allow emergence and maintenance of SSD via sex-specific architecture of body size and thus its sex-independent evolution.

Abstract ID: 2142
Poster board number:
P681

Fixation probabilities in network structured meta-populations

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The effect of population structure on evolutionary dynamics is a long-lasting research topic in evolutionary ecology and population genetics. Evolutionary graph theory is a popular approach to this problem, where individuals are located on the nodes of a network and can replace each other via links. We study the effect of complex network structure on the fixation probability, but instead of networks of individuals, we model a network of sub-populations with a probability of migration between them. We ask how the structure of such a meta-population and the rate of migration affect the fixation probability. Many of the known results for networks of individuals carry over to meta-populations, in particular for regular networks or low symmetric migration probabilities. However, when patch sizes differ we find interesting deviations between structured meta-populations and networks of individuals. For example, a two-patch structure with unequal population size suppresses selection for low migration probabilities.

Abstract ID: 2154
Poster board number:
P682

The role of evolvability, robustness, and tunability of transcription factors in regulatory rewiring

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Mutations in operator sites play an important role in the evolution of gene expression. It may affect the strength of binding of the coordinate transcription factor or change the specificity of binding of transcription factors. These changes in regulatory connection

describe **regulatory rewiring** - one of the mechanisms upon which gene regulatory networks evolve. A number of empirical studies investigated the mechanistic basis behind regulatory rewiring. However, the role of intrinsic properties of transcription factors in the evolution of gene regulatory networks is poorly understood. In the present work, we investigated how the properties of transcription factors (**robustness**, **evolvability,** and **tunability**) shape the evolutionary potential for regulatory rewiring. For this purpose, we used the canonical system to study gene expression - the genetic switch of lambdoid phages. From *in vivo* molecular measurements of repression levels, we explored the empirical support for established theoretical findings: although on the genotypic level robustness and evolvability are antagonistic, on the phenotypic level they facilitate each other; whereas tunability is in trade-off with robustness and evolvability.

Abstract ID: 2185
Poster board number:
P683

The changing effect of social class on fertility through the demographic transition in Switzerland

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Resource availability is one of the key factors that drive human evolution as evolutionary theory predicts individuals with high resources produce more offspring. In humans, resource availability is closely linked to social class and therefore affects fertility (number of offspring) which ultimately affects fitness. However, in contrast to evolutionary theory human family size began to decrease in higher social classes after the demographic transition. This may be due to cultural changes. In this study, we aim to determine why human fertility has changed over the demographic transition using individual records of fertility from a historical dataset that spans from the 16th century to the 20th century in Swiss canton Glarus, including 7840 individuals. We use a novel historical social stratification system (HISCAM - Historical Social Interaction and Stratification Scales) to assign each individual a social stratification score based on their occupation. Firstly, we examine the effect of parental social class on their offspring which enable us to understand better determinants of social class. Secondly, we examine the effect of inter-generational changes in social class on fertility which allows us to elucidate why human fertility is decreased in high social class after the demographic transition. From the inter-disciplinary perspective, it is predicted that social learning and modernisation outweigh the evolutionary dynamics. Therefore, we aim to explain the dynamics of these changes with an inter-disciplinary approach in addition to explain how social class affects the change in human family size through time.

Abstract ID: 2186
Poster board number:
P684

Adaptive introgressions have driven the domestication of the apple tree

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Domestication processes in long-lived plants are often characterized by a large extent of genetic exchanges between crop and wild populations. Several wild species (*Malus sylvestris, M. orientalis, M. baccata*) have contributed to wild-to crop introgression to the genetic make-up of cultivated apples (*M. domestica*). However, the genomic architecture (number and which genes/alleles involved) of these introgressions in the cultivated apple genome remains a topic of intense investigations. We investigated the genomic landscape of admixture and selection in hundreds of genomes (SNPs called from Illumina sequencing) of cider and dessert apple varieties, and of wild apple relatives to *M. domestica*. Population genomics analyses indicated that both dessert and cider apples showed large introgression tracts from *M. sylvestris* from Western Europe, and selected genes in these introgressed regions are associated with plant hormone signal transduction and plant-pathogen interaction. This study revealed that gene flow drives adaptation during apple domestication and provides a starting point for breeding programs.

Abstract ID: 2188
Poster board number:
P685

Identifying the environmental drivers of functional biodiversity loss in a freshwater lake

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Biodiversity underpins essential ecosystem functions and services, yet threats to biodiversity are ever increasing. Climate change, invasive species, land use change and pollution threaten functional and phylogenetic biodiversity, contributing to its ongoing decline and the loss of vital ecosystem services. These challenges occur over decade-to-century time scales, which are difficult to study directly. Here, we investigate a freshwater lake which has been subject to historical anthropogenic impact, using a sedimentary archive spanning the past century. We reconstruct the past biological community of the lake using eDNA metabarcoding and use targeted mass spectrometry to measure persistent pollutants from the lake. We investigate long term trends in community dynamics and relationships between the biological community, anthropogenic pollution and climate change. Using sparse canonical correlation analysis, we identify the top factors with an adverse effect on the community which could be targeted for remediation or policy intervention.

Abstract ID: 2199
Poster board number:
P686

Transposable elements and genome size evolution in the plant genus *Curcuma* (Zingiberaceae)

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Genome size (GS) is an important feature of an organism that impacts cell-level processes like replication and thus could influence and determine species biology and ecology. Changes in GS are largely influenced by the activity of repetitive or transposable elements (TEs). These repetitive elements make up the major proportion of all the nuclear DNA in most eukaryotic genomes, however, the impact of their activity on genome functioning is mostly unknown in non-model organisms. We measured GS (using flow cytometry) for ca. 200 accessions from the genus *Curcuma* L. (Zingiberaceae), a herbaceous plant genus native to the Indo-Malayan region. The genus is classified into four major genetic lineages which hybridized and/or polyploidized in the past. Genome size distribution showed different patterns among the lineages mirroring also diverse degrees of polyploidization. For 20 species we quantified TEs from shallow-level genome sequencing using RepeatExplorer2 pipeline. We observed a certain link between TE content and GS where LTR-elements (*Ty1/Copia* and *Ty3/Gypsy*) were especially responsible for increasing the GS. However, lineage-specific TE composition was detected and phylogenetic analysis of selected repeats showed a pattern compatible with the phylogenetic tree from previous studies.

Keywords: *Curcuma*, genome size, polyploid, repeats, transposable elements, Zingiberaceae

Abstract ID: 2201
Poster board number:
P687

Atlantic vs. Mediterranean: Different evolutionary pathways of populations of goby *Gobius niger*

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The black goby (*Gobius niger*, Gobiiformes) belongs to Gobiidae, one of the most diverse and most successful fish families. It is a sedentary marine goby living in shallow protected waters of the north-east Atlantic, the Mediterranean and the Black seas. Although the black goby is very common, easily accessible, and its biology and ecology are well known, its phylogeography has never been profoundly studied. Due to its sedentary lifestyle, its dispersal depends mainly on the dispersion of its pelagic larvae, and therefore the connectivity of the populations can be influenced by external factors, particularly marine currents. In our study, the phylogeography of the black goby was deeply examined using two mitochondrial markers (*D-loop* and *cytochrome b* genes). According to our analyses of 455 individuals from 29 localities across the distribution range, while the populations throughout the north-east Atlantic are well interconnected and are connected to the western Mediterranean populations, the populations from the eastern Mediterranean, north Adriatic and the Black seas show marked division among each other. Moreover, a possible anthropogenic influence was revealed: the haplotype transfer between the Black Sea and the western Mediterranean, and the eastern Mediterranean and the North Sea was detected. The variability between the populations accounted for most genetic variability within the species distribution range. The study revealed different recent evolutionary histories of distinct populations.

Abstract ID: 2211
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P688

Seeking the smoking gun of fisheries induced selection using covariance-based temporal genome scans

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Temporal genome scans including covariance analyses of allele frequencies across multiple time points are powerful tools to directly assess evolutionary change in

populations in response to selection. Here, we apply such methods for the first time to a heavily overexploited fish stock, the Eastern Baltic cod (*Gadus Morhua*). Adapted to the low salinity environment of the Baltic Sea, they are biologically and genetically differentiated to their neighboring ecotype, Western Baltic cod, allowing us to exclude the possibility of migration. Taking advantage of full genome sequences that we were able to reconstruct from dried otolith (ear-bone) material from 1996-2019, we hypothesized that selection by size-selective trawling caused a dramatic change of length at maturity, which in turn would be reflected in genomic changes. While genome-wide genetic diversity and temporal Fst values showed little change, genome-wide temporal covariance showed signs of selection over time. Selection scans including examining haplotype statistics along with the temporal covariance analysis pinpoint specific regions of selection. We also examined whether large inverted regions in LG2, 7 and 12, might have responded to selection, as they occur in all Atlantic cod populations albeit in different frequencies and are known to be involved in adaptation. Together with the phenotypic data of the same individuals and the environmental data in hand, information earned from temporal genome scan will guide us through connecting dots of fisheries induced evolution.

Abstract ID: 2237
Poster board number:
P689

Ray of light: vegetation cover is the main driver of color brightness evolution in squamates

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The colored integument has an important role on the ecology of organisms, but the underlying mechanisms regulating its variation are not well-understood yet. Squamates are an ideal study group to investigate which eco-environmental pressures influence color brightness variation, as these organisms not only rely on coloration for concealment, mimicry, social signaling, or sexual selection, but also for thermoregulation. Here, we hypothesized that environments exposed to strong solar radiation will select for brighter integuments to be concealed with the surrounding and avoid overheating by reflecting the incoming heat, whereas environments with limited solar exposure for darker integuments for opposing reasonings. To test this, we analyzed the dorsal brightness of 1233 species from 9909 images, collected life history traits and ecological information (vegetation cover, latitudinal and altitudinal distributions, body mass, concealment, polymorphism, and circadian rhythm) from the literature, and made use of previously published phylogenies to produce comparative models. Surprisingly, we found that only vegetation cover is the main driver of color brightness evolution, where open habitats select for brighter integuments possibly to better reflect the incoming heat. Clade-dependent analyses showed that body mass negatively influenced brightness but only in groups with relatively large organisms, suggesting contrasting evolutionary pressures between large and small species. Other eco-environmental pressures influencing brightness are clade-specific, likely reflecting life history strategies of species. The results provide insights on the complexity and trade-offs between the mechanisms

driving color variation in squamates and suggest that global patterns of trait variation should be carefully interpreted.

Abstract ID: 2252
Poster board number:
P690

New stygomorphic freshwater crab from Laos offers insights into the adaptation to cave life

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Do freshwater potamid crabs adapt to the cave environment morphologically? To answer this question, free-living and cave-dwelling freshwater crabs from Laos are compared in an undergraduate final year project. The morphology, morphometry and genetics of 16 crabs are analysed. A new stygomorphic crab from the Khammouan area can be reported. Cave-crabs from Khammouan and Vientiane show similar characteristics that distinguish them from free-living crabs: e.g. strongly elongated legs, a wide carapace and a vestigial orbit. The traits occur independently of phylogenetic relationship and geographic location. These observations suggest that the environmental factors prevailing in caves, e.g. darkness and food shortage - lead to convergent evolution of troglomorphic traits in potamid crabs.

Abstract ID: 2268
Poster board number:
P691

Major urinary proteins profile and copy number variation in commensal and noncommensal mouse species

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Major urinary proteins (MUPs) transport and protect volatile ligands but they can themselves act as olfactory cues. Since MUPs contribute to complex information about the donor they can play an important role in divergence between nascent species. Despite being intensively studied, the majority of the studies focused on the “classical” inbred strain C57BL while wild house mouse populations have scarcely been studied. Therefore, we involved wild-derived strains of 3 commensal and 3 non-commensal mouse (sub)species in our study. Although the house mouse, namely its subspecies *Mus musculus domesticus*, is known to possess at least 21 functional *Mup* genes arrayed in ~ 2 Mb long gene cluster, the situation in other closely relative species remained unknown. To fill this knowledge gap, we focused on *Mup* gene expression at the protein level as well as on the potential contribution of copy number variation (CNV) to the (sub)species-specific patterns as CNV represents a substantial part of genetic variability and high CNV may be expected particularly in large gene clusters. Moreover, our results enable assessing to what extent MUPs production reflects species-specific phylogenetic and ecological differences.

Abstract ID: 2270
Poster board number:
P692

Mate choice and reproductive success in a warming planet

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Much information exists on the influence of thermal stress on the reproductive fitness of the exposed organisms. However, less is known about the effects of heat on the ability of choosy individuals to perceive and obtain reliable information about the potential mate. A crucial sensory channel for intersexual communication is olfaction. I tested the thermal sensitivity of sex pheromone communication and several reproductive traits in a species in which odours play a crucial role in mating decisions, the collembolan *Orchesella cincta*. Like in many soil arthropods, *O. cincta* males advertise their presence to females by means of packets of sperm (spermatophores) deposited in the environment. A female selects and picks up one spermatophore guided solely by the spermatophore-associated sex pheromone. Experimental evidence suggests that in this species some reproductive traits are more sensitive to heat stress than others.

Abstract ID: 2272
Poster board number:
P693

A reference genome assembly of the chaetognath Flaccisagitta enflata

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Chaetognaths, commonly known as arrow worms, are transparent marine predators widely distributed at various depths in all oceans. They form an enigmatic clade whose phylogenetic position is still discussed: they were initially considered as deuterostomians due to their development, but analyses placed them among protostomians. Based on transcriptomic data, they were hypothesized to belong to the clade Gnathifera, which gathers Gnathostomulida, Micrognathozoa and Rotifera. To this day, there is no genome assembly available for the whole phylum Chaetognatha, although this resource could help resolve and refine their phylogenetic position. We assembled a reference chromosome-level assembly for *Flaccisagitta enflata*, a species of epipelagic chaetognaths from the family Sagittidae, using Oxford Nanopore, Illumina and Hi-C reads. This haploid assembly consists of 9 chromosomes, encompassing 794 Megabases with a BUSCO score of 93.3% (based on the Metazoa dataset), and will serve as a basis for phylogenomic analyses to elucidate the position of chaetognaths

Abstract ID: 2279
Poster board number:
P694

Consequences of evolution under juvenile malnutrition for adult metabolism and fitness.

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Juvenile undernutrition has lasting effects on adult metabolism of the affected individuals, a form of phenotypic plasticity. However, it is unclear to what degree these plastic responses predict how adult physiology would be shaped over evolutionary time by natural selection driven by juvenile undernutrition. We used experimental evolution combined with RNAseq and metabolomics to study the consequences of adaptation to juvenile undernutrition for metabolism of reproductively active adult females of *Drosophila melanogaster*. Fly populations maintained for over 230 generations on a nutrient-poor larval diet evolved major changes in adult gene expression and metabolite abundance, in particular affecting amino-acid and purine metabolism, and the abundance of key electron carriers (NAD, NADP and FAD). The evolutionary changes in gene expression profiles and metabolite abundance were not in general predicted by phenotypically plastic responses to diet. Rather, the metabolic profile of the larval-undernutrition-adapted flies, even when well fed, resembled that of flies subject to starvation. Our results also suggest widespread genetic constraints on independent evolution of larval and adult gene expression profiles, even in a species where the two stages are separated by metamorphosis, with negative consequences for adult reproductive performance. Our results imply that evolutionary adaptation to juvenile undernutrition has large pleiotropic consequences for adult metabolism, and that they are costly rather than adaptive for adult fitness.

Abstract ID: 2296
Poster board number:
P695

Conservation genomics of the Finnish wolf population

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Human impact has led to biodiversity loss, causing extirpations and declines in local abundances of species and populations. A key to undertaking effective conservation actions for such species is to understand the importance of different factors affecting the performance of populations. These include population dynamics, environment, stochasticity, and genetic processes. Genetics are important for population viability since, in small populations, the impact of inbreeding and genetic drift becomes prevalent. These processes can lead to a loss in standing genetic variation and less efficient purifying selection, reducing the population's adaptive potential. The Finnish wolf population has experienced severe declines, getting close to extirpation during the bottleneck at least twice (at 1920s and 1970s) and remaining at low population sizes until the 1990s. Here, we studied conservation genomics of the Finnish wolf population. We had whole-genome sequence data from 95 Finnish wolves sampled between the years 2000 and 2016. For 81 individuals the birth year had been estimated, suggesting that these wolves were born between years 1994 and 2016. We estimated the effective population size (Ne), Ne/Nc-ratios, level of inbreeding, and the temporal patterns in

them. Our results help to assess the genetic viability of the Finnish wolves and can be used to produce a favorable reference value for the Finnish wolf population.

Abstract ID: 2301
Poster board number:
P696

Gene expression of distinct shell phenotypes between ecotypes of *Littorina saxatilis*.

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Parallel evolution arises when similar phenotypes evolve repeatedly and independently in response to local adaptation in a similar environment. The marine snail, *L. saxatilis*, has evolved ecotypes that are locally adapted to different shoreline microhabitats, and this has occurred repeatedly in populations in Sweden, the United Kingdom and Spain. The “crab” ecotype exists where there is less disturbance from wave action and where crab predation is high. These snails are larger, have a thick shell, and shy behavior. The “wave” ecotype exists in exposed areas where there is substantial wave action. These snails are smaller, have thinner shells, and bolder behavior than the crab ecotype. The mantle tissue is involved in shell formation and is a likely candidate for shell-related differences in these ecotypes. In order to understand the genetic basis of shell differences between these forms, we sequenced mRNA from mantle tissue from both ecotypes from two distant populations, one from Sweden and one from Spain. Our findings comparing the ecotypes and populations, as well as basic identification of the genes transcribed in the mantle tissue will be presented.

Abstract ID: 2306
Poster board number:
P697

Phylogeography and evolutionary history of the *Crocidura poensis-hildegardeae* species complex

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The *Crocidura* genus is the most speciose of all mammal genera. It is particularly diversified in Africa, with more than 100 species. The African *Crocidura* have been split into many different species complexes throughout history, ranging from 4 to 22 possible clusters based on morphological criteria. Among those, it was previously believed that the *C. poensis* and *C. hildegardeae* species complexes formed two different units, discriminated mainly by their body size, tail length and pelage coloring. Recent

sequencing efforts oppose this view, the *C. poensis* complex appearing as a monophyletic group embedded within the *C. hildegardeae* complex. The monophyletic *C. poensis* complex was recently reviewed using multilocus data and 10 genetic lineages were retrieved out of the 12 described species. The *C. hildegardeae* complex appears to be genetically very diversified, with many more lineages than the 3 species currently described. Here, we present a molecular phylogeny of the *C. poensis-hildegardeae* species complex, and discuss its taxonomy and history in an integrative framework, incorporating morphological and geographical data.

Abstract ID: 2323
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P698

Opsin gene expression and vision modification during ontogeny in European cyprinid fishes

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Vision plays a key role in life of vertebrates. Photoreceptive cell layer on retina contains rods and cones sensitive to specific parts of visible light spectrum. Cones, used for photopic vision, allow for colour perception thanks to the expression of opsin genes sensitive to ultraviolet (SWS1), blue (SWS2), green (RH2) and red light (LWS). On the rods, only RH1 gene is expressed, allowing for scotopic vision during dim-light conditions. During the evolution of cyprinid fishes, mainly RH1 and RH2 opsin genes were duplicated, creating gene copies further evolving in various adaptations in specific light conditions. Opsin gene expression varies during ontogeny of the fish, modifying their visual abilities by expressing alternative opsin combinations (palettes) in different stages of development. Such plasticity in expression may serve for adaptation to various environmental conditions they encounter in life, e. g. influencing their trophic ecology or habitat preference. In our study, we focused on larvae, juveniles and adults of common freshwater cyprinid fish species of subfamily Leuciscinae of Central Europe. Using transcriptome sequencing we have identified the level of opsin gene expression in each individual and compared the expression patterns between different ontogenetic stages of studied species. We found that the vision of adult cyprinids is based on the most dominant red photoreceptor, whereas larvae rely on short wavelength-sensitive opsins SWS1 and SWS2. We report more differences observed between adults and larvae and we hypothesized the importance of opsin gene expression for function of fish vision.
Keywords: opsin, vision, adaptation, cyprinid, teleost fishes

Abstract ID: 2329
Poster board number:
P699

Male mating success evolves in response to increased levels of male-male competition.

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Male-biased operational sex ratios can increase male-male competition and can potentially select for both increased pre-and post-copulatory male success. In the present study, using populations of *Drosophila melanogaster* evolved under male-biased (M) or female-biased (F) sex ratios, we asked whether (a) male mating success can evolve (b) males are better at mating females that they have co-evolved with (c) males mating success is affected by female mating status and (d) male mating success is correlated with their courtship effort. We directly competed M and F males for mating with (a) virgin ancestral (common) females, (b) virgin females from the M and F populations and (c) singly mated females from the M and F populations. We also assessed the courtship frequency of the males when paired with mated M or F females. Our results show that M males, evolving under an increased level of male-male competition, have higher mating success than F males irrespective of the female evolutionary history. However, the difference in mating success is more pronounced if the females had mated before. M males also have a higher courtship frequency than F males, but we did not find any correlation between mating success and courtship frequency.

Abstract ID: 2331
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P700

South-eastern Europe - a hotspot of genetic diversity of the European bitterling

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Hotspots of intraspecific genetic diversity are often associated with glacial refugia – regions where populations of thermophilic species survive the Quaternary glacial cycles. South-east Europe and adjacent West Asia (northwestern Middle East: Asia Minor, Caucasian and Caspian regions) are important hotspots of genetic diversity for a number of taxa with many locally endemic lineages. A combination of the effects of historical climate, topography and dramatic changes in sea level during the last 5 million years resulted in variable patterns of continental colonization from this refugium for different taxa. We used 12 polymorphic microsatellite loci and partial mitochondrial gene of cytochrome b on a set of 1038 individuals from 68 localities to describe genetic variability and detailed spatial structure across the *Rhodeus* species complex distribution in the western Palearctic with a focus on south-eastern Europe and the Caspian-Caucasian region and to infer population contribution to contemporary continental distribution. Our analysis revealed six well-supported lineages, with limited local co-occurrence. Two lineages expanded throughout Europe, with two zones of secondary contact. Another two lineages were restricted to the Ponto-Aegean region of Greece, the place which harboured highest bitterling diversity. The final two lineages were restricted south of the Caucasus mountains. The west Transcaucasian (Georgian) region of the Black Sea basin is inhabited by lineage described as a separate species, *Rhodeus colchicus*. And

bitterling populations from the Caspian watershed of the southern Caucasian region (Azerbaijan, Iran) formed a separate, well-characterised lineage.

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P701

An approach based on molecular data to relationship of Fannia (Fanniidae: Diptera) from Colombia

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Fannia Robineau-Desvoidy, 1830, (Diptera: Fanniidae) is a cosmopolitan genus of little house flies and the most diverse in the family. It occurs in numerous habitats, and most species inhabit wild environments; however, few species have developed a close association with man; some species are of forensic, medical, veterinary, ecological, and agronomic importance. Around 110 species have been reported in the neotropical region, 37 in Colombia, where still new species are being described. Species morphological identification is a challenge due to their close similarity. We aim to outline an approach to the molecular identification and delimitation of the most common *Fannia* species occurring in the four biogeographical provinces of Colombia based on molecular data. Sequences of the mitochondrial genes Cytochrome c oxidase I (COI) and Cytochrome b – Serine transfer RNA gene and Dehydrogenate subunit I gene fragment (Cytb-ARNtSer-ND1) were used to set the approach. Identical morphological specimens were clustered into monophyletic clades (82–100% bootstrap branch support). Despite low interspecific divergence, the species-level resolution was informative, and its relationships are meticulously discussed. The Cytb-ARNtSer-ND1 region allowed to delimitate the taxa assessed. This study offers molecular data on six neotropical species for the first time. It also allowed the association of conspecific males and females hindered by sexual dimorphism, minimizing the taxonomic impediment of these dipterans in Colombia and the Neotropic. It is desirable to include a complete set of neotropical *Fannia* species-groups in further studies for their better phylogenetic understanding.

Abstract ID: 2335
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P702

Host specificity influence how fungal pathogens navigate nutritional landscapes of their insect host

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Nutrition often mediates the outcomes of host-pathogen interactions. These effects can be indirect when a host's immune response is constrained by specific nutritional deficiencies (*e.g.* iron or glutamine), or direct when pathogens colonize the heterogeneous nutritional landscape comprised of host organs and tissues. Here we use nutritional geometry to study these dynamics as ecological niches in two steps. First, we measured the fundamental nutritional niche (FNN) breadth of insect-pathogenic *Metarhizium* fungi in simulated *in vitro* host environments. Second, we measured how these pathogens navigate nutritional landscapes to acquire a realized nutritional niche (RNN) in simulated host environments of semi-solid liquid media to determine nutrient-specific intake. We further compared nutritional niche evolution across three *Metarhizium* species with different levels of host specificity from propagule introduction to onset of spore dispersal. Host-specificity did not influence FNN dimensions for fungal growth, as each fungal pathogen species grew maximally across a broad range of carbohydrates (C), assuming protein (P) was present above a minimal threshold. Fungal pathogens also similarly initiated dispersal behaviors leading to sporulation when either C or P became depleted. In contrast, host specialists and generalists prioritized P and C intake differently. The host specialist *M. acridum* always prioritized C intake, but the generalists *M. anisopliae* and *M. robertsii* prioritized P and C equally, with P:C intake reflecting diet media P:C ratios. In this way, pathogens may span a continuum of dietary specialization corresponding to degrees of host specificity, similar to that used to predict the success of potential invasive species.

Abstract ID: 2339
Poster board number:
P703

Museomics to resolve the genomic and wing-pattern relationships of burnet moths (*Zygaena*).

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Burnet moths (Zygaenidae: *Zygaena*) are amongst the most striking Lepidoptera and often termed honorary butterflies for their day-flying habits, bright aposematic colours and utter fascination set upon naturalists. Most of this interest stems from the sheer diversity and variability of their wing-patterns, showing both geographically structured, environmentally induced and individual differentiation patterns. However, although morphological work has been undertaken since the 19th century zygaenologists, deciphering the evolutionary patterns amongst the 108 species in the genus and allied relatives has proven a challenge. Even after numerous attempts, often involving extensive genetic sequencing the group is far from being resolved. Additionally, the relationships among the different wing-pattern ground plans are not clear and may actually impose a confounding aspect to phylogenetic inference. Whilst the table is set with extensive morphological data gathered, and an existing backbone of genetic data has already been proposed, the next step needs to be taken. In this study we take the chance and harness the power of museomics approaches using the most comprehensive *Zygaena* collections in the world, combine it with targetted fieldwork to fill-in the gaps of *Zygaena* phylogenomics and complement it with artificial-intelligence wing-pattern analyses. Our aims are two-fold: 1) to resolve the relationships among *Zygaena* species and 2) decipher the evolutionary paths and molecular evolution of such complex, dynamic and stunning wing-patterns.

Abstract ID: 2357
Poster board number:
P704

Hybridisation of cyprinid fishes of the subfamily Leuciscinae in the Czech Republic

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This project aims to determine species of subfamily Leuciscinae involved in hybridization, level of such hybridization and to evaluate possibly ongoing introgression in several reservoirs of Czech Republic (Lipno, Jordán, Klíčava, Římov, Žlutice). We collected and identified the hybrids based on morphological characters (soft rays counts, lateral line scale counts, main shape, and colour of body) and to confirm a mother of each specimen we use barcoding of COI gene. We performed the ddRAD sequencing on the selected candidate hybrids and parental species to mainly identify hybridizing species, the further generation reproduction, and back crossing to parental species in our reservoirs. Further, we present the association of morphological characters with the genetic identity. We analysed and quantified shape features by 2D morphometry and we focused on the pharyngeal dentition using the CT scanning. These two techniques reveal the morphological consequences of introgressive hybridization. Typical F1 hybrids are usually somewhere in the middle in these features, while the next-generation hybrids are less recognizable by the morphological characters, such as soft rays counts in the fins. We identified common hybridization between: Rutilus rutilus, Abramis brama, Alburnus alburnus, Scardinius erythrophthalmus, Squalius cephalus and Blicca bjoerkna. We further noticed that some characters traditionally used in the identification key should be slightly expanded in their range (such as fin ray counts) and we aim to suggest a set of such characters in this project.

Abstract ID: 2358
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P705

Teach and outreach: promoting public understanding of evolution through collections–based learning

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Museum object-based learning is appreciated among scholars and practitioners for its capacity to facilitate and promote understanding of the nature of science. When it comes to evolution, natural history collections have a particular didactic and communication power, transitioning the boundaries between formal and nonformal science education and promoting the trust in science. The natural history collections' didactic use can foster evolution acceptance and better understanding of environmental issues. Here, we discuss the effects of longstanding collaboration between Natural History Museum

Belgrade and Chair of Genetics and Evolution, Faculty of Biology, University of Belgrade. Since 2001, workshops for undergraduates have been organized within the introductory course on Evolutionary biology yearly, with the exception of 2020 due to COVID-19 pandemics. Average group size was 70 students (range 22-125). Workshops have been based on the museum collections illustrating paleodiversity, fossilization and transformation processes, and focused on discussions addressing various evolutionary issues. This collaboration has been providing students with hands-on experience of fossil material as primary factual evidence of evolutionary processes. Our approach included students' surveys and supporting their follow-up activities. Students were encouraged to join ongoing or create their own outreach programs and activities aimed at general public (e.g. student project on dinosaur nervous system or volunteering as guides at evolution exhibitions). In addition, this experience has been contributing to promoting students' interest to later pursue the scientific career.

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Poster board number:
P706

Ploidy as an imperfect speciation barrier: what drives interploidy gene flow in natural populations?

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Whole genome duplication is a dominant force in sympatric speciation in plants. Ploidy acts as an instant hybridization barrier between diploids and their polyploid derivatives. Generally, triploids arise as a result of crosses between diploid and tetraploid individuals of the same or related species. Such crosses often result in the failure of seed formation, a phenomenon called ‘triploid block’. Triploid block can result in an instant postzygotic reproductive isolation between tetraploids and their diploid progenitors and triploid hybrids often do not survive until maturity in the wild. However, recent flow cytometric and population genetic surveys have revealed signs of widespread inter-ploidy introgression in several ploidy-variable species. Here, we review novel knowledge concerning the variations in the strength of triploid block angiosperm-wide and the mechanisms driving such variations. We revisit the developmental basis of triploid block to account for the causes of these variations. Evidence suggests that the strength of triploid block varies among taxa with different developmental patterns, such as triploid block appears to be stronger in species with cellular and/or permanent endosperm as compared to those with nuclear and/or transient endosperm. However, a scarcity of studies in a natural diploid-autotetraploid system and a virtual lack of integration with population genomic approaches leaves the underlying mechanisms and levels of realised interploidy gene flow in nature largely unknown. We discuss how knowledge of variation in the strength of reproductive barriers may increase our understanding of the interploidy gene flow and its consequences on polyploid speciation.

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P707

Identifying non-recurrent rare variants in Anopheles mosquitoes to infer evolutionary processes

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Population genomic analyses utilising patterns of rare genetic variants have the potential to provide new information for evolutionary inference that may be otherwise undetectable by traditional approaches. Existing methods rely on the assumption that different copies of rare mutations are all descended from a single common ancestor, i.e. are identical by descent. However, this assumption may frequently be violated in taxa with high mutation rates or large effective population sizes, so that, by chance, the same rare mutations have in fact arisen independently. For example, such “recurrent” rare mutations are thought to be appreciable in non-model organisms like the malaria vector mosquito *Anopheles gambiae*. To address this, we devise a new method to identify non-recurrent rare mutations from a sample of individuals, utilising the composition of their surrounding shared haplotypes. Based on differences in the sharing of rare variants between rare variant haplotypes, we determine a likelihood for a given haplotype being non-recurrent, which can then be confidently used for downstream analysis. We applied this method to data from the *Anopheles gambiae* 1000 genomes project (Ag1000G). We find that concern over recurrent mutation is valid in *A. gambiae*, but that our method can effectively identify non-recurrent mutants for this species. This approach can then be used to make various downstream inferences, such as the impacts of selection, site conservation, and chromosomal location effects on rare variants, and on the utility of such variants for population level inferences.

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P708

Phylogenetic and molecular clock study of plastid encoded genes untangle archaeplastidia evolution

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Photosynthetic eukaryotes play a key role in the Earth's biosphere by converting light into organic compounds in specialized organelles called plastids. Plastids evolved from free living cyanobacteria engulfed by a heterotrophic unicellular eukaryote in a process called primary plastid endosymbiosis. Two cases of primary plastid establishment have been reported. The first gave rise to three eukaryotic lineages: glaucophytes, rhodophytes and green plants, all united into the supergroup of Archaeplastida. The second occurred much later within the rhizarian genus *Paulinella*. There are also cases of plastid secondary endosymbioses where an organism already bearing a plastid becomes an endosymbiont of another heterotrophic eukaryote. In order to untangle plastid evolution, we performed phylogenetic and molecular clock analyses based on a concatenated set of 30 highly conserved plastid-encoded proteins derived from 108 taxa, representing a large diversity of cyanobacteria and plastid bearing eukaryotes. We used PSI-BLAST to build datasets of homologous plastid-encoded proteins and computed multiple alignments with MAFFT using L-INS-I algorithm. To eliminate poorly aligned positions and divergent regions we used TrimAl gappyout alghoritm. Phylogenetic analyses were performed in Beast, RaxML, IQtree and MrBayes using best-fit partitioned schemes calculated in Partition Finder. Molecular clock analyses were conducted using relaxed clock methods: autocorrelated in Phylobayes and MrBayes as well as uncorrelated in Phylobayes, MrBayes and Beast. Our results indicate that the cyanobacterial endosymbioses that gave rise to the Archaeplastida and

photosynthetic *Paulinella* occurred much earlier than postulated 1.600 and 90-140 million years ago, respectively. We also estimate the age of plastid secondary endosymbioses.

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P709

Cooperation and competition across the evolutionary transition to multicellularity

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From organic compounds in a primordial soup to the remarkable diversity of modern organisms, the evolution of life has been driven by pivotal moments of cooperation and competition. In what instances are individuals driven to cooperate, rather than compete? The most paradigmatic of these dynamics are observed in Major Evolutionary Transitions (METs), where transitions in individuality require the formation of a cooperative group with sufficiently minimal within-group conflict to overcome competition between groups. While key drivers of METs remain unknown, some transitions are reproducible in the laboratory. Previous work used settling selection to drive the transition to multicellularity in the yeast system, *S. cerevisiae*, allowing for real-time analysis of the causes and consequences of multicellularity. Yet, populations rarely evolve in isolation, raising the question: How does interspecific competition impact the origin of multicellularity? In this study, we explored the evolution of multicellularity in co-cultures of two yeast species, *S. cerevisiae* and *K. lactis*, examining how competition influenced the emergence of cooperative multicellular groups. We found that while *K. lactis* evolved multicellularity first, interspecific competition did not lead to exclusion of *S. cerevisiae*. When rare, each species could invade the other, illuminating how the interplay of cooperation and competition across this MET altered the eco-evolutionary landscape between species.

Abstract ID: 2431
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P710

Habitat determines convergent evolution of cephalic horns in vipers

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Convergence in similar environments provides insights into the evolutionary processes shaping phenotypic evolution. Horn-like cephalic appendages have evolved under various selective pressures among squamate reptiles, including selection for defence, crypsis and sexual selection. Yet, among snakes, where horns are most abundant in vipers, the functional and evolutionary significance of horns are unknown. Using a comparative phylogenetic approach, we shed light on the evolution of horns in vipers. Horns are evolutionarily labile with frequent fluctuations in the extent of character states as lineages diversified. We detected significant correlations between the presence of horns and taxon association with habitat, where the relative positions of horns are ecologically divergent. Supranasal horns are positively correlated with terrestrial forest habitats while supraocular horns are negatively correlated with terrestrial forest habitats and instead associated with arboreal or sparsely vegetated terrestrial habitats. Multiple

independent origins of horns in lineages with similar ecologies provides evidence of adaptive convergence.

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P711

Predictive genotype-phenotype-fitness mapping of the tetracycline efflux pump regulatory elements

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Antibiotic resistance is rapidly becoming one of the biggest healthcare problems globally. To tackle this problem, we need a dramatically better ability to predict how antibiotic resistance evolves. Doing this requires the development of predictive genotype-phenotype-fitness maps for key resistance mechanisms. In this study we aim to generate a predictive genotype-phenotype-fitness map for the resistance gained through changes in the regulation of the tetracycline efflux pumps, a major mechanism of resistance across bacterial species. Doing this would allow predicting how mutations in the regulatory elements of the pumps (promoters and transcription factors) can mutate in order for the organism to develop resistance. We developed an experimental system that would allow us to obtain high-throughput measurements of mutational effects in promoters and transcription factors regulating the expression of the pump. We are currently in the process of generating a large-scale experimental dataset, which will form the foundation of a mechanistic model based on statistical thermodynamics of protein-DNA binding. This model will allow us to predict the effects of mutations in gene regulatory elements (genotype) not only on the gene expression phenotype, but also on the fitness of the organism in the presence of a range of antibiotics.

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Poster board number:
P712

Genomes on a Tree (GoaT) - informing planning and progress of eukaryotic genome sequencing globally

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Under the Earth BioGenome Project (EBP) umbrella, several initiatives have pledged to sequence all known eukaryotic species. This ambitious goal requires coordination of targets and effort among projects in this global network. To maximise synergy between initiatives and prevent duplication of effort, the Tree of Life programme has developed Genomes on a Tree (GoaT), a taxon-centred database for genome-relevant metadata. GoaT offers collation of target lists, priority declarations and sequencing status for EBP affiliates, as well as a compilation of genome-relevant metadata (genome size, karyotype, assembly metrics, etc.) from a plurality of trusted sources. Missing data are estimated based on phylogeny. GoaT currently holds values for over 40 taxon and 30 assembly attributes across 1.5 million eukaryotic species. The depth and breadth of curated data, frequent updates, and versatility of possible queries makes GoaT a powerful data aggregator and portal to explore and report underlying data for eukaryotes. GoaT can be queried via API or web front-end which allows data summary visualisations

(https://goat.genomehubs.org/). Herein we present a series of use cases where GoaT can help with planning, execution and reporting of sequencing within and outside the EBP community. Examples include: defining target lists based on gap-analysis, predicting sequencing effort based on genome size and ploidy, and reporting quality metrics for assembly subsets. The ease of visualisation of attributes across trees allows quick detection of outlier taxa and biological features meriting further investigation. Real-time summary of reference genome sequencing provided by GoaT will facilitate collaboration between projects in the global community.

Abstract ID: 2443
Poster board number:
P713

Dispersal can play a crucial role in evolutionary dynamics of flightless beetles

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Limited dispersal ability, along with geographic isolation, belongs to key drivers of speciation. While the dispersal ability is influenced by species traits, e. g., by loss of wings, geographic isolation among populations can be strengthened by cryptic lifestyle and habitat fragmentation. However, occasional dispersal events and expansions can occur, becoming evolutionary drivers in poorly dispersing organisms. In our study, we show the effects of both strong geographic isolation and occasional dispersal events in evolutionary dynamics of flightless moss-inhabiting flea beetles. Our work combines population genetics and integrative taxonomy to study their speciation and diversification on various scales. We studied two different models to understand moss-inhabiting flea beetle species evolution. In the case of the beetles from the Chabria group in Taiwan, we revealed that moss-inhabiting flea beetles dispersed on long distances despite to their limited dispersal abilities. In the second model system (the European genus Mniophila), we found an unexpected cryptic diversity of possibly Tertiary origin. Glaciations subsequently shaped the intraspecific population structures in Mniophila, surviving Quaternary in the forested montane refugia, and Central European microrefugia. Then, several genotypes quickly expanded through Europe in some species. Both examples show that dispersal events can be very important factor shaping the diversification in flightless beetles, which seem to have poor dispersal abilities.

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P714

Surviving ice ages by going south or up? - Biogeography of the European butterfly *Erebia medusa*

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Interglacial and glacial periods had an impact on many biogeographic patterns of extant European species. Most temperate species spread northward during interglacials and were restricted to southern, usually Mediterranean, refugia during glacial periods. In contrast, it has generally been accepted that arctic-alpine species were able to survive on nunataks, non-glaciated mountain summits, during the ice ages. However,

researchers hypothesize that temperate species with broad continental distributions may also have survived in such peri-Alpine refugia. The Woodland Ringlet butterfly (*Erebia medusa*) is such a species with a wide European distribution and preferences for mountain ranges. So far, little is known about its fine-scaled population structure in mountainous regions. Some dispersal centers have been identified in the Romanian Carpathians. These probably resulted from a glacial differentiation process, but whether the species used high-altitude refugia in the Alps or dispersed southward during the ice ages is still uncertain. Our goal is to investigate the genetic structure of alpine and non-alpine populations using ddRAD data. Our sample set includes more than 40 populations distributed across the European Alps and their adjacent areas. The SNP data obtained by ddRAD sequencing will help us to analyze whether the biogeographic history of *Erebia medusa* is consistent with the occurrence of peri-Alpine refugia during the Würm glaciation (ca. 115,000 to 11,700 years ago) and served as glacial differentiation centers, and whether hybridization zones exist today. In addition, we will address the challenge of applying a genome-reduced approach to low molecular weight DNA.

Abstract ID: 2445
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P715

On the relativity of species, or the probabilistic solution to the species problem

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For centuries, both scientists and philosophers have discussed the nature of species resulting in c. 35 species concepts proposed to date. However, in our opinion, none of them incorporated neither recent advances in evolutionary genomics nor dimensionality of species in befitting depth. Our attempt to do so resulted in the following conclusions. Due to the continuous nature of evolution (regardless of its rate and constancy), species are inevitably undefinable as natural discontinuous units (except those originating in saltatory speciation) whenever the time dimension is taken into consideration. Therefore, the very existence of species as a natural discontinuous entity is relative to its dimensionality. A direct consequence of the relativity of species is the duality of speciators (e.g., incipient species) meaning that, in a given time, they may be perceived as both being and not being a species. Finally, the most accurate way to reflect both the relativity of species and the duality of speciators in species delimitation is probabilistic. While the novelty of some of these ideas may be debatable, they still deserve more extensive attention from the scientific community. Here, we hope to draw such attention by outlining one of the possible pathways toward a new kind of probabilistic species delimitation method based on the probability of irreversible divergence of evolutionary lineages. We anticipate that our probabilistic view of speciation has the potential to facilitate some of the most serious and universal issues of current taxonomy and to ensure unity of the species-level taxonomy across the tree of life.

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P716

Evolutionary history of livestock guarding dogs

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Livestock guarding dogs (LGDs) are a set of large dog breeds specialized in protecting livestock from predators induced by a strong bond to the herds established since early ages. Despite this important role, there have been surprisingly few systematic investigations into the evolutionary history of these dog breeds. In this work, we aim to study the genetic diversity, differentiation and gene flow for 36 LGD breeds using genome-wide genotype data from > 300 dogs, generated with the Illumina CanineHD BeadChip, to elucidate the evolutionary history of livestock guarding dog breeds across Eurasia.
Preliminary results indicate that LGDs display high genetic diversity and low inbreeding coefficients relative to other pure breeds, likely a result of a relaxed pedigree management and the absence of strong selection for extreme phenotypes. LGD breeds are structured according to their original regions showing that geographic isolation could have been the most relevant driving force for the differentiation of breeds. However, events of genetic migration between LGD breeds separated by large geographical distances support the assumption that gene flow has continued through time and the continued mixed ancestry composition of breeds from the same region supports the hypothesis that livestock movements, like transhumance, potentiated gene flow between breeds.
LGD breed formation is likely the result of differentiation after human and livestock migration events, with geographic and cultural barriers influencing the establishment of locally differentiated dog populations.

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P717

Population dynamics of the Late Pleistocene narrow-headed voles reconstructed using ancient DNA

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Narrow-headed voles, together with collared lemmings and common voles, were the most abundant small mammal species across the Eurasian Late Pleistocene steppe-tundra environments. Previous ancient DNA studies of the latter tworevealed a dynamic past population history shaped by climatic fluctuations. To investigate the extent to which species with similar adaptations share common evolutionary histories, we generated a dataset comprising mitochondrial genomes of 139 ancient and 6 modern narrow-headed voles from multiple sites across Europe and western Asia and covering the last ca. 100 thousand years (ka). We inferred Bayesian time-aware phylogenies with the ages of directly radiocarbon-dated samples used for molecular clock calibration. We found that across the three species, divergence of the main mtDNA lineages took place during Marine Isotope Stages (MIS) 7 and MIS 5 suggesting common responses of species adapted to open habitats to interglacial environments. In European narrow-headed voles we identified multiple time-structured mtDNA lineages, implying population turnovers. Timing of some of these turnovers was synchronous across all three species, allowing us to identify the main drivers of the Late Pleistocene dynamics of steppe- and cold-adapted species.

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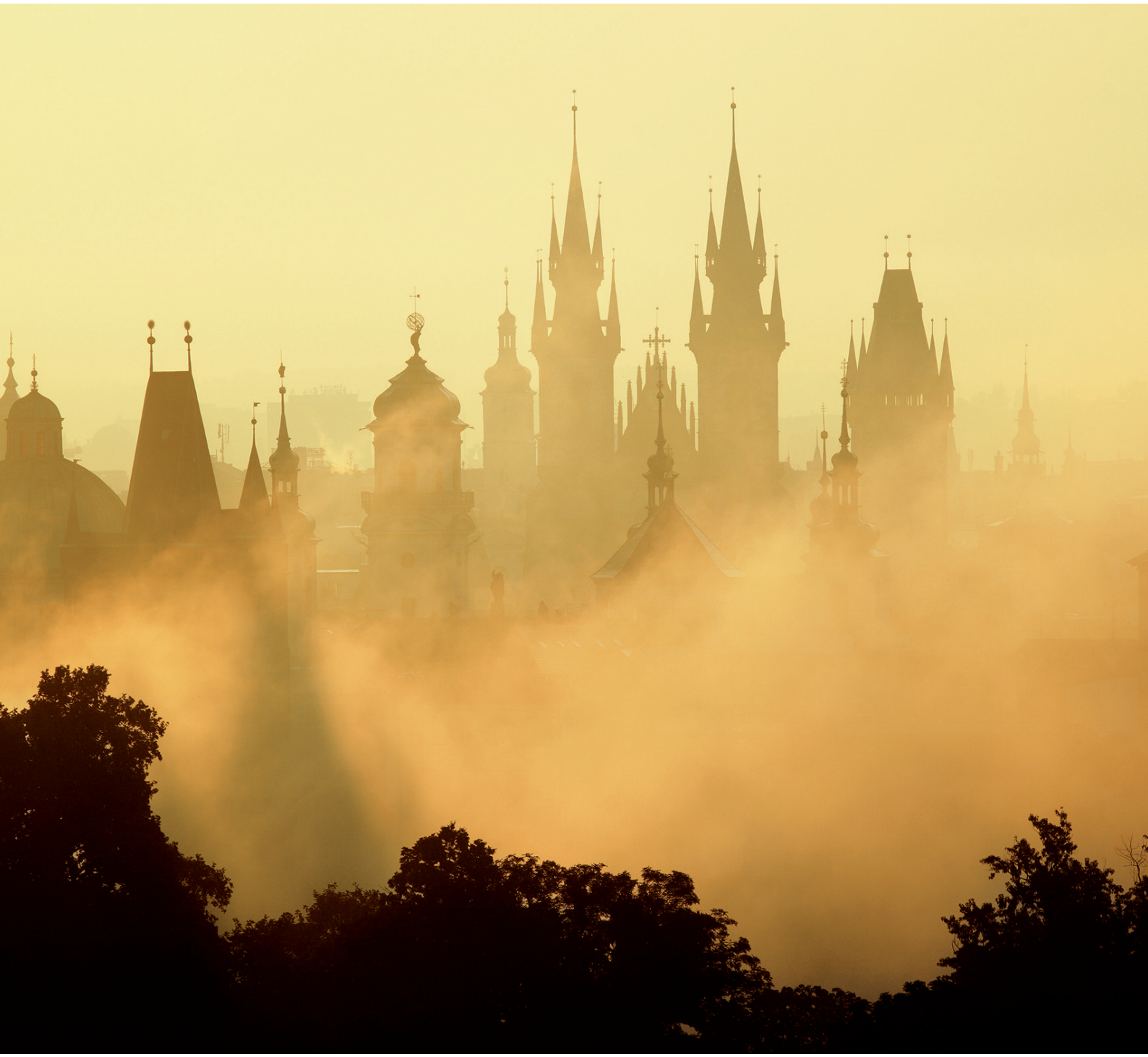

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