ESEB2025

BARCELONA 17-22 AUGUST 2025

CONGRESS OF THE EUROPEAN SOCIETY FOR EVOLUTIONARY BIOLOGY

KEYNOTE AND INVITED SPEAKER PRESENTATION SUMMARIES

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Keynote Presentation Summaries

Drift, Mutation, and the Origin of Cellular Features

Dr. Michael Lynch[1]
[1]Biodesign Center for Mechanisms of Evolution, Tempe, United States

Plenary Talk – Keynote Speaker MICHAEL LYNCH

PLENARY SESSION (113-117), August 18, 2025, 9:00 AM - 9:45 AM

As in physics and chemistry, evolutionary processes proceed by specific rules that generalize across the entire Tree of Life, embodied in the theory of population genetics. However, convinced that all aspects of biodiversity are driven entirely by natural selection, most biologists remain content to ignore all other evolutionary forces. Moreover, it is commonly assumed that the ultimate target of selection is the emergence of complexity. This is a bit of a problem given that the vast majority of phylogenetic lineages have remained simple for over three billion years. The idea that prokaryotic lineages are condemned to a perpetual state of simplicity by energetic limitations has not held up to close scrutiny.

An alternative view is that natural selection is not all powerful, with the power of random genetic drift ultimately dictating what selection can and cannot accomplish. Many prokaryotes may reside in population-genetic environments where the limits to selection are indeed dictated only by the constraints of cell biology. However, in the eukaryotic domain, larger organism size is typically associated with a reduction in effective population size (Ne), which passively induces coevolutionary side effects leading to more complex and less efficient phenotypes.

The integration of new theory with comparative analyses is starting to provide a mechanistic understanding of patterns of diversification at the molecular and cellular levels, leading to the emergence of a formal field of evolutionary cell biology. Many issues remain to be resolved, but these general ideas will be illustrated with examples on observations ranging from intracellular error rates at the level of genome replication, transcription, and translation to maximum growth capacities and the allocation of cellular resources. For reasons that remain unclear, some traits appear to be much more recalcitrant to the thousand-fold range in effective population sizes across the Tree of Life than others.

Sex (and lack thereof) in Artemia brine shrimp

Prof. Beatriz Vicoso[1]
[1]ISTA

Plenary Talk – Keynote Speaker BEATRIZ VICOSO

PLENARY SESSION (113-117), August 19, 2025, 8:45 AM - 9:30 AM

Sexual reproduction is ancestral to animals, but how males and females are generated varies widely, with some species some using environmental cues and others carrying highly specialized sex chromosomes. Why such a fundamental process is subject to so much variability remains an open question. Many lineages have lost sexual reproduction entirely, and not much is known about the molecular pathways underlying these transitions. Our lab has contributed to developing Artemia brine shrimp as tractable models for investigating some of these questions. We have characterized their ZW pair of sex chromosomes, and their evolutionary and regulatory patterns throughout the clade, including a mechanism of dosage compensation that is highly convergent with the mechanism found in Drosophila. A locus on the Z chromosome containing a highly modified version of the key oogenesis gene Itpr is responsible a switch to asexuality in this group, providing important information on the molecular steps required for such an evolutionary transition.

Red Queen dynamics from months to megayears

Mr. Dieter Ebert[1]
[1]University of Basel, Zoologie, Basel, Switzerland

Plenary Talk – Distinguished Fellow Talk DIETER EBERT

PLENARY SESSION (113-117), August 19, 2025, 9:30 AM - 10:15 AM

Hosts evolve to minimize the fitness reduction caused by parasites, while parasites optimize 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, potentially forever. This mechanism is believed to explain the high genetic diversity observed at coevolving loci in hosts and parasites. 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. In my presentation, I combine a series of experimental and genomic studies with particular focus on the time scale, 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. 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 for millions of years.

Evolutionary insights from deep-time palaeogenomes

Prof. Love Dalén[1]
[1]Stockholm University, Stockholm, Sweden

Plenary Talk – Keynote Speaker LOVE DALÉN

PLENARY SESSION (113-117), August 20, 2025, 9:00 AM - 9:45 AM

In recent years, the recovery of ancient DNA has been pushed further back in time, sometimes reaching as far back as the Early Pleistocene. This has enabled genomic studies across timescales of several hundred thousand years, making it possible to study macroevolutionary processes as they occurred, including speciation, extinction, and adaptation. Ongoing research using such deep-time genomic datasets has resulted in the identification of previously unknown lineages, new insights into species origins, and a better understanding of the timing and rate of gene evolution. This type of studies will also help place current biodiversity into a broader context, and can open the door to investigating how environmental changes, such as repeated glacial cycles, have shaped the gene pool of present-day taxa.

Zombihaviour: Unraveling the zombie-making strategies of Ophiocordyceps fungi to hijack ant behaviour

Dr. Charissa de Bekker[1]
[1]Utrecht University, Utrecht, Netherlands

Plenary Talk – Keynote Speaker CHARISSA DE BEKKER

PLENARY SESSION (113-117), August 21, 2025, 9:00 AM - 9:45 AM

The evolutionary arms race between parasites and their hosts can culminate into complex extended phenotypes that further disease progression and transmission. The fungus-adaptive changes in behaviour as seen in Ophiocordyceps-infected carpenter ants are a prime example. These “zombie ants” exhibit a suite of behaviours that circumvent the colony’s social immune responses. Eventually, the hijacked ant climbs and attaches itself to an elevated position that benefits fungal spore development and dispersal. These extended phenotypes are not unique to Ophiocordyceps since parallel behaviours are observed in invertebrates infected by other fungi, viruses and trematodes. However, the precise mechanisms underlying these convergently evolved behavioural phenotypes are unknown.
To unravel these mechanisms, we have developed the Ophiocordyceps-ant interaction into an integrative model system. By combining data from field studies with fungal culturing and lab infections, quantitative behavioural assays and multi-omics approaches, we propose several comprehensive mechanistic hypotheses about the fungal proteins and ant receptors involved in parasitic hijacking of host behaviour. These include specific fungal “manipulation” effectors and ant targets involved in e.g., light perception, biogenic amine binding, and neurotransmitter release. To test these hypotheses, we are currently, for the first time in this model, integrating functional genetics assays to determine the function of Ophiocordyceps effectors, the host behaviours they elicit, and the host pathways underlying these phenotypes. Our results will provide molecular insights into fungus-insect interactions and animal behaviour in general, while advancing our understanding of parasite extended phenotypes in particular.

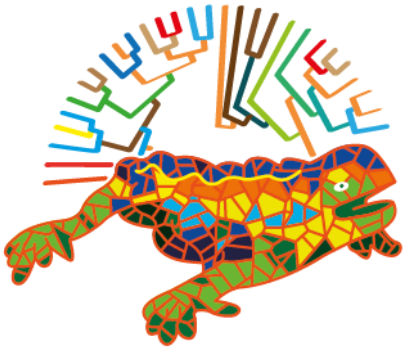
Signals of Survival: The Genetics and Ecology of Looking Dangerous

Prof. Johanna Mappes[1]
[1]University of Helsinki

Plenary Talk – Keynote Speaker JOHANNA MAPPES

PLENARY SESSION (114-117), August 22, 2025, 9:00 AM - 9:45 AM

To understand how phenotypic diversity arises and why it persists under natural selection, warning signals provide a particularly revealing model. These traits, which advertise prey unprofitability to predators, are predicted to experience strong stabilizing selection for uniformity—yet striking variation and stable polymorphism are common. The wood tiger moth (Arctia plantaginis) has become my primary model system in this work. This species is chemically defended against birds (via volatile pyrazines), displays warning coloration in both larval and adult stages, and exhibits considerable variation in signal appearance. Male hindwing colour is a discrete polymorphism in many populations, and recent work has revealed that the underling architecture of white and yellow morphs is associated with a duplication of a yellow family gene, valkea, which is present and highly expressed in white morphs. Our research investigates how genetic architecture, predator communities, and sexual selection interact in shaping the evolutionary trajectories of warning signals. I will summarize my team's findings showing that spatial variation in predator communities shapes the strength and direction of selection on warning signals, supporting the concept of a geographic mosaic of selection. This context-dependent selection, together with underlying genetic architecture and sex-specific fitness consequences, contributes to the persistence of warning signal polymorphism across landscapes.



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Invited Speaker
Presentation Summaries

Next generation experimental citizen science: when research meets the needs of forestry facing climate change

Dr. Katalin Csilléry[1], Dr Daniella Schweizer[1], Dr Marjorie Bison[1], Dr Nicole Ponta[1]
[1]Swiss Federal Research Institute WSL, Birmensdorf, Switzerland

S01 - Adaptation to environmental changes in trees through the lens of common gardens and genomics

MEETING ROOM 122+123, August 18, 2025, 10:30 AM - 12:30 PM

Advances in ecology and evolutionary biology increasingly require the integration of insights gained at local levels to regional or global scales to build predictive models. Expanding the temporal or spatial scale of studies, such as using Coordinated Distributed Experiments, is undoubtedly the best way to observe evolutionary change and validate/discover general patterns. Forestry research and its provenance trials have pioneered such large-scale experiments on non-domesticated organisms. However, many provenance trials are being abandoned and/or tested only with a limited selection of provenances at artificial open field sites that limit the evidence-based adaptation in forest management to climate and global change.

Today, citizen science is a common approach to obtaining a large amount of data collected over large spatial and temporal scales. Our analysis of the history of citizen science revealed an apparent trade-off between scale and experimental complexity, with most global projects using elementary protocols with the general public. However, citizens can do highly engaged experimental work with the right match between a specialized group of citizens and a research question. I will call this approach next-generation citizen science and present MyGardenOfTrees as an example of such a project.

MyGardenOfTrees recruited over 300 foresters across the multilingual and multicultural landscape of Europe. We engaged them to set up and follow a small unit of large-scale experiments for at least five years with a selection of seeds from two species across their entire ranges. Participants have been monitoring several life-history traits of the developing seedlings since spring 2024. After combining with genomic data, we will develop a prediction tool to provide guidelines for assisted migration decisions in Europe. I will present the recruitment strategy, the experimental design, and the protocols of this unprecedented experiment, as well as the first results of the performance of different provenances across Europe.

Towards understanding the pangenomic basis of environmental adaptation in European beech using common gardens

Ms. Desanka Lazic[1], Cornelia Geßner[1], Katharina J. Liepe[1], Isabelle Lesur-Kupin[2], Malte Mader[1], Céline Blanc-Jolivet[1], Dušan Gömöry[3], Mirko Liesebach[1], Santiago C. González-Martínez[2], Matthias Fladung[1], Bernd Degen[1], Niels A. Müller[1]
[1]Thünen Institute of Forest Genetics, Grosshansdorf, Germany, [2]BIOGECO, INRAE, University of Bordeaux, Cestas, France, [3]Faculty of Forestry, Technical University in Zvolen, Zvolen, Slovakia

S01 - Adaptation to environmental changes in trees through the lens of common gardens and genomics

MEETING ROOM 122+123, August 18, 2025, 10:30 AM - 12:30 PM

Understanding the genetic basis of environmental adaptation is key to predicting species future maladaptation and ecosystem stability in the face of climate change. This is especially important for long-lived organisms like trees, which may struggle to keep pace with rapid shifts in environmental conditions. Here, we resequenced 874 individuals from 100 range-wide populations in European beech (Fagus sylvatica L.), a wide-spread forest tree species in Europe. We found that genetic variation closely mirrors geography, with clear isolation-by-distance patterns. Genotype-environment association (GEA) analyses identified a limited number of robust adaptive signals after accounting for extensive number of false positives. We found a high-confidence locus potentially linked to winter temperature adaptation through modulation of spring phenology. However, reciprocal transplant experiments of trees supposedly adapted to two contrasting climates suggest that phenotypic plasticity plays a major role. Additionally, genome-wide association studies indicate extensive missing heritability. To better resolve the complexity of adaptive variation and address the missing heritability, we are building a European beech pangenome, based on 70 high-quality haplotype-resolved assemblies using PacBio HiFi long-read sequencing with an average contig N50 of 25 Mb. While still in progress, the pangenome – being a more representative and inclusive resource of genomic diversity - allows us to explore structural variation and to zoom in on GEA regions. Together, these approaches highlight both the challenges and the potential of combined genomic resources for understanding forest tree adaptation and their behaviour under climate change.

Genomic signatures of intra-chromosomal epistasis in hybrid populations

Prof. Claudia Bank[1]
[1]Institute Of Ecology And Evolution, University Of Bern, Bern, Switzerland

S02 - Addressing new and long-standing evolutionary questions with linkage disequilibrium based approaches

MEETING ROOM 129+130, August 20, 2025, 10:30 AM - 12:45 PM

Linkage-disequilibrium (LD) based methods have revealed that detrimental genetic interactions between alleles or genes from hybridizing species are common, with up to hundreds of pairs of epistatically interacting alleles segregating simultaneously in a hybrid population. The LD signature leveraged by these methods is caused by selection acting on pairs of alleles which, in the absence of an interaction, should segregate independently. Detecting interacting pairs of alleles is more difficult within a chromosome, where physical linkage maintains LD locally. However, intra-chromosomal epistatic interactions distort the frequencies of two-locus haplotypes in ways that can be distinguished from LD due to physical linkage. Here, we present conceptually how epistatic interactions affect LD and LD-related statistics, and how these statistics can be used to identify interacting alleles. Moreover, we show how epistatic alleles leave complex genomic signatures in linked neutral variation also after the detrimental variation has been purged from a hybrid population.

Inferring human evolutionary history using linkage disequilibrium

Prof. Aaron P Ragsdale[1]
[1]University Of Wisconsin-Madison, Madison, United States

S02 - Addressing new and long-standing evolutionary questions with linkage disequilibrium based approaches

MEETING ROOM 129+130, August 20, 2025, 10:30 AM - 12:45 PM

Population history and genome biology combine to shape the composition of genetic variation among individuals, and many methods exist to infer those evolutionary processes using varying summaries of genetic variation in present-day and ancient populations. One summary that is particularly informative about historical population sizes, structure and gene flow is linkage disequilibrium (LD). LD, or the correlation of variation between pairs of loci, is generated by the combined effects of mutation, drift and migration, and broken down by recombination. By comparing model predictions to observed LD at different genetic distances, ranging from tightly to loosely linked loci, we can infer demographic history over both the recent and distant past. We recently showed that cross-population LD allows us to distinguish between competing models for early human history, finding that long-lasting population structure with ongoing gene flow shared by all contemporary populations provides a better fit to genetic data than proposed models of unidentified “ghost” introgression. Here, we discuss the robustness and limits of LD-based methods for multi-population demographic inference. We further show that multi-population demographic history can be inferred using two-locus diversity from single individuals, and we present an application to ancient and archaic individuals from Eurasia, including high-coverage ancient humans, Neanderthals and Denisovans. We recapitulate and expand upon previously inferred history connecting humans and Neanderthals, and we show that two-locus diversity supports a model of recurrent gene flow between those lineages rather than strict isolation after their initial divergence.

Which theoretical tools should be our toolbox?

Prof. Hanna Kokko[1], Dr. Tom Keaney[1]
[1]University Of Mainz, Mainz, Germany

S03 - Advances in technology, mathematical and statistical models and their application in evolutionary ecology: the dawn of a new era

MEETING ROOM 129+130, August 18, 2025, 10:30 AM - 12:30 PM

Someone somewhere expressed tongue-in-cheek surprise that we always thought AI would come in the form of a nerdy introverted robot, instead with ChatGPT we got a verbose bullshitter. In a world like that, it is challenging to decide what tools to teach to our students. Large language models form associations from pre-existing patterns of covariation, and it is useful to be reminded how unlikely it is that they give you the spark of unique insight that might happen when reading some long forgotten work. We will reflect on this avoiding too much philosophy, and instead focus on modelling the same problem (which happens to have anthropogenic evolution of tusklessness in elephants in it) with three different approaches, one of them somewhat neglected in evolutionary ecology: ordinary differential equations, a method going back to Newton and Leibniz. This, of course, is not long forgotten work in the sciences in general - but there may be imbalances in what methods biologists are comfortable with, and in our experience, most people go for discrete-time models even if, say, elephants do not have discrete generations. As our aim is to produce a textbook of modelling, we will very much welcome feedback on whether our examples are pedagogically useful.

Using machine learning to measure phenotypic evolution: butterflies as a case study for emerging technologies

Dr Jennifer Hoyal-Cuthill[1], Dr Nicholas Guttenberg[2], **Dr. Callum McLean**[1], Dr Blanca Huertas[3]
[1]University Of Essex, Colchester, United Kingdom, [2]Cross Labs, Cross Compass, Tokyo , Japan, [3]Natural History Museum, London, United Kingdom

S03 - Advances in technology, mathematical and statistical models and their application in evolutionary ecology: the dawn of a new era

MEETING ROOM 129+130, August 19, 2025, 11:00 AM - 1:00 PM

This talk will describe our recent uses of machine learning to measure the extent of phenotypic evolution, including representation of whole-specimen butterfly images in multi-dimensional "embedding" spaces that capture image similarity. New biological applications of machine learning present a range of methodological opportunities, and questions, in the emerging field of phenomics. Such methods allow us to capture extents and patterns of phenotypic evolution, for example, against predictions of mimicry in Heliconius, and sexual versus natural selection in birdwing butterflies. Machine learning, therefore, offers insights into longstanding questions in evolution, such as the relative roles of survival versus sex, and the contributions of males and females to inter-species evolution.

'Lenses' bring ageing into focus: Senescence in a tiny, floating macrophyte

Dr. Robert Laird[1], Suzanne Chmilar[1], Athita Senayai[2], Amanda Luzardo[1], Priyanka Dutt[1], Victoria Thwaites[1], Nicola Herman[1], Abbe Pawluk[1], Julian Ketler[1]
[1]University of Lethbridge, Lethbridge, Canada, [2]Kasetsart University, Bangkok, Thailand

S04 - Ageing outside of the box: insights from unusual and non-model species

MEETING ROOM 129+130, August 19, 2025, 2:00 PM - 5:15 PM

Duckweeds – also known as 'water lenses' – are tiny aquatic angiosperms in the family Lemnaceae. They have been used sporadically for more than seven decades as a highly effective means of studying senescence (i.e., 'aging'), due to their ease of cultivation, small size, rapid reproduction, and short lifespan at the ramet level. I will use these 'lenses' to 'focus' on three themes explored by my research group: (1) Parental age effects, whereby offspring of older parents are less fit than offspring of younger parents; (2) Lifespan extension by caloric restriction, whereby individuals subjected to dim light (and therefore reduced photosynthesis) live longer than individuals in bright conditions; and (3) temporal scaling of aging trajectories, whereby lifespan distributions in varying environments differ from one another due to the apparent 'stretching of time'.

Death might keep the clone alive

Prof. Thorsten Reusch[1], Dr. Benjamin Werner[2], Prof. Iliana B. Baums[3]
[1]Geomar Helmholtz Center For Ocean Research Kiel, Kiel, Germany, [2]Barts Cancer Institute, Queen Mary University London, London, United Kingdom, [3]Helmholtz-Institute for Functional Marine Biodiversity at the University of Oldenburg (HIFMB), Oldenburg, Germany

S04 - Ageing outside of the box: insights from unusual and non-model species

MEETING ROOM 129+130, August 19, 2025, 2:00 PM - 5:15 PM

Clonal species, multicellular organisms that reproduce asexually via the iteration of a modular bauplan, are widespread among the animal, plant, algal and fungal kingdom, but are often neglected in evolutionary biology. A genet (synonymous to clone) originating from sexual reproduction gives rise to an asexual population of independent modules (=ramets) that collectively can grow to very large size (km2). In several clonal species, genet age based on spatial extent has been estimated to be >1000 yrs, prompting the question as to how these individuals can prevent mutational meltdown, as somatic mutations are incurred during mitosis during genet proliferation. High-coverage genome resequencing along with the application of somatic mutation callers revealed that somatic genetic variation (SOGV) appears first in a genetic mosaic status but subsequently segregates among modules as the founding cell population for new modules is small. In the emerging model seagrass Zostera marina, we recently found that this process of somatic genetic drift only depends on the mitotic mutation rate, permitting the application of a somatic genetic clock to precisely age clonal individuals. We also found evidence for purifying selection at the cell lineage level compared to the somatic genetic load among ramets. Importantly, the segregation of SOGV among modules also permits purging of deleterious mutants at the ramet level. Hence, module death might keep the genet alive and explain the extreme longevity of large coral, seagrass or algal genets. Further research needs to analyze cell line dynamics within ramets and to assess their demography to resolve the enigma of methuselah genets and their secret to longevity.

Marine Aliens: How They Impact Biodiversity and Evolution in Urban Marine Environments

Dr. Frédérique Viard[1]
[1]CNRS (ISE-M), Montpellier, France

S05 - Aliens among us: ecological drivers, evolutionary dynamics, and rapid ecosystem reshaping by biological Invasions

MEETING ROOM 120+121, August 18, 2025, 10:30 AM - 12:30 PM

Human-mediated species translocations across the oceans are increasing with the growth of international maritime trade. Ports thus act as major introduction hotspots, providing novel habitats for a wide range of marine non-indigenous species. These species interact with resident biota, leading to the formation of unique assemblages and distinctive evolutionary dynamics. Examples include i) admixture driven by high propagule pressure due to recurrent introductions from genetically distinct sources, ii) mosaic genetic structures resulting from a mix of short- and long-distance dispersal in port-dwelling species, and iii) hybridization and introgression -sometimes adaptive- resulting from secondary contact between native and non-native taxa that were previously in allopatry. Together, these patterns illustrate how marine invasions and coastal urbanization -two facets of global change- can interact cumulatively, fostering novel ecological interactions and promoting the emergence of new evolutionary lineages.

Comparative Oncology: Discovering Natural Cancer Defense Mechanisms Across Species to Inspire Future Therapies

Prof. Lisa Abegglen[1]
[1]Huntsman Cancer Institute, University of Utah, Salt Lake City, United States

S06 - Cancer in an evolutionary framework: across species and within individuals

MEETING ROOM 122+123, August 22, 2025, 10:30 AM - 12:30 PM

Cancer susceptibility varies widely across the animal kingdom, with some species exhibiting remarkably low cancer incidence despite large body size or long lifespans—traits typically associated with higher cancer risk. These natural outliers evolved enhanced cancer defense strategies over millions of years. By collecting, curating, and analyzing cancer incidence data across species, we can identify those with exceptional resistance. Genomic analysis of these species can reveal candidate alterations that may underlie their enhanced tumor suppression capabilities. Through comparative biology approaches we can investigate how these alterations contribute to cancer resistance. With molecular and cellular tools, including gene editing and in vivo modeling, we can validate these alterations and identify the mechanisms they encode. Importantly, these mechanisms may offer novel therapeutic targets or inspire entirely new strategies for human cancer treatment. This evolutionary framework not only deepens our understanding of cancer biology but also expands the toolkit for translational research. In this presentation, I will highlight promising examples of this cross-species approach to cancer research, including recent discoveries from cancer resistant species. These cases illustrate the promise of combining evolutionary insight with functional genomics to uncover natural solutions to cancer that may ultimately benefit human health.

Microbiome-mediated adaptation and niche construction

Dr. Carola Petersen[1], Inga Käthe Hamerich[1], Dr. Karen L. Adair[2], Hanne Griem-Krey[1], Prof. Dr. Brendan J. Bohannan[2], Prof. Dr. Hinrich Schulenburg[1]
[1]Christian-Albrechts University of Kiel, Zoological Institute, Kiel, Germany, [2]University of Oregon, Eugene, USA

S07 - Contribution of the microbiome to host adaptation and plasticity

MEETING ROOM 116, August 18, 2025, 10:30 AM - 12:30 PM

Host-associated microbiomes may enable rapid adaptation of metaorganisms to new environments, as they evolve faster than host genomes. How hosts and their microbiomes interact to drive adaptation remains unclear. One hypothesis is that hosts shape microbial communities in their environment to improve fitness through niche construction.

In an ongoing experiment, we are using the nematode Caenorhabditis elegans and a natural microbial community as a model to study the roles of host, microbiome, or both in adaptation to a new environment and niche construction. We developed compost mesocosms containing C. elegans and the microbial community in the lab. Over time, we collected microbial samples from worms and compost. After 100 days (~30 host generations), we tested worms and microbiomes in a common garden experiment to assess the effects of microbiome composition and host genetics on adaptation. We also tracked long-term changes over 500 days (~150 host generations) in the worms and their compost environment to explore reciprocal influences between host and microbiome and potential niche construction by the worms.

Our protocol supported thriving C. elegans populations for over 1300 days in compost mesocosms. Adaptation patterns varied: some worm lines increased in fitness, while others declined. These changes were linked to host-microbiome interactions. Specific shifts in bacterial and fungal communities, as well as host gene expression, were associated with fitness outcomes. Microbiomes in worm-free composts differed from those with worms. Although worm presence did not alter overall microbiome richness or diversity, worm and compost microbiomes became more similar over time, suggesting host-driven niche construction.

These findings demonstrate that both host and microbiome contribute to adaptation and suggest that C. elegans can influence its microbial environment to establish a favorable niche. This highlights the importance of host–microbiome co-adaptation in shaping evolutionary outcomes in complex environments.

Adaptation through symbiosis

Dr. Hassan Salem[1]
[1]Max Planck Institute For Biology, Tuebingen, Germany

S07 - Contribution of the microbiome to host adaptation and plasticity

MEETING ROOM 116, August 18, 2025, 2:00 PM - 5:00 PM

Symbiosis binds organisms from all domains of life. In animals, these interactions have evolved repeatedly, giving rise to striking functional diversity. Many animal traits are shaped by beneficial microbes, and our research group explores how symbiosis drives adaptation. By investigating how these partnerships are regulated and transmitted across generations, we uncover the mechanisms that maintain host–microbe specificity. Using leaf beetles as a model system, I will present (i) the molecular, developmental, and behavioural strategies that ensure symbiont retention and transmission, (ii) the nutritional and defensive benefits microbes provide, (iii) the ecological context that modulates these relationships, and (iv) the evolutionary fidelity resulting from 60 million years of co-dependence. Throughout, I will emphasize how the timing of symbiont acquisition, relative to host evolutionary history, reveals the adaptive potential of these associations. This theme is further explored through our work on mutualism breakdown and the metabolic consequences of going it alone.

Microbes as socially transferred materials: Origin and evolution of a defensive symbiosis in tortoise leaf beetles.

Dr. Aileen Berasategui[1]
[1]Vrije Universiteit Amsterdam, Amsterdam, Netherlands

S08 - Cooperation, Conflict and the Evolution of Socially Transferred Materials

MEETING ROOM 131 +132, August 21, 2025, 10:30 AM - 12:30 PM

Socially transferred materials (STMs) have been traditionally studied for their roles in delivering genetic material, nutrition, or regulatory molecules between conspecifics, and are increasingly recognized as key drivers of behavior, physiology, and evolutionary processes. While the functional impacts of STMs are gaining scientific attention, their microbial dimension remains notably underexplored.

In many systems, STMs act as vehicles for symbionts, shaping the microbiomes and metabolism of the host. Here, we describe a mutualistic relationship between the fungus Fusarium oxysporum and the leaf beetle Chelymorpha alternans. This vertically transmitted symbiont rapidly proliferates during pupation, forming a conspicuous coating that protects the beetle against predation. Eliminating the fungus reduces pupal survival, highlighting its defensive role. In return, emerging beetles disperse Fusarium to host plants, where it retains its phytopathogenic traits, causing wilt disease. Comparative genomics of ten symbiont strains from Cassidinae beetles revealed high functional conservation relative to non-insect-associated Fusarium lineages. Defensive symbionts evolved smaller genomes with fewer protein-coding and tRNA genes, as well as fewer repeats, underscoring the link between genome reduction and symbiosis.

Our findings shed light on a mutualism predicated on pupal protection of an herbivorous beetle in exchange for symbiont dissemination and highlight the importance of microbes as socially transferred materials.

Predictions from signalling theory about the molecular properties of socially transferred materials

Dr. Jen Perry[1]
[1]St. Francis Xavier University, Antigonish, Canada

S08 - Cooperation, Conflict and the Evolution of Socially Transferred Materials

MEETING ROOM 131 +132, August 21, 2025, 10:30 AM - 12:30 PM

Many interactions within species involve the transfer of endogenously-produced material from one individual to another. Examples of such socially-transferred materials (STMs) include seminal proteins, nuptial gifts, milk, and yolk. Many STMs transfer resources between individuals. All STMs are likely to bear information – for example, about the state of the producer or the environment – that receivers might evolve to perceive and respond to. It is therefore of interest to consider STMs in the context of signalling theory. In this talk, I will consider how predictions drawn from signalling theory might apply to molecular signals transferred via STMs.

Genomic and developmental foundations of adaptive tooth shape evolution

Dr. Alexa Sadier[1], Mr. Benoît Moison[1], Dr. Marcela Herrera Sarrias[1], Dr. David Grossnickle[4], Prof. Karen Sears[3], Prof. Sharlene Santana[2]
[1]CNRS - ISEM, [2]University of Washington, [3]UCLA, [4]Natural Sciences Department, Oregon Institute of Technology

S09 - Craniofacial Evolution in Vertebrates

MEETING ROOM 118+119, August 21, 2025, 2:00 PM - 4:00 PM

Teeth are serial structures that have evolved a remarkable diversity of shapes during their adaptation to various diets. Despite this diversity, teeth develop from well-conserved genomic and developmental programs. How, then, does such variation arise from these conserved mechanisms? One hypothesis to explain this paradox is the existence of both conserved and variable phases of development that constrain the evolution of shape while allowing variation along preferential developmental trajectories. To explore this hypothesis, we use the highly diverse adaptive radiation of Noctilionoid bat as a model system, combining genomic, developmental, morphological and computational data in multiple species. In tandem with the colonization of various ecological niches, this group of bats have evolved all possible mammalians diets (i.e. insects, fruits, nectar, pollen, small vertebrates, and even blood) resulting in an incredible diversity of molar shape. We first characterized the morphological signature of bat molars, using geometric morphometrics on the first lower molar. Specifically, we identified the principal axes of molar shape variation and found that molar shapes cluster according to diet within the morphospace. To uncover the developmental changes driving these differences, we reconstructed molar development using PTA-stained CT scans in bats and other mammals, spanning 35 species and six developmental stages. We identified two main developmental trajectories and heterochronic shifts that recapitulate the morphological patterns observed in adults. We further conducted RNA-seq analyses of developing molars in eight species across four developmental stages, linking gene expression dynamics to morphological variation. These combined approaches allowed us to identify both shape-specific and species-specific genomic and developmental signatures associated with distinct morphologies and developmental trajectories. Together, our results demonstrate that the rapid evolution of tooth shape during can be explained by both conserved and divergent genomic and developmental modules that direct the evolution of tooth shape along preferential developmental trajectories. More broadly, these findings can be extended to other serial organs, such as ectodermal appendages.

The Metamorphic Blueprint: How life cycle type shapes salamander skulls

Prof. Anne-Claire Fabre[1], Dr. Kévin Le Verger, Julien Clavel, Ms. Morgane Fournier, Dr. Vivien Louppe, Isabelle Toussaint-Lardé, Dr. Anthony Herrel, Dr. Olivia Plateau
[1]Bern Universitat

S09 - Craniofacial Evolution in Vertebrates

MEETING ROOM 118+119, August 21, 2025, 2:00 PM - 4:00 PM

Salamanders and newts exhibit the greatest diversity in life cycle strategies among tetrapods. Remarkably, they have independently evolved different developmental modes multiple times, resulting in distinct ontogenetic trajectories. Some species follow a complex, biphasic life cycle, transitioning from aquatic larvae to terrestrial adults and exploiting different environments at each stage. Others show direct development, bypassing the larval stage entirely and hatching as terrestrial, adult-like juveniles. Paedomorphic species, by contrast, retain larval traits and remain fully aquatic even after reaching reproductive maturity. Additionally, certain species exhibit facultative life cycles, allowing for phenotypic flexibility in response to environmental variability. This spectrum of reproductive strategies—from fixed life cycles adapted to stable environments, to plastic ones suited to ephemeral habitats—provides an ideal framework for testing how developmental pathways influence morphological and functional diversity. Specifically, it allows us to explore whether developmental strategies act as a driver of biodiversity. Given the diversity in lifestyles and feeding strategies among salamanders, we expect ontogenetic shifts to be reflected in morphological changes, particularly in the head. The head is a highly complex and integrative structure: it supports sensory input, protects the brain, and plays a central role in feeding. In this presentation, we focus on cranial morphology and how it evolves across life stages in relation to changes in feeding ecology. Using an interdisciplinary approach—combining functional morphology, developmental biology, macroevolutionary analyses, and statistical modeling—we investigate how life cycle complexity influences morphological diversification. Our findings show that the impact of life cycle strategy can vary by anatomical region, sometimes constraining, other times facilitating, morphological evolution. Ultimately, developmental strategy plays a crucial role in shaping patterns of morphological diversity across species.

The Secret Life of Inteins

Ms Danielle Arsenault[1], Dr. Sopha Gosselin[1], Ms Gabrielle Stack[1], **Prof. J.Peter Gogarten**[1]
[1]University of Connecticut

S10 - Eco-evolutionary dynamics driven by mobile genetic elements

MEETING ROOM 122+123, August 18, 2025, 2:00 PM - 5:00 PM

Inteins, aka protein introns, are selfish genetic elements found in cellular organisms and in viruses. Inteins target conserved parts of conserved proteins, e.g., the motifs characteristic for nucleotide binding sites. Most inteins consist of a self-splicing and a homing endonuclease (HE) domain. These two domains are in a mutualistic relationship: the self-splicing domain formed by the beginning and end of the intein removes the intein from the host protein, aka the extein, thereby allowing the extein to function as before invasion by the intein; the HE domain provides mobility allowing the intein to invade intein free target sites. Inteins rely on naturally occurring gene flow (sex, gene transfer, co-infection) to get into a cell that harbors a gene encoding an intein free homolog.

My presentation will focus on inteins in Archaea and Actinobacteriophages, two groups in which inteins occur frequently. For most inteins we find a sporadic and disjunct distribution, revealing frequent gain and loss of the inteins.

Divergent inteins often target different insertion sites in the same protein family (e.g., ATPases, terminases, helicases, portal proteins). For example, eleven distinct sites in archaeal MCM helicases (previously known as CDC21) are targeted by inteins; in the mcm helicase from Haloquadratum walsbyi four different inteins are found in the same gene. Most of intein insertion sites in MCM are close to the ATP binding site or the channel through which the single stranded DNA is pulled. Although homologous phage genes often harbor inteins in different sites, to date we have not found more than one intein per individual phage gene.

We found evidence for a highly effective gene drive operating in local phage populations: related but divergent phages in the same geographical location harbor identical inteins. This reveals the recent invasion of related but divergent phages. In both Haloarchaea and in phages we detected mutation that lead to resistance to intein invasion by amino acid substitutions that prevent the self-splicing reaction, but do not prevent homing, resulting in resistance by suicide.

We discovered several atypical intein architectures, where the homing endonuclease is not encoded in the same reading frame as the extein, but in a frame different from the extein and the self-splicing domain. In one case the homing endonuclease is encoded on a reading frame on the opposite DNA strand. Phylogenetic analysis reveals that these inteins remain able to invade the targeted insertion site.

Finally, I will discuss three models for intein persistence: the traditional homing cycle; a model based on intransitive fitness relationship; and the long-term and stable coexistence of alleles with and without intein in a structured environment with local differences in growth rates.

References:

Gosselin SP, Arsenault D, Gogarten JP. Actinobacteriophage Inteins: Host Diversity, Local Dissemination, and Non-Canonical Architecture. bioRxiv. 2025;:2025.01.02.630785.

Gosselin SP, Arsenault D, Jennings CA, Gogarten JP. The Evolutionary History of a DNA Methylase Reveals Frequent Horizontal Transfer and Within-Gene Recombination. Genes. 2023;14.

Arsenault D, Gosselin SP, Gogarten JP. An Actively Homing Insertion Element in a Phage Methylase Contains a Hidden HNH Endonuclease. Genes. 2025;16:178.

Turgeman-Grott I, et al. Neighboring inteins interfere with one another's homing capacity. PNAS Nexus. 2023;2:pgad354.

Mechanisms of virus-microbe adaptation, innovation, and coexistence

Dr. Adriana Lucia-Sanz[1,2], Mr. Javier Mancheño-Bonillo[1], Prof. Alberto Marina[1], Dr. Joshua Borin[3], Prof. Justin Meyer[3], Dr. Shengyun Peng[2], Prof. Joshua Weitz[2,4]
[1]Institute Of Biomedicine Of Valencia (CSIC), Valencia, Spain, [2]Georgia Institute of Technology, Atlanta, United States of America, [3]University of California San Diego, San Diego, United States of America, [4]University of Maryland, College Park, United States of America

S10 - Eco-evolutionary dynamics driven by mobile genetic elements

MEETING ROOM 122+123, August 18, 2025, 2:00 PM - 5:00 PM

Microbial communities form complex interaction networks, shaped by the infection dynamics between viruses and their microbial hosts. Our previous works showed that these interactions can evolve rapidly under experimental conditions, are predictable and driven by simple adaptive processes of mutation and counter-selection. Yet, in natural environments, key viral innovations often lead to more unpredictable evolutionary outcomes. Lysogeny is a viral innovation, understood as a survival strategy, whereby the viral genome integrates into the host chromosome effectively uniting virus and microbe into a single unit of selection. In our recent work we investigated how viral communication systems, mediated by small quorum-sensing peptides, influence the eco-evolutionary dynamics of lysogeny. We found that such signaling significantly increases lysogeny rates under nutrient-limited conditions and can promote the diversity and coexistence of different lysogens through cross-communication among viral strains. These findings point to a previously underappreciated role for viral social behaviors in shaping microbial diversity and coevolution across environments, from the mammalian gut to marine ecosystems.

Transforming Science Culture: Inclusive Meta-Research for Transparency

Dr. Malgorzata Lagisz[1]
[1]University of New South Wales Sydney, Sydney, Australia

S11 - Enhancing Diversity and Transparency in Ecology and Evolution: Reliable Practices for Research and Organisations

MEETING ROOM 122+123, August 19, 2025, 2:00 PM - 4:00 PM

Science is a powerful driver of discovery yet faces persistent challenges in reproducibility, trust, and equity. Open Science practices—such as preregistration, transparent reporting, data and code sharing—can address these challenges by promoting robustness, reproducibility, and collaboration. Meta-research, which uses scientific methods to study the research process itself, generates empirical evidence on practices ranging from methodological rigor and reporting quality to evaluation mechanisms and incentive structures.

This presentation showcases a series of open, international, and collaborative, meta-research initiatives in ecology and evolutionary biology that elevate transparency, access, and inclusivity, across scientific system.

Key examples include:

1. Studies of transparency and equity in academic prizes and awards, within and across disciplines.

2. An analysis of membership fees across learned societies related to ecology and evolutionary biology, providing concrete recommendations for greater affordability.
3. An assessment of structures related to equity, diversity, and inclusion (EDI) within the learned societies, identifying gaps and proposing strategies for more representative leadership.

Notably, many contributors of the above projects come from backgrounds that are underrepresented or historically excluded in science, ensuring diverse perspectives guide both the inquiry and its recommendations. Our collaborative meta-research delivers three benefits:

1. Rigorous evaluation of the current state of science producing actionable evidence.

2. Immersing participants in Open Science principles—facilitating their adoption in future research.

3. An inclusive model of inquiry that empowers underrepresented researchers.

By coupling empirical insights with participatory team-building and hands-on training, collaborative meta-research could catalyse systemic change at both organizational and disciplinary levels. By working together, we can harness meta-research as a tool for evidence-based reform and community-building—advancing a more transparent, equitable, and resilient science.

The role of journals in promoting a diverse, credible and open research culture in ecology and evolutionary biology

Dr. Joel Pick[1]
[1]University Of Edinburgh, Edinburgh, United Kingdom

S11 - Enhancing Diversity and Transparency in Ecology and Evolution: Reliable Practices for Research and Organisations

MEETING ROOM 122+123, August 19, 2025, 2:00 PM - 4:00 PM

As with many other quantitative fields, Ecology and Evolutionary Biology are facing a crisis. We are surrounded by low powered studies and strong publication bias, and work in an inequitable research environment which incentivises questionable research practices. As a consequence, the published literature is full of inflated effects sizes and false positives, and fails to provide a good representation of research conducted and, ultimately, the phenomena we study. This 'replication crisis' is the antithesis of what we aim to achieve as academics.

While many researchers either do not realise the potential scale of this crisis, or choose to bury their heads in the sand, journals are in a unique position to change the way we conduct and communicate our research. When working effectively, journals, and the peer review system, is often considered a gatekeeper of quality - we presume that published, peer-reviewed papers are generally higher quality, and have undergone more scrutiny than, for example, pre-prints. We now need journals to be a further gatekeeper of credibility, and act to increase the transparency, and so trust, in science.

With particular reference to key journals in evolutionary biology, I will outline several steps that journals can take to help move us from a replication crisis to a credibility revolution. I will focus on four aspects: Replication studies (tackling the replication crisis head on), Registered Reports (fighting the causes of the crisis; low power and publication bias), Data and code quality control (enhancing credibility and building trust) and Open access policy (ensuring equitable opportunities to access and publish research).

Genomic and epigenomic variation contribute to local adaptation to temperature in the sea

Dr. Dafni Anastasiadi[1]
[1]The New Zealand Institute of Plant and Food Research, Nelson, New Zealand

S12 - Epigenetics and adaptation to global change: climate and biotic interactions

MEETING ROOM 120+121, August 22, 2025, 10:30 AM - 12:30 PM

In ocean ecosystems, temperature shifts are critical for poikilothermic species. When triggered during key developmental windows, epigenetic changes can lock in lasting phenotypic effects—marking both long-term warming trends and extremes like marine heatwaves. While epigenetic variation may aid thermal adaptation in the wild, studies linking field data with experimental validation remain rare. We studied the relative importance of genomic vs epigenetic variation to local temperature adaptation using a marine teleost (Australasian snapper, Chrysophrys auratus). Snapper are distributed along New Zealand's coastline following a thermal gradient—a natural Darwinian testbed. We sequenced individual genomes and DNA methylomes—a stable, well-studied epigenetic mark—along parallel transects of both west and east coasts. To compare the contribution of genetic vs methylation signals, we identified polymorphic CpGs close to promoters with variable methylation. Sea surface temperature was the main driver of polymorphic CpGs variation. CpG methylation associated with temperature from one coast accurately predicted temperature of the other coast, indicating strong parallelism of epigenetic variants. Parallel temperature-associated polymorphic CpGs were in the same genes as differential methylation induced by temperature changes in captive broodstock populations. Captive broodstock offspring carried methylation and gene expression changes suggesting transgenerational inheritance with functional implications. Temperature challenges resulted in higher growth gain, a proxy for fitness, in offspring of parents subjected to higher temperatures, showing adaptive consequences of matched parent-offspring environments. Our results highlight temperature as a causative driver of variation in polymorphic CpGs with consistent responses in independent wild populations and captive individuals. Importantly, we show that parental thermal experience can pre-condition offspring for enhanced performance in similar environments—linking epigenetic change not only to environmental history, but also to adaptive potential. This work advances a crucial frontier in evolutionary biology, demonstrating that heritable epigenetic variation can shape local adaptation in marine species facing rapid climate change.

Taming the Genome: Epigenetic Contributions to Domestication and Sex-Specific Regulation in Chickens

Dr Carlos Guerrero Bosagna[1]
[1]Department of Organismal Biology, Physiology and Environmental Toxicology; Uppsala University, Uppsala, Sweden

S12 - Epigenetics and adaptation to global change: climate and biotic interactions

MEETING ROOM 120+121, August 22, 2025, 10:30 AM - 12:30 PM

Domestication has profoundly influenced animal genomes, leading to marked phenotypic and behavioral changes. While traditional genetic studies have elucidated many aspects of this process, emerging evidence highlights the pivotal role of epigenetic mechanisms in domestication-driven phenotypic differentiation.

We have performed several integrative genome-wide studies to explore how epigenetic mechanisms have contributed to chicken domestication, testing the idea that selection for increased tameness could be the initial step driving the domestication syndrome. In Red Junglefowl lineages divergently selected for high or low fear of humans, we observed, within only five generations, divergence in both thalamic and sperm DNA methylation profiles. Genetically, loci associated with tameness co-localize with loci linked to brain composition and anxiety behavior. By integrating genetic and epigenetic data, we identified sperm DNA methylation changes that overlap with QTLs for fear of humans, brain structure, and anxiety behavior.

By using advanced intercrosses between populations of Red Junglefowl and domestic White Leghorn chickens, we have also investigated the role of DNA methylation in regulating sex-specific gene expression on the chromosome Z. We have identified multiple Male Hyper-Methylated (MHM) regions that downregulate, but do not fully silence, local gene expression in males, thereby contributing to sex balancing in the absence of global dosage compensation in chickens. This methylation variation is modulated by both cis- and trans- loci and exhibits substantial inter-individual variability.

These combined studies show that DNA methylation plays a crucial and diverse role in domestication, by responding to selection processes and by shaping sex-specific gene regulation.

‘Who’s afraid of assisted gene flow?’ & other thorny questions about evolution at range edges

Prof. Anna Hargreaves[1]
[1]Mcgill University, Montreal, Canada

S14 - Evolution at species range margins

MEETING ROOM 129+130, August 18, 2025, 2:00 PM - 5:15 PM

Theory about species ranges makes contradictory predictions about the nature and conservation value of range-edge populations, which in turn imply contradictory management practices. Despite decades of sustained interest, it is still unclear which of these predictions are right, or when. This talk will explore recent empirical evidence, from global data syntheses of local adaptation to in-depth experimental tests, what this evidence implies about our ability to predict responses to environmental change, and mis-matches between modern scientific evidence and modern conservation policy.

Niche evolution at expanding range margins

Prof. Lesley Lancaster[1]
[1]University Of Aberdeen, Aberdeen, United Kingdom

S14 - Evolution at species range margins

MEETING ROOM 129+130, August 18, 2025, 2:00 PM - 5:15 PM

This presentation explores the premise that climate-mediated range expansions facilitate rapid niche evolution in marginal populations, enabling new phenotypes to emerge in ways perhaps unexpected under evolve-in-place scenarios.

A typical paradigm for understanding the capacity for species to adapt to climate change is summarised as 'adapt or move', which introduces a false dichotomy between range shifts that track climate (no evolution required or occurring), vs. in situ adaptation to novel conditions.

In fact, range shifts will, by their very nature, strongly invoke microevolutionary processes of (directional) gene flow and drift (including spatial sorting). These spatially-dynamic evolutionary processes may facilitate rapid evolution of niche breadth, even if populations are (at least initially) shifting to track their ancestral niches.

Here I show evidence of the genetic basis of such processes, and how they can contribute to resilient high-latitude populations and lead to the emergence of macroecological gradients in niche breadth and range size. Implications of the findings for warming tolerance of high latitude populations and the nature of genetic limits on future spread are discussed.

Crazy reproduction in crazy ants

Dr. Hugo Darras[1]
[1]Johannes Gutenberg University Mainz, Mainz, Germany

S15 - Evolution in and of diverse genetic systems

MEETING ROOM 118+119, August 20, 2025, 10:30 AM - 12:30 PM

Ant societies are characterized by a reproductive division of labor and a haplodiploid sex determination mechanism. In most species, females are produced by sexual reproduction and develop into queens or workers depending on environmental factors, while males develop from unfertilized, haploid eggs. The combination of eusociality and haplodiploidy has, however, led to the emergence of unusual reproductive strategies in several ant taxa.
We recently discovered another unique reproductive system in the yellow crazy ant, Anoplolepis gracilipes. Males of this species are all chimeras of haploid cells from divergent lineages. Chimerism occurs when parental nuclei bypass syngamy and divide separately within the same egg. When syngamy occurs, the diploid offspring either develops into a queen or a worker female, depending on the genotype of the sperm. Genetic analyses suggest that this unusual mode of reproduction is probably the result of a genetic conflict between a bisexual lineage and an androgenetic lineage.

Evolution and function of Programmed DNA Elimination in Mesorhabditis nematodes

Dr. Brice Letcher[1]
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S15 - Evolution in and of diverse genetic systems

MEETING ROOM 118+119, August 21, 2025, 10:30 AM - 12:30 PM

Several distantly related eukaryotes undergo Programmed DNA Elimination (PDE), a process that systematically destroys parts of the genome in somatic cells during early embryonic development. By contrast the germline genome remains intact.

Though PDE was first observed cytologically in parasitic nematodes as early as the 1880s, the evolution and function of this process have not been elucidated, in part due to a lack of lab-tractable systems.

We recently discovered that free-living *Mesorhabditis* nematodes undergo substantial PDE (15-35% of the genome removed in somatic cells), and have established functional genetic assays to probe the process. In parallel we assembled and compared the somatic and germline genomes of multiple species, to characterise PDE genomically.

Our most intriguing finding so far is the discovery of a highly conserved sequence motif that precisely specifies the location of elimination breakpoints. Several lines of evidence suggest this motif has originated from a transposable element. This, together with comparative analysis of the eliminated DNA (genes, transposable elements, satellite DNA), has led me to hypothesise that PDE has evolved as a mechanism to tolerate transposable elements in host genomes.

In this talk I will present the results currently in support of this hypothesis, and how we will definitively test it in the future.

Altogether, our work has possibly uncovered yet another intriguing cellular process resulting from co-evolution between host genomes and their selfish genetic elements (here, transposable elements).

Evolutionary legacies of demographic collapse: Genomic time series reveal dynamics of small populations

Dr. Hernán Morales[1]
[1]University of Copenhagen, Copenhagen, Denmark

S16 - Evolution in small populations

MEETING ROOM 115, August 19, 2025, 11:00 AM - 1:15 PM

Small populations are shaped by an interplay of drift, selection, and demography—forces that leave lasting evolutionary signatures. Yet our ability to trace these dynamics over recent time has been limited by the lack of temporally resolved genomic data. Leveraging whole-genome time series from several endangered bird species with exceptionally well-documented demographic histories, we investigate how population collapse and subsequent demographic recovery affect genomic erosion.

By comparing historical (100+ year-old museum specimens) and modern genomes, we quantify changes in genome-wide, inmunogenetic, and deleterious variation. Forward-in-time simulations, parameterised with species-specific histories, allow us to explore how the severity of decline, time since collapse, and connectivity modulate the pace and extent of genomic erosion. Across species, we observe a consistent pattern of "drift debt" - a delayed loss of genetic diversity that persists even after demographic numbers recover, revealing how different evolutionary regimes emerge depending on demographic legacies.

This work provides new insights into the tempo and mode of evolution in small populations, emphasising the long-term consequences of demographic collapse. We underscore the importance of integrating genomic monitoring into conservation planning to account for the drift debt and ensure long-term resilience of species in a rapidly changing world.

Who let the frogs out? Insights from an experimental island population

Prof. Eva Ringler[1], Max Ringler, Mélissa Peignier
[1]University Of Bern

S16 - Evolution in small populations

MEETING ROOM 115, August 19, 2025, 2:00 PM - 5:00 PM

Animal populations in closed settings allow for unbiased estimates of fitness. In 2012, we established an experimental population of the dendrobatid frog Allobates femoralis on a river island to investigate a variety of questions ranging from space and resource use, orientation, animal personality, and communication. We took advantage of the colonization phase of the island, and used molecular parentage analysis to establish cross-generational pedigrees and reconstructed tadpole transport trajectories of frog parents. In the past years, we investigated how individual frogs differ in their levels of aggression, exploration, and boldness and how this impact on individual space use, mate choice, and parental care; and how these differences ultimately affect an individual's survival and reproductive performance. The combination of population monitoring, standardized behavioural testing, habitat manipulation experiments, and genetic parentage analysis revealed that poison frogs show strategic and flexible parental strategies, have elaborate navigation and communication skills, and exhibit consistent individual differences in behavioural profiles.

The evolution of brain structures in mammals linked to behavioural ecology and from the perspective of the fossil record

Dr. Ornella Bertrand[1]
[1]Institut Català de Paleontologia Miquel Crusafont, Cerdanyola Del Vallès, España

S17 - Evolution of behavioural diversity: from ecology to genes and neural systems

MEETING ROOM 115, August 18, 2025, 2:00 PM - 5:00 PM

Mammals exhibit a wide array of brain sizes and morphologies. Many different factors contribute to the brain organization in mammals including development, ecology and evolutionary history. To better appreciate how and why this brain diversity emerged in mammals, relying solely on extant species can lead to instances of false synapomorphies. In this regard, the fossil record demonstrates that convergence is frequent and therefore a combined approach provides more accurate ancestral state reconstructions. Virtual brain endocasts of extinct species contribute valuable insight into the evolutionary context of why the size of brain regions has changed throughout time and as a function of ecology. The combination of osteological elements and the size of brain structures can be used as a proxy for ecological behaviour in extinct species. Here, I present examples of how the fossil record can improve our understanding of the evolution of mammalian brain structures in relation to behavioural ecology. The Oligocene caviomorph Incamys has exposed caudal colliculi, which might relate to enhanced auditory capabilities and may have been crucial in the evolution of group-living in Chinchillidae. Modern arboreal and terrestrial squirrels have relatively large neocortices. This trait was likely acquired during the transition to arboreality 33 million years ago. Terrestrial squirrels have smaller visual cortices and larger somatosensory areas in contrast to arboreal squirrels, suggesting a reorganization of the neocortex in Sciuridae influenced by ecology. Finally, the petrosal lobule (eye movement control) size greatly varies among Paleocene placental mammals. They progressively increase in size during the first 10 million years of the Cenozoic, which might be linked to the re-invasion of the arboreal niche after forests recovered from the end-Cretaceous mass extinction event. Ultimately, considering that shifts in brain structure sizes and associated functions likely evolved in completely different environments than today will improve our understanding of brain evolution.

New and old genes to generate novel neural systems: the origin of the Turbanate eyes in mayflies.

Dr. Isabel Almudi Cabrero[1], Dr Maria Rossello, Tòt Senar, Rafath Chowdhury, Dr. Helena García-Castro, Sophie Tandonnet, Noelle Anderson, Scott Roy, Fernando Casares, Dr. Jordi Solana
[1]Genetics & IRBio, UB, [2]Oxford Brookes University, [3]University of Exeter, [4]Andalusian Centre Developmental Biology, [5]San Francisco State University

S17 - Evolution of behavioural diversity: from ecology to genes and neural systems

MEETING ROOM 115, August 18, 2025, 10:30 AM - 12:30 PM

Mayflies are a key order to understanding the evolution of insects due to their phylogenetic position. Within this lineage, the family of Baetidae has evolved a striking sexual dimorphism: in addition to the lateral compound eyes, males develop an extra pair of extremely large dorsal, turban-shaped eyes. Thus, by comparing males versus females, these insects are a privileged system to understand the origin and integration of new visual structures.
For this, we have successfully established the mayfly Cloeon dipterum as a model species with a continuous culture in the lab and a high-quality reference genome that allows as describe the development of the eye and its integration with the optic lobes of male and female Cloeon nymphs using confocal and electronic microscopy. Furthermore, we compare sex-specific gene expression in nymphal heads at single cell resolution, to show a set of candidate genes specifically expressed in male cell populations. Together with ATAC-seq and CRISPR/Cas we uncover the GRN responsible for the origin of this new visual system, which constitutes a great advantage for males to detect other objects and individuals in the swarms that adults form to mate.

Mutualistic networks in the face of global change

Prof. Jordi Bascompte[1]
[1]University of Zurich, Zurich, Switzerland

S18 - Evolution of biotic interactions across scales

MEETING ROOM 113, August 18, 2025, 10:30 AM - 12:30 PM

The mutualistic interactions between plants and the animals that pollinate them or disperse their seeds can form complex networks involving dozens or hundreds of species. These coevolutionary networks are highly heterogeneous, nested, and built upon weak and asymmetric links among species. Such general architectural patterns maximize the number of coexisting species and increase the range of variability that these mutualistic networks can withstand before one or more species goes extinct. As a result of such interdependence, however, species extinctions induced by climate change may trigger coextinction cascades, thus driving extinct many more species than originally predicted by models of climate change. Importantly, these coextinction cascades also change the way extant species are selected from the evolutionary and functional trees, with potential implications for the functioning and robustness of the resulting communities. Beyond its effects on extinctions, global environmental change may shift the outcoumes of interactions from mutualistic to antagonistic. This leads to selection imposed by direct partners outweighing that imposed by indirect partners, resulting in communities composed of species with dissimilar traits and fast rates of adaptation.

Phage warfare: Understanding the importance of prophage-encoded anti-phage defence in Pseudomonas aeruginosa.

Prof. Stineke van Houte[1]
[1]University of Exeter, Penryn, United Kingdom

S18 - Evolution of biotic interactions across scales

MEETING ROOM 113, August 18, 2025, 2:00 PM - 5:00 PM

Bacteriophages are a major force in shaping microbial evolution and microbial community composition. In response, bacteria have evolved a wide repertoire of anti-phage defense responses. Our lab studies interactions between bacteriophages and their bacterial hosts, using a combination of molecular genetics, experimental evolution approaches and bioinformatics. While we traditionally studied the (co)evolutionary interactions between one type of phage and its host, and how anti-phage defence shapes these interactions, more recently we have begun to study how different bacteriophages interact (and often compete) within the same host, and the key role that anti-phage defenses play in this. I will talk about our latest findings, using the opportunistic pathogen Pseudomonas aeruginosa and its bacteriophages as a model system.

Anaerobic protist survival in microcosms is dependent on microbiome metabolic function.

Dr. Courtney Stairs[1,2], Karla Iveth Aquilera Campos[1], Julie Boisard[1], Viktor Törnblom[1]
[1]Department of Biology, Lund University, [2]Science for Life Laboratory, Department of Biology

S19 - Evolution of symbioses and interactions in microbial eukaryotes

MEETING ROOM 131 +132, August 19, 2025, 11:00 AM - 1:00 PM

Anaerobic environments serve as habitats for diverse microorganisms, including unicellular eukaryotes (protists) and prokaryotes. To thrive in low-oxygen environments, protists and prokaryotes often establish specialized metabolic cross-feeding associations, such as syntrophy, with other microorganisms. Previous studies show that the breviate protist Lenisia limosa engages in a mutualistic association with a denitrifying Arcobacter bacterium based on hydrogen exchange. Here, we investigate if the ability to form metabolic interactions is conserved in other breviates by studying five diverse breviate microcosms and their associated bacteria. We show that five laboratory microcosms of marine breviates live with multiple hydrogen-consuming prokaryotes that are predicted to have different preferences for terminal electron acceptors using genome-resolved metagenomics. Growth of the prokaryotes and protists within the microcosms respond differently to electron acceptors depending on the make-up of the prokaryotic community. We find that the metabolic capabilities of the bacteria and not their taxonomic affiliations determine protist growth and survival and present new potential protist-interacting bacteria from the Arcobacteraceae, Desulfovibrioaceae and Terasakiella lineages. This investigation uncovers potential nitrogen and sulfur cycling pathways within these bacterial populations, hinting at their roles in syntrophic interactions with the protists via hydrogen exchange.

Unlocking the molecular complexity of endosymbiosis in diverse model systems

Dr. Ben Jenkins[1]
[1]University of Cambridge, Cambridge, United Kingdom, [2]University of Oxford, Oxford, United Kingdom

S19 - Evolution of symbioses and interactions in microbial eukaryotes

MEETING ROOM 131 +132, August 19, 2025, 11:00 AM - 1:00 PM

Endosymbiosis – one cell living within another – is a fundamental biological process which sparked an explosion of evolutionary innovation. Endosymbiosis is responsible for the origin of photosynthetic organelles and their spread across the tree of life, the formation of reef-building coral symbioses, and the persistence of notorious intracellular parasites. In order to understand the mechanisms that underpin endosymbiosis, we must explore how these complex interactions are maintained in diverse model systems.

Firstly, I describe an immune-like glycan-sensing/processing network, partly assembled through horizontal gene-transfers (HGTs), that enables the ciliate Paramecium bursaria to control its algal endosymbionts. Using phylogenetics, RNA-interference (RNAi), and metabolite exposure experiments, we show that P. bursaria uses glycan-sensing/processing to regulate endosymbiont destruction, enabling plasticity to maximize host fitness across ecological conditions. This network includes a eukaryotic-wide chitin-binding chitinase-like protein (CLP), localized to the host phago-lysosome, which is homologous to a human phagocyte-associated innate immune factor. These findings reveal how immune functions can be alternatively adapted and expanded to enable endosymbiotic control, and may be augmented through HGT.

Secondly, I have used spatial proteomics (LOPIT) to generate a sub-cellular protein atlas of endosymbiosis in a model for corals, Exaiptasia diaphana (Aiptasia). We identify ~100 host proteins associated with the symbiosome organelle – a modified phagosome which houses endosymbiotic algal cells – and trace the expression of these genes across distinct endosymbiotic cell-states using single-cell transcriptomics. Several of these proteins share homology with immune regulation and cellular autophagy pathways in mammals but never before described in corals. Using RNA-interference based gene knock-down and cellular imaging, we can investigate the function of these proteins during endosymbiosis establishment and break-down (i.e. bleaching). Comparative phylogenetics with broader reef-building coral species now allow us to identify the core cellular machinery that governs endosymbiosis in corals and understand how these ecologically-significant interactions have evolved.

Don’t you know we’re talking ‘bout (rapid) evolution: recombination and copy-number variation in Wolbachia shift cytoplasmic incompatibility phenotypes.

Dr. Alice Namias[1,2], Dr. Julien Martinez[3], Mrs Sandra Unal[2], Mr Patrick Makoundou[2], Mrs Fabienne Justy[2], Pr Mathieu Sicard[2], Dr Mylène Weill[2]
[1]CNRS, Université Paris-Saclay, AgroParisTech, Ecologie Société Evolution, Gif Sur Yvette, France, [2]ISEM, Université de Montpellier, CNRS, IRD, EPHE, Montpellier, France, [3]MRC-University of Glasgow, Centre for Virus Research, Glasgow, United Kingdom

S20 - Evolutionary biology meets genetic pest control

MEETING ROOM 118+119, August 18, 2025, 10:30 AM - 12:45 PM

Wolbachia are maternally-transmitted endosymbiotic bacteria infecting roughly 50% of insect species. They induce a wide range of reproductive manipulations, of which cytoplasmic incompatibility (CI) is the most common. In its simplest form, CI is a reduced embryo viability in crosses between an infected male and an uninfected female. In mosquitoes, Wolbachia can also suppress the replication of pathogens such as Dengue and Zika arboviruses. With these two properties, Wolbachia are of key use for vector or pest control strategies.
In Culex pipiens, infected with the Wolbachia wPip, compatibility patterns are highly complex. We previously showed that these patterns diversity is caused by the amplification and diversification of CI causal genes, named cid. The cid operon functions as a toxin-antidote system, in which cidB is the toxin and cidA the antidote.
By repeating crosses between Culex isofemale lines over a 17 years period, we documented the emergence of a new compatibility type in real type, and linked it to a change in cid genes genotype. We show a rapid loss of a cid antidote in the genome, which causes a loss of compatibility. This antidote had an original recombinant sequence at its binding interface, corresponding to the original sequence at the toxin’s binding interface. The lost variants are organized in a palindrome, which was likely excised in a single event. Palindromic organization seems to result from a horizontal transfer from a distinct Wolbachia, wNaev, hosted by the moth Rhopobota naevana.
Variation through recombination and horizontal transfers, rather than point mutations, seem to be at the heart of rapid diversification and changes in the Wolbachia genomes. These transfers and rapid evolution abilities have to be taken into account by regular monitoring when releasing massive amount of Wolbachia-infected insects in the wild.

Predicting the invasiveness of threshold-dependent gene drives

Mr. Philipp Messer

S20 - Evolutionary biology meets genetic pest control

MEETING ROOM 118+119, August 18, 2025, 10:30 AM - 12:45 PM

Gene drives have generated considerable excitement for their potential to spread desirable genes through populations or to eliminate harmful populations, such as disease vectors. However, most current drive designs can spread from extremely low frequencies, meaning that even a minor spillover could result in the modification or eradication of an off-target population. Threshold-dependent gene drives, which require a larger release size to spread, are generally considered a safer alternative, yet their invasion criteria in real-world populations remain poorly understood. In this talk, I will show how reaction-diffusion models can be used to predict the invasiveness of threshold-dependent gene drives in populations distributed across large geographic ranges. Previous studies suggest that such systems will only spread if released above a so-called “critical propagule,” in which the local introduction frequency exceeds the invasion threshold by a sufficient amount and across a sufficient area. Unfortunately, these mathematical results rely on assumptions that often fail to hold in actual target populations. Using individual-based simulations and numerical reaction-diffusion models, I will examine how different introduction scenarios, stochastic effects, and variations in population density influence the spread of gene drives in continuous-space populations. I will also discuss how these results can inform assessments of the invasiveness of specific drive designs under real-world conditions.

Early germline sequestration in a basidiomycete fungus

Prof. Hanna Johannesson[1], Dr Markus Hiltunen Thorén, Dr Peter Jan Vonk, Boel Olsson, Dr. Mattias Siljestam, Dr Johan Reimegård, Dr Martin Ryberg
[1]Stockholm University

S21 - Evolutionary consequences of heterokaryosis, mosaicisms, chimeras and other monsters

MEETING ROOM 122+123, August 21, 2025, 2:00 PM - 4:15 PM

In sexual organisms, inheritance of new mutations is highly dependent on the timing of germline definition. Here, we used the fairy-ring forming fungus Marasmius oreades to challenge the general assumption of a late germline separation in the Fungi. We collected mushrooms from different parts of rings over a seven-year period, and identified new mutations in different tissues by whole-genome sequencing. We found evidence that sterile and fertile tissues had accumulated different mutations, suggesting that cell fate in this species is predetermined, and that the germline, destined for spore production, is already defined in the mycelium. Moreover, the germline carried fewer mutations than sterile tissues, indicating a lower mutation rate. Our findings suggest that early germline sequestration is more widespread than previously considered across multicellular life.

Choosing Cooperation: Invasive Multicellularity in Fonticula alba and Beyond

Prof. Marko Kaksonen[1], Dr Christopher Toret
[1]University Of Geneva, Geneva, Switzerland

S21 - Evolutionary consequences of heterokaryosis, mosaicisms, chimeras and other monsters

MEETING ROOM 122+123, August 21, 2025, 2:00 PM - 4:15 PM

Fonticula alba is a cellular slime mold and the only known species in its genus that belongs to a clade that is a sister group to fungi. It has been isolated from the wild only once. F. alba cells can engage in at least two separate forms of multicellularity. One form gives rise to spore-forming fruiting bodies, while the other, more recently discovered behavior, is a cooperative migration to invade bacterial biofilms that F. alba feeds on. In this collective invasion, individual amoebae form transient groups that can cover distance faster than individual cells, possibly representing an adaptation for rapid resource exploitation.
Both types of multicellular behavior are facultative, with F. alba choosing to engage in these cooperative behaviors depending on the population density and environmental cues. We have shown that the signal promoting collective invasion is derived from mature bacterial biofilms. Using this insight, we attempted to find new wild isolates of Fonticula from environmental samples by culturing them on mature bacterial biofilms. Although we have not yet succeeded in obtaining new Fonticula isolates, we have, to our surprise, frequently observed collective invasion on bacterial biofilms by species from groups throughout the eukaryotic tree, including Amoebozoa, Rhizaria and Discoba. This suggests that collective invasion is an ancient and broadly distributed behavior in eukaryotes and may have been a driver for the evolution of multicellularity in certain clades.

The bacterial march to endosymbiosis: on-ramps and off-ramps

Ms. Marjolein Bruijning[1], Andrew H. Moeller, Gavriela Carver, Mohamed S. Donia, Britt Koskella, Prerna Singh, C. Jessica E. Metcalf
[1]University Of Amsterdam, Amsterdam, Netherlands

S22 - Evolutionary Ecology of Microbial Symbioses

MEETING ROOM 116, August 20, 2025, 10:30 AM - 12:30 PM

Host-associated bacteria are found across the tree of life and can have crucial influences on the performance of their hosts. Despite the clear importance of such intimate host-microbe associations for individual hosts, it remains a mystery how and when these associations establish, and how these may impact host evolution and adaptation. This knowledge gap is partly due to the lack of theoretical frameworks that capture the evolutionary dynamics of host-microbiome systems. I explore to what extent the foundation for such frameworks lies in existing evolutionary theory. For this talk, I merge insights from classical population genetics, quantitative genetics and evolutionary ecology to highlight three key drivers that shape the fate of a host-microbe association: Host life history, chance and ecological context. By seeking general principles emerging from broad features of host and microbe, and benefiting from the wealth of theory existing the field of evolutionary biology, this work paves the way for future empirical tests to unravel the origin, function and evolution of the vast ubuiquity of the host-microbe associations surrounding us.

Insect facultative symbionts: a horizontal gene pool for eukaryotes

Dr. Lee Henry[1]
[1]Queen Mary University of London, London, United Kingdom

S22 - Evolutionary Ecology of Microbial Symbioses

MEETING ROOM 116, August 21, 2025, 10:30 AM - 12:30 PM

Bacterial symbionts are widespread in eukaryotes and often provide beneficial functions that profoundly influence host biology. Many eukaryotes rely on obligate bacterial symbionts to synthesise nutrients absent from their diets and to perform other essential functions. Even more widespread are heritable facultative symbionts, which, while not essential for host survival, can offer important ecologically relevant benefits, such as protection against natural enemies or abiotic stresses. In insects, facultative symbionts can be horizontally transferred between hosts and are often non-randomly distributed among plant-adapted insect populations and species, suggesting a role in host adaptation. This has led researchers to propose that facultative symbionts may act as a “horizontal gene pool,” transferring adaptive genes across lineages in a manner analogous to plasmids and other mobile genetic elements in bacteria. The persistence of these interactions raises key questions, many of which parallel those concerning the maintenance of plasmids in bacteria. In this seminar, I will present evidence from aphid facultative symbionts to explore and better understand the dynamics of this recently discovered and highly unusual phenomenon.

Pleiotropy as a constraint on physiological adaptation to changing environmental conditions

Prof. Cameron Ghalambor[1], Dr. Alexander Mauro[1]
[1]Norwegian University Of Science & Technology (ntnu), Trondheim, Norway

S23 - Evolutionary Genomics: Understanding and Adapting to Climate Change (organised by the journals Molecular Ecology & Evolutionary Applications)

MEETING ROOM 114, August 19, 2025, 11:00 AM - 1:00 PM

A fundamental challenge to understanding biological responses to environmental change is the capacity for populations to adaptively evolve a broader ecological niche. Because organisms are highly integrated systems, functional trade-offs and genes with pleiotropic effects represent a potential constraint on evolutionary responses to selection. Yet, few examples demonstrate how pleiotropy can constrain niche breadth and adaptive evolution. Here we build on previous results showing that Trinidadian guppies avoid brackish water in nature despite being euryhaline. Brackish water sites in Trinidad are occupied by close relative and lab breeding experiments exhibit a negative genetic correlation between salinity tolerance and competitive ability with the close relative. These results led to the hypothesis that guppies are unable to adapt to brackish water because it would come at the expense of their competitive ability. Using lab salinity exposure experiments and transcriptomics we find that transfer from freshwater to brackish water results in a loss of body condition when guppies are forced to compete with a close relative, but not when they compete with other guppies. Patterns of gene expression in the gills reveals differential expression of genes associated with osmoregulation. However, changes in gene expression in the brain reveal evidence for hormonally mediated pleiotropy between pathways involved in osmoregulation and those associated with aggression and competitive ability. Collectively, these results suggest that adaptation to increased salinity, as is expected due to sea level rise and terrestrial runoff, will come at the expense of competitive ability. Results from other studies suggest pleiotropy may be a common mechanism constraining adaptive responses.

Adaptation to Climate in European Conifers: Lessons Learned

Dr. Santiago González Martínez[1]
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S23 - Evolutionary Genomics: Understanding and Adapting to Climate Change (organised by the journals Molecular Ecology & Evolutionary Applications)

MEETING ROOM 114, August 18, 2025, 10:30 AM - 12:30 PM

European conifers represent a diverse group of long-lived forest species occupying a broad range of climatic environments across the continent. In this talk, I will present insights from our research on past, present, and future climate adaptation in four conifer species with contrasting demographic histories: stone pine (Pinus pinea), maritime pine (P. pinaster), Scots pine (P. sylvestris), and English yew (Taxus baccata). The divergent demographic backgrounds have shaped distinct levels of genetic diversity and population structure—from exceptionally low diversity in stone pine to extensive standing variation observed in Scots and maritime pines; the two latter species having also contrasted capacity for adaptive evolution (higher in maritime pine than in Scots pine). Our analyses consistently reveal a polygenic basis for adaptive traits, with, for example, around 6% of SNPs showing non-zero effects on key phenotypes in maritime pine. This complex genomic architecture presents challenges for pinpointing climate-associated candidate genes. Moreover, despite the prevalence of phenotypic clines in European conifers—particularly in traits such as growth phenology—rigorous tests for local adaptation often reveal adaptation lags and cases of population maladaptation. In English yew, such patterns appear to be exacerbated by strong population isolation. Furthermore, demographic history influences the dynamics of genetic load: from an excess of fixed deleterious alleles in stone pine to evidence of purging in marginal maritime pine populations, with no clear effects in Scots pine. Finally, I will discuss the application of predictive frameworks, such as the calculation of genomic offsets, across these species. While these approaches offer promising tools for forecasting climate vulnerability, I will argue that their interpretation must be contextualised and approached with caution. Moreover, using complementary statistics together with genomic offsets has the potential to provide more meaningful predictions.

Two explanations for variation in the predictability of evolution

Mr. Patrik Nosil[1]
[1]SETE/CNRS, Moulis, France

S24 - Forecasting evolution in natural populations

MEETING ROOM 129+130, August 22, 2025, 10:30 AM - 12:30 PM

The extent to which evolution is predictable remains debated, but is central to understanding the role of determinism and chance in the history of life. Variation in the ability of scientists to predict evolution can be due to: (1) random processes and (2) data limitations that cause poor understanding of deterministic natural selection. I evaluate these explanations using >30 years of field data from replicate populations of a stick insect, combined with theory, genomic analyses, and experiments. Color-pattern morph frequencies exhibit predictable “up-and-down” fluctuations in all populations, due to negative frequency-dependent selection. Thus, evolution from existing variation is predictable and repeatable. However, random mutation adds complexity at longer-time scales, even for traits controlled by large structural genome re-arrangements. I place these results from stick insects in the context of other study systems, to show how predicting evolution requires understanding of how selection and mutation drive evolution around dynamic equilibria.

From non-coding to coding: the de novo emerging proteome

Dr. Aaron Wacholder[1]
[1]University of Pittsburgh, Pittsburgh, United States

S25 - Gene Content Across Genomes: Models and Genomic Data

MEETING ROOM 118+119, August 22, 2025, 10:30 AM - 12:30 PM

All genomes contain genes whose sequences appear unique to a given species or lineage to the exclusion of all others. These “orphan” genes cannot be related to any known gene family; they are considered evolutionarily novel and are thought to mediate species-specific traits and adaptations. Many orphan genes have evolved from genomic regions that were ancestrally non-coding through an enigmatic process called “de novo gene birth”. I will present a series of integrated computational and experimental analyses in budding yeast that begin to shed light on the molecular mechanisms of de novo gene birth. Serendipitously, these analyses reveal the existence of thousands of previously unsuspected translated elements that are emerging de novo and appear to mediate beneficial phenotypes yet are evolutionarily transient: the “dark proteome”. I will discuss the implications of these findings for our understanding of cellular biology and evolution.

Exploring Biodiversity Genomics to Reveal Soil Invertebrates' Role in the Carbon Cycle

Hannah Muelbaier[1], Freya Arthen[1], Dr. Vinh Tran[1], Felix Langschied[1], **Prof. Ingo Ebersberger**[1,2]
[1]Goethe University Frankfurt, [2]Senckenberg Biodiversity and Climate Research Centre Frankfurt (S-BIK-F)

S25 - Gene Content Across Genomes: Models and Genomic Data

MEETING ROOM 118+119, August 22, 2025, 2:00 PM - 3:00 PM

Biodiversity genomics provides a wealth of assembled genomes, yet precomputed orthology collections lag behind, diminishing taxonomic representation. Consequently, it is hard to tap this wealth of novel data for studies investigating the presence/absence pattern of genes and their function at a precision that is provided by state-of-the-art orthology assignment tools. Here we show how a multi-scale phylogenetic profiling approach using a targeted and feature-aware ortholog search both in annotated gene sets and in un-annotated genomes augmented with a post-hoc contamination check can close this gap. We trace 300+ proteins involved in plant cell wall- and chitin degradation across 18,000 species distributed across the three domains of life. We introduce a UMAP as a novel way to visualize and explore the resulting phylogenetic profiles. This renders the identification of individual lineage-specific changes in the repertoire of carbohydrate active enzymes even with this wealth of data straightforward. Investigating animals, we find plant cell wall degradation is rare, except for some soil invertebrates like springtails. This prompts a critical reassessment of soil invertebrates' role in terrestrial decomposition. Such revelations may position them as crucial players in the global carbon cycle, reshaping ecosystem dynamics and carbon sequestration strategies.

Predictive ecological genomics: can we use correlative models to inform assisted gene flow?

Dr. Thibaut Capblancq[1]
[1]LECA - University of Grenoble, Grenoble, France

S26 - Gene flow to the rescue: Assessing the need, effectiveness, risks and ethical implications of manipulating gene flow to improve adaptation to climate change

MEETING ROOM 120+121, August 19, 2025, 11:00 AM - 1:00 PM

Species often exhibit adaptive variation across their ranges, meaning climate change will not affect all populations equally. To account for this intraspecific diversity, researchers are increasingly integrating genomic data into models that assess maladaptation risk under future climate scenarios. These predictive ecological genomics approaches combine large-scale genomic datasets with fine-scale environmental variables to estimate gene–climate associations and identify populations most at risk. They also offer a promising framework for identifying source populations best suited to specific climate conditions, informing assisted gene flow and other adaptive conservation strategies. However, these approaches typically rely on correlative models, often extrapolated from other correlative predictions, raising concerns about their validation and reliability. Despite this seemingly precarious foundation, many of these models perform surprisingly well when validated spatially. Yet, their performance over time, especially under rapidly changing climates, remains uncertain. In this talk, I will explore the promise and pitfalls of using predictive ecological genomics to guide conservation interventions such as assisted gene flow. I will discuss the challenges of model validation, highlight emerging best practices, and consider how these tools can be applied to mitigate climate change impacts on natural populations.

Genetic monitoring of plant translocations in practice

Dr. Fabienne Van Rossum[1], Mrs Cécile Godé[2], Mrs Sarah Le Pajolec[1], Prof. Dr. Ludwig Triest[3], Prof. Dr. Olivier J. Hardy[4]
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S26 - Gene flow to the rescue: Assessing the need, effectiveness, risks and ethical implications of manipulating gene flow to improve adaptation to climate change

MEETING ROOM 120+121, August 19, 2025, 11:00 AM - 1:00 PM

Assisted gene flow is often implemented by plant translocations. The purpose of plant translocations is to restore viable populations of species that are to the bridge of extinction in the short or medium term, especially when habitat restoration and management are insufficient to recover large and viable populations. However, implementation of plant translocations can still remain challenging, with uncertain translocation outcomes. Besides, given the urgency of preventing immediate species extinction as a result of habitat fragmentation and degradation, most translocations involve source populations that are selected for current habitat conditions. However, attention is increasingly paid to restore genetic diversity and to increase plant fitness to guarantee population evolutionary potential in the long term. Many unknowns still remain about the practical implementation of translocations which takes climate-change adaptation into account. Assessing the effectiveness of plant translocations under current ecological conditions and management practices can certainly provide guidelines for future implementation of assisted gene flow aiming to improve adaptation to climate change. For this purpose, a precise monitoring has to be conducted, to understand the reasons of translocation success or failure. In particular, genetic monitoring combining molecular markers and fitness-related quantitative traits can contribute to identify post-translocation processes associated with translocation success (or failure) that are not assessed by demographic monitoring, such as mating processes, the relative contribution of clonality and sexual reproduction to population expansion, pollen and seed dispersal patterns, and how translocated populations can enhance connectivity by gene flow for the extant populations. It can also contribute to a finer assessment of inbreeding and of selective or rescue processes, which may have long-term consequences for population dynamics and viability. This can provide information for proposing adaptation-oriented management of the populations. The present talk will illustrate through practical studies the interest of short-term to long-term genetic monitoring for evaluating translocation outcomes.

Evolutionary Arms Races Shaping the Mammalian Epigenome

Dr. Antoine Molaro[1]
[1]Institute of Genetics Reproduction and Development, Clermont Ferrand, France

S27 - Genetic conflict: Evolutionary and Genomic consequences

MEETING ROOM 120+121, August 18, 2025, 2:00 PM - 5:00 PM

Germline chromatin pathways are key to the stable inheritance of genetic and epigenetic information. They also participate in intense evolutionary battles between genetic entities with opposite incentives during reproduction. These include conflicts between transposons and host genomes, between chromosomes during meiosis, and between maternal and paternal epigenomes. Such genetic conflicts are predicted to drive evolutionary arms races leading to rapid genetic and epigenetic innovations. Contrary to current dogmas focusing on conserved features, our research group explicitly tackles the functional consequences of epigenome rapid evolution during mammalian reproduction and disease, including in humans.

Here, I will first present our most recent findings on the arms race driving the rapid functional diversification of short histone H2A variants in placental mammals. I will discuss the molecular mechanisms and antagonistic interactions underlying their imprinting-like function during reproduction. Then, I will present our ongoing phylogenomic efforts to identify novel cases of rapid evolution in mammalian genomes tied to genetic conflicts. Most notably, our investigation of repeated domain sub-functionalization that turned a family of immune factors into speciation genes in rodents.

The evolution of Programmed DNA elimination in insects.

Prof. Laura Ross[1]
[1]Institute of Ecology and Evolution, University of Edinburgh, Edinburgh, United Kingdom

S27 - Genetic conflict: Evolutionary and Genomic consequences

MEETING ROOM 120+121, August 18, 2025, 2:00 PM - 5:00 PM

Chromosome segregation during mitosis and meiosis constitutes the foundation of Mendelian genetics. Faithful segregation of homologous chromosomes during meiosis, which reduces the ploidy by half, lies at the core of Mendel's laws of inheritance. Faithful segregation of sister chromatids during mitotic divisions is also critically important to integrate Mendelian genetics with the process of natural selection. It ensures that all genetic information inherited from the parents has the opportunity to be 'seen' by natural selection. These core rules of Mendelian chromosome segregation predominantly frame our understanding of inheritance. However, there are many examples in nature that do not follow these rules, thereby challenging the ubiquity of Mendelian genetics. Genomic conflicts are often evoked as a key driver in the evolution of non-Mendelian genetics, even though the empirical support for this remains limited. Here I will present data from a variety of insect models aimed at understanding why, when and how the transmission of genes from one generation to the next deviate from Mendel's laws. All species we study undergo "Programmed DNA elimination", where individuals systematically eliminate a subset of their genome from specific cells: Some carry germline-restricted chromosomes, which are eliminated from somatic cells. Others undergo somatic elimination of X chromosomes, as part of their sex determining mechanisms. And finally many undergo male germline elimination of parentally-derived chromosomes. I will discuss how these types of DNA elimination might have evolved, and to what extend genomic conflicts play role in their evolution. I will also discuss insights into the molecular mechanisms that govern the elimination and how these phenomena affect genome evolution.

Escaping the trap! How flies evolved new sex chromosomes

Dr. Melissa Toups[1], Dr. Clementine Lasne[2], Dr. Marwan Elkrewi[2], Lorena Layana[2], Ariana Macon[2], Prof. Beatriz Vicoso[2]
[1]University Of Louisiana At Lafayette, [2]Institute of Science and Technology Austria

S28 - Genome Architecture and Their Role in Evolution

MEETING ROOM 113, August 20, 2025, 10:30 AM - 12:30 PM

Sex chromosomes are widespread among animals and are known to have evolved independently multiple times. However, why some sex chromosomes turnover rapidly whereas others persist for hundreds of millions of years is unknown. Here, we evaluate the homology of insect sex chromosomes across 450 million years. We find that the highly heteromorphic X chromosomes of 8 orders of insects, plus the outgroup order Collembola, are homologous. While most insect orders have retained the ancestral X chromosome, within Diptera there has been recurrent turnover of sex chromosomes. Dipterans have a small ancestral sex chromosome, containing only about 200 genes, while the rest of the insect orders examined have X chromosomes have several hundred to thousands of genes. Through sequencing the scorpionfly, Panorpa cognata (order Mecoptera), a close sister group to Dipterans, we demonstrate that the reduction of gene content on the X occurred within the lineage leading to Dipterans. This shrinking of the X chromosome may be one means of escaping the “evolutionary trap” of highly heteromorphic sex chromosomes, allowing sex-chromosome turnover.

Genomic rearrangements involved in speciation and evolution of sexual system in nematodes.

Dr. Kohta Yoshida[1]
[1]Niigata University, Niigata, Japan

S28 - Genome Architecture and Their Role in Evolution

MEETING ROOM 113, August 21, 2025, 10:30 AM - 12:30 PM

Large genomic rearrangements are involved in various genetic processes such as recombination and segregation, and they have the potential to impact speciation and the evolution of reproductive systems. Chromosome fusions are a classic example that have long been thought to influence evolutionary processes, although their role in speciation has remained controversial. My colleagues and I recently discovered that Pristionchus nematodes exhibit independent chromosome fusions between two closely related species. These fusions altered the recombination landscapes of the two species and also accumulated QTLs for hybrid sterility of different sexes. Genetic analyses revealed that hybrid sterility between these species is partially explained by segregation distortion and hybrid-specific recombination abnormalities. We therefore conclude that chromosome fusions have promoted the evolution of reproductive isolation through multiple mechanisms.

To further explore the evolutionary roles of genomic rearrangements in this genus, we karyotyped an additional 45 Pristionchus species, revealing rapid chromosome evolution in the genus. Notably, chromosome fusions frequently occurred between the X chromosome and an autosome, resulting in transitions from an XX/XO to an XX/XY sex chromosome system. Several XX/XY lineages independently evolved androdioecy, consisting of hermaphrodites and males, whereas ancestral lineages are dioecious, consisting of females and males. In an XX/XY system, if hermaphrodites are XX, they cannot produce males through self-fertilization, which is the typical reproduction for them. Subsequent genomic and genetic analyses revealed that these species secondarily evolved thermosensitive stochastic sex determination, wherein individuals with the same XX genotype stochastically develop into either males or hermaphrodites. These hermaphrodites can produce XX males capable of outcrossing with other hermaphrodites. Remarkably, X chromosomes have been conserved as sex chromosomes for over 300 million years in nematodes. The unexpected switch in sex determination systems is linked to the evolution of sexual systems, which was triggered by ancestral chromosome fusion events.

Chromosome chains and genome structural changes in termite sex chromosome evolution

Prof. Ann Kathrin Huylmans[1]
[1]Johannes Gutenberg-Universität Mainz, Mainz, Germany

S29 - Genomic Basis of Evolutionary Innovations (organised by GEVOL)

MEETING ROOM 113, August 19, 2025, 11:00 AM - 1:00 PM

Termites, in contrast to social hymenopterans, are not haplo-diploid but diplo-diploid with XY sex determination and both sexes usually present in all castes of the colonies. The XY sex determination system in termites evolved from an X0 system still present in wood- and cockroaches most probably via sex chromosome turn-over. We could show that, while there may be more variety and additional changes in sex chromosomes, at least some species show hallmarks of differentiated sex chromosomes such as obvious genomic coverage differences and dosage compensation mechanisms. The sex chromosomes in many termite species are furthermore involved in the formation of meiotic chains during male meiosis. The number of chromosomes present in these chains can vary quite drastically between and even within species and the chains are assumed to mitigate inbreeding effects by maintenance of heterozygosity. We are investigating multiple European species of termites of the genus Reticulitermes and find interesting polymorphisms in karyotypes in male meiotic cells, especially in the Italian species Reticulitermes lucifugus. Our current research investigates causes and consequences of this ring formation. Specifically, we hypothesise that chains form due to reciprocal translocations and that chromosomes in the chain can thus be considered neo-sex chromosomes. These are potentially drivers of speciation as they may represent barriers to reproduction. This systems thus offers insights in how sex chromosomes can drive important evolutionary processes such as population differentiation and sympatric speciation via structural genomic changes.

Arthropod comparative evolutionary and functional genomics

Dr. Robert Waterhouse[1]
[1]SIB Swiss Institute of Bioinformatics, Lausanne, Switzerland

S29 - Genomic Basis of Evolutionary Innovations (organised by GEVOL)

MEETING ROOM 113, August 19, 2025, 2:00 PM - 5:00 PM

The countless adaptations observed across insects and other arthropods mean that they are ideal for investigating how conservation or divergence of functional genomic elements give rise to the splendour of animal biology. The rapid accumulation of high-quality genomic resources for species from across the arthropod phylogeny supports new avenues of research investigating biological innovations. Comparative evolutionary and functional genomics approaches exploiting these data are beginning to trace how changes in gene repertoires – gene family expansions and contractions as well as gene gains, losses, and emergences – are associated with variable traits such as diet and digestion or immunity and moulting. Exploiting such large-scale datasets to quantify genetic and genomic changes requires methodological advances in genomics analysis and visualisation tools. In parallel, aiming to understand how such changes relate to phenotypic differences requires new literature mining approaches to liberate knowledge from publications at scale.

Evolution of genetic variation associated with adult migration timing in Chinook Salmon & Steelhead

Dr. Shawn Narum[1]
[1]University Of Idaho / CRITFC, Hagerman, United States

S30 - Genomic insights into evolutionary adaptation and species movements in a changing climate

MEETING ROOM 120+121, August 21, 2025, 2:00 PM - 5:15 PM

With the discovery of a major effect region (GREB1L, ROCK1) for adult migration timing in genomes of both Chinook Salmon and Steelhead, several subsequent studies have investigated the effect size and distribution of early and late migration alleles among populations in the major lineages of these species. Whole genome studies with high marker density have provided extensive insight to SNPs most associated with adult migration timing, and suites of markers for each species have been genotyped in large numbers of individuals to further validate phenotypic effects. For Steelhead, the largest phenotypic effect sizes have been observed in the coastal lineage (36% of variation for passage timing at Bonneville Dam; 43% of variation for tributary arrival timing) compared to the inland lineage (7.5% of variation for passage timing at Bonneville Dam; 8.4% of variation for tributary arrival timing) that over-winter in freshwater prior to spawning. For Chinook Salmon, large effect sizes have been observed in all three lineages for multiple adult migration phenotypes (Coastal lineage: percentage of variation of 27.9% for passage timing at Bonneville Dam, 28.7% for arrival timing for spawning; Interior ocean-type: percentage of variation of 47.6% for passage timing at Bonneville Dam, 39.6% for tributary arrival timing, 77.9% for arrival timing for spawning; Interior stream-type: percentage of variation of 35.3% for passage at Bonneville Dam, 9.8% for tributary arrival timing, 4.7% for arrival timing for spawning). Together, these results have extended our understanding of genetic variation associated with life history diversity and evolutionary processes that maintain this variation. However, much research remains necessary to determine the causal mechanism for this major effect region on migration timing in these species.

Can ecological genomics predict population maladaptation under climate change? Lessons learned from 10 years of working with genomic offsets

Prof. Matthew Fitzpatrick[1], Dr. Stephen Keller
[1]University Of Maryland Center for Environmental Science

S30 - Genomic insights into evolutionary adaptation and species movements in a changing climate

MEETING ROOM 120+121, August 21, 2025, 2:00 PM - 5:15 PM

The growing availability of dense genomic and environmental data sets has opened the possibility of integrating genomics into forecasting models of climate change impacts for many species. Of particular interest is assessing the potential for near-term disruption of genotype-environment associations and thereby identifying where populations may be most prone to climate maladaptation. One approach that is accessible to nearly any non-model organism (but most applicable to sessile, long-lived organisms for which the pace of environmental change is likely to be rapid relative to generation time and dispersal ability) is to use landscape genomic data paired with climate forecasts to derive the expected shift in the genotype-climate association between current and future climates, allowing quantitative predictions about the degree of expected maladaptation -- a metric termed “genomic offset”. Now 10 years old, genomic offset and related metrics of predicted maladaptation have seen development, application, testing, and sensitivity analyses conducted across a range of taxa, contexts, and parameter spaces. In this talk, we will discuss the conceptual underpinnings of genomic offset and different inferences that can be derived from their application. I will also summarize key findings from several recent studies that have used common garden and simulation experiments to validate genomic offsets, highlighting areas where there is growing agreement and understanding of the ability to predict climate maladaptation and where areas of uncertainty remain. Central to this discussion is a frank assessment of assumptions and limitations behind genomic offsets, and how the interpretation and potential applications of these metrics in conservation may hold promise but must be approached cautiously. Lastly, we will discuss a few research areas viewed as important next steps in the development of the field.

Magic meadows: the future of seagrasses under global change

Prof. Thorsten Reusch[1]
[1]Geomar Helmholtz Center for Ocean Research Kiel, 24148 Kiel, Germany

S31 - Habitat-forming species and global change: a multidisciplinary perspective on their evolution and adaptive potential to improve their conservation

MEETING ROOM 131 +132, August 18, 2025, 3:30 PM - 5:00 PM

Seagrasses are important foundation species that are increasingly threatened by ocean change. Along with carbon sequestration, their meadows provide important ecosystem functions such as wave attenuation, sediment stabilization, nutrient capture and biodiversity enhancement. Many meadows, particularly in the Atlantic, feature zero species-level diversity as they consist of only a single species. Understanding population-level processes determining the persistence of seagrasses is thus a pressing question in coastal ecology and conservation. Most seagrasses feature a mixture of sexual reproduction and vegetative proliferation by growth and branching of rhizomes (=clonal reproduction). Both reproductive modes deserve separate attention. Analogous to current conservation efforts in corals, active restoration of seagrass beds through leaf shoots or seeds is now increasingly addressing how to enhance natural adaptation processes through assisted evolution, for example by targeting genetically diverse and locally adapted donor beds, by applying assisted gene flow or via targeted hybridization and breeding. Yet, the diversity paradox is even more puzzling when looking at some locations where single clones extend over several kilometers, thus apparently lacking any genetic diversity in rather stressful and changing environments. Resolving this riddle of large and possibly old clones is currently an area of intense research. One hypothesis posits that accumulating somatic genetic variation segregating among clone mates of the same genet can contribute to adaptation. Moreover, and mutually non-exclusive, large “super”-clones might have particularly broad reaction norms (plasticity) to cope with changing environmental conditions. Ongoing work tries to detect asexual selective sweeps among clonal lineages for which methods from cancer evolutionary genetics are adapted to free-living clones. Findings of within-genet genetic diversity have implications for defining individuality in modular species, and suggest that some conservation genetic rules need to be revisited for clonal species if “super-clones” do really exist.

Life history constrains adaptation to climate change in habitat-forming species: insights from 3 models

Dr. Ophélie Ronce[1], Dr. Olivier Cotto[2], Dr Adele Erlichman[4], Prof. Sarah Otto[3], Prof. Sally Aitken[3], Dr. Linnea Sandell[4]
[1]CNRS Institut des Sciences de l'Evolution, Montpellier, France, [2]INRAE PHIM, Montpellier, France, [3]UBC, Vancouver, Canada, [4]MNHN, Paris, France, [5]KTH, Stokholm, Sweden

S31 - Habitat-forming species and global change: a multidisciplinary perspective on their evolution and adaptive potential to improve their conservation

MEETING ROOM 131 +132, August 18, 2025, 3:30 PM - 5:00 PM

Habitat-forming species, such as trees or corals, share life cycle features, such as ecological differences across developmental stages or a long sessile life-span. I will here illustrate with several theoretical models unexpected feedbacks between life history evolution and adaptation to a warming climate. In the first example, we show how faster climate change can result in the evolution of accelerated aging in long-lived populations when genes conferring adaptation to a warmer climate have effects that increase with age. Ultimately, this pattern is due to the weakening of natural selection with increasing age, which has been extensively discussed in the literature concerned with the evolution of senescence, but little considered when predicting patterns of adaptation to climate change. In the second example, we show how the imperfect adaptive tracking of a changing climate in a long-lived species can results in maladaptive shifts in life history, with some traits such as fecundity increasing at the expense of others such as survival. These shifts could easily be confounded with warmer climate selecting for a different trade-off between history traits, while they signal decreasing net fitness and increasing risk of collapse for the population. Considering the impact of climate warming on the entire life cycle is thus critical Finally, the last example will discuss how to optimize practices of assisted gene flow to accelerate adaptation to a warming climate in very long-lived species where individuals do not experience the same climate at the end and beginning of their life. Our model suggests that anticipating climate warming is risky if the young stages in the life cycle are the most sensitive to temperature. Our theoretical results also call for quantitative estimates of how thermal tolerance changes across the life cycle, as the optimal design for assisted gene flow critically depends on this unknown parameter.

The role of reductive evolution in animal terrestrialisation

Dr. Rosa Fernandez[1]
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S32 - Letting go: reductive evolution across the tree of life

MEETING ROOM 131 +132, August 21, 2025, 2:00 PM - 3:30 PM

Animal terrestrialisation marks a pivotal evolutionary transition that underpins the extraordinary biodiversity found on land today. Understanding how animals adapted to terrestrial environments is essential for reconstructing the origins of major physiological, morphological, and genomic innovations in evolution. Traditionally, the emphasis has been on gene gain as a driver of these innovations. However, emerging evidence challenges this view. In this talk, I will explore the central role of reductive evolution, specifically gene loss, in facilitating key adaptations during the transition from aquatic to terrestrial life across the Animal Tree of Life. Drawing on a kingdom-wide analysis of gene repertoire evolution across ca. 1,000 animal species, I will discuss that gene loss occurs at rates nearly ten times higher than gene gain in multiple independent terrestrial lineages, challenging the prevailing emphasis on gene acquisition as the main driver of evolutionary innovation. Using annelids as a case study, I will then focus on how such pervasive gene loss can act as a trigger for large-scale changes in genome architecture, potentially facilitating the out-of-the-sea transition and their adaptation to freshwater and terrestrial environments. These findings invite a reevaluation of how we define genetic innovation and highlight gene loss as a powerful, yet often overlooked, evolutionary force, with an important impact on both the linear genome and its 3D organisation. By reframing terrestrialization through the lens of reductive evolution, this talk contributes to a broader understanding of how an initial genomic simplification can lead to complexity and innovation in evolutionary trajectories, ultimately shaping the remarkable diversity of animal life on land.

Terrestrial triumph, genetic trim: Bryophyte genome reduction and the need to serve mitochondria and plastids

MSc Maria Lozano Quiles[1], MSc Parth Raval[1], **Prof. Sven Gould**[1]
[1]Heinrich-Heine-University Düsseldorf, Düsseldorf, Germany

S32 - Letting go: reductive evolution across the tree of life

MEETING ROOM 131 +132, August 21, 2025, 2:00 PM - 3:30 PM

Bryophytes unite the non-vascular plants that are mosses, liverworts and hornworts. Due to their simpler body plans in comparison to vascular land plants and their early-branching among embryophyte phylogeny, they are often considered to represent what we imagine early land plants might have looked like. Their genomes, however, reveal that their phenotypes are also the result of a significant genome reduction. We asked to what degree this reduction affected the biology of mitochondria and plastids, the two organelles of endosymbiotic origin that harbour their own genome and are characterized by complex biology and bioenergetic membranes. Based on organelle proteome data and the genomes of 168 phototrophic eukaryotes, we identified 1,648 and 706 protein families that are predicted to have operated in the ancestral plastid and mitochondrion of the bryopyhte ancestor, respectively. This does not differ significantly from the number of organelle proteins predicted for the ancestor of all land plants (1565 and 673) and this is because overall not gene families, but rather individual genes of a family were lost. Among the single copy genes that is otherwise encoded by several paralogs in canonical land plant genomes is FRIENDLY/REC. This protein family regulates the overall mass of mitochondria and plastids in an unknown manner. While model plants such as Arabidopsis or maize encode several copies to serve specifically either the plastid or mitochondrion, the liverwort Marchantia polymorpha encodes only a single homolog. Our data shows that its knockout affects both mitochondria and plastids and that organelle specificity is likely achieved by the alternative splicing of a single exon that alters the confirmation of a protein-binding TPR-motif in the C-terminus. We found similar examples of other single copy genes that serve both organelles through different means of dual targeting. Bryophytes hence present an example of how, after a genome reduction event, a taxon can efficiently use single copy genes to serve both compartments of endosymbiotic origin to remain an evolutionary successful lineage.

Supergene evolution between coadaptation and degeneration

Dr. Mathieu Joron[1]
[1]CNRS, University of Montpellier, Montpellier, France

S33 - Linking recombination rates and supergene evolution with the genomics of complex traits

MEETING ROOM 120+121, August 19, 2025, 2:00 PM - 4:00 PM

Supergenes control the co-variation of multiple traits, acting as genetic switches between alternative integrated phenotypes. Under supergene inheritance, distinct combinations of traits segregate within populations as alleles of a single Mendelian locus, without forming intermediates. The molecular bases of supergenes are now being unravelled, often pointing to complex loci with structural rearrangements. This explains how supergenes act as recombination coldspots maintaining long-term associations of coadapted mutations in linked genes, and evolving into differentiated haplotypes. However, although supergene haplotypes are often thought to lock together coadaptated allele combinations, recombination suppression causes selective interferences between the multiple genes and variants in linkage. Our research on butterfly supergenes have shown that supergene formation has occurred via selection on genes captured by multiple linked inversions, combined with introgression, explaining the cosegregation of many wing patterning genes. However, deleterious mutations are also trapped in the inversions, translating into a strong heterozygote advantage. Recent research has revealed that the maintenance of wing pattern polymorphism is explained by disassortative mating via both visual and olfactory cues. In sum, although recombination suppression may owe to selection on coadapted sets of alleles, coadaptation is not the sole element explaining the maintenance of polymorphism itself. Instead, balanced polymorphism at the mimicry supergenes reflects selection of mimicry and a rich series of phenotypic effects including deleterious mutations. I will discuss how supergene evolution in many different systems appears to respond to dual forces associated with recombination suppression, driving coadaptation of linked polymorphisms, but also degeneration.

What determines interspecific gene flow in butterflies?

Dr. Konrad Lohse[1]
[1]University of Edinburgh, Edinburgh, United Kingdom

S33 - Linking recombination rates and supergene evolution with the genomics of complex traits

MEETING ROOM 120+121, August 19, 2025, 2:00 PM - 4:00 PM

Most species barriers can be viewed as polygenic traits that are due to the effects of many loci in the genome. However, even in the presence of strong multilocus barriers many "good species" continue to exchange genetic variation. Classic models for the evolution of intrinsic incompatibilites predict that loci contributing to species barriers should be concentrated on X (and Z) chromosomes and in regions of low recombination. We used genome polarisation to characterize recent introgression in 21 sister species pairs of European butterfly to test these predictions. Our analysis reveals ubiquitous large-Z effects and allows us to test the extent to which the direction of introgression between species mirrors their asymmetry in effective population size, as predicted by genetic load arguments.

Eco-evolutionary dynamics within small bacterial communities

Prof. Sara Mitri[1]
[1]University of Lausanne, Lausanne, Switzerland

S34 - Mechanisms of adaptation to changing conditions in microorganisms

MEETING ROOM 129+130, August 21, 2025, 10:30 AM - 12:30 PM

Bacteria are excellent model systems to study evolution in the lab. Such studies are typically carried out on single species in isolation, for example to understand how they evolve resistance to antibiotics. In natural environments instead, bacteria are evolving within complex multi-species communities, which are likely to influence their evolutionary trajectories. In addition, in my lab we are interested in how the environment - in particular its toxicity - can shape interactions between bacterial species. My talk will focus on the intersection of these topics: how the environment shapes interactions between species within a community and how these interactions affect how the species evolve over time. I will talk about two studies using small bacterial communities in vitro: The first involves a long-term evolution experiment with four bacterial species that can survive in and degrade toxic pollutants. We compare how these species evolve when together versus when they are alone. In the second study we use mathematical modeling and experiments to ask how the evolution of resistance to antibiotics in a focal species might be affected by its interactions with others. Overall, my goal for this talk is to motivate a better integration of ecology into studies of bacterial evolution.

Horizontal gene transfer as an evolutionary lifeline in intracellular bacteria

Prof. Matthias Horn[1]
[1]University of Vienna, Vienna, Österreich

S35 - Mechanisms, barriers, and impacts of horizontal gene transfer across the Tree of Life

MEETING ROOM 131 +132, August 20, 2025, 10:30 AM - 12:30 PM

Obligate intracellular bacteria, including diverse symbionts and pathogens like Chlamydia and Rickettsia, exhibit characteristic genome reduction as an adaptation to their host-dependent lifestyle. The availability of host metabolites often renders bacterial metabolic pathways redundant, leading to gene loss. While limited access to the gene pool of free-living bacteria seemingly hamper gene acquisition, horizontal gene transfer (HGT) still plays a pivotal role in shaping their genomes. The phylum Chlamydiota exemplifies these dynamics. Ancestral genome reconstruction indicates their last common ancestor, around 1 billion years ago, was already intracellular with a reduced genome and key virulence factors. HGT has significantly influenced chlamydial evolution, particularly in protist symbionts, facilitating adaptations such as oxygen tolerance and increased metabolic versatility. Protists likely served as a ‘training ground’ and genetic ‘melting pot’ fostering inter-domain gene flow. Notably, the acquisition of host genes has driven the evolution of effector proteins used to manipulate host cellular pathways during infection. In conclusion, HGT is a crucial evolutionary force for obligate intracellular bacteria, facilitating host adaptation, enhancing metabolic capabilities, and shaping their pathogenic potential despite genome reduction trends.

Who Moves Whom and For Whose Benefit?

Dr. Eduardo Rocha[1]
[1]Institut Pasteur, Paris, France

S35 - Mechanisms, barriers, and impacts of horizontal gene transfer across the Tree of Life

MEETING ROOM 131 +132, August 20, 2025, 10:30 AM - 12:30 PM

Horizontal 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 in terms of their gene repertoires. This is partly because transfer is costly, their traits are often under balancing selection, and vectors of horizontal transfer compete within genomes. As a result, bacterial genomes are littered with mobile genetic elements that encode immune systems protecting them, and eventually their host, from other mobile genetic elements. Our most recent work shows that many, if not most, mobile genetic elements need to hijack the machinery of other mobile genetic elements to spread across microbial communities. Hence, changes in the gene repertoires of bacterial genomes are driven by tripartite interactions evolving within a parasitism-mutualism continuum.

Phenotypic trade-offs as a bridge in micro- and macroevolution

Dr. Lee Hsiang Liow[1]
[1]Natural History Museum, University of Oslo, Oslo, Norway

S36 - Microevolutionary processes and Macroevolutionary patterns

MEETING ROOM 114, August 19, 2025, 2:00 PM - 5:00 PM

Trade-offs are often used to frame the study of phenotypic evolution. Trait values that maximize survival may negatively impact reproduction and growth, and vice versa, but some balance among such competiting interests is often found via evolutionary processes, including selection. Here, I use cheilostome bryozoans, a commonly-occurring group of marine colonial invertebrates, to explore phenotypic trade-offs observed within contemporary and fossilized populations, as well as such trade-offs in a comparative phylogeneic context. Cheilostomes have calcified phenotypic structures that reflect colony-level fecundity (reproduction), defense (survival), fossilizable behaviour that is interpretable as inter-colony competition (survival). Moreover, a bryozoan's investment in colony growth, and temporal changes in their population growth can both be estimated, even in the fossil record. Given a recent molecular phylogeny of cheilostomes, the trade-offs between different classes of traits (reproduction, defense) in cheilostome lineages will also be estimated and discussed. This talk will showcase cheilostomes as a model system for linking microevolutionary and macroevolutionary approaches, but also discuss the complexities of scaling from population measures to macrevolutionary outcomes.

Conceptual and empirical bridges between micro- and macroevolution

Dr. Jonathan Rolland[1]
[1]CNRS - CRBE - University of Toulouse, Toulouse, France

S36 - Microevolutionary processes and Macroevolutionary patterns

MEETING ROOM 114, August 20, 2025, 10:30 AM - 12:30 PM

Since the beginning of the 20th century and the modern synthesis, evolutionary biology has been divided between microevolution (below the species level) and macroevolution (above the species level). Conceptual frameworks, terminology and mathematical models remain largely separate among those scales, leading to several paradoxes, such as the paradox of stasis.
In this talk, I will present some opportunities to unite scales exploring major questions that require bridging the gap between micro and macroevolution:
For example: Why does the rate of evolution appear to accelerate close to the present time?
Why is there stasis over long evolutionary timescales?
Do bursts of phenotypic evolution and speciation occur at the same time?
Do ecological interactions leave a predictable signature on macroevolution?
I will also present some of the avenues explored in the last years in my research group, mostly related to adaptations across latitudinal clines and species range shifts.

Museomics for understanding adaptive potential - what else do we need to develop to reach this goal?

Prof. M. Thomas P. Gilbert[1]
[1]Globe Institute, University of Copenhagen, Copenhagen, Denmark

S37 - Museomics: Challenges and Possibilities

MEETING ROOM 120+121, August 20, 2025, 10:30 AM - 12:30 PM

Temporal datasets are critical for understanding biodiversity loss, whether based on counts of individuals, or how their genomes are shaped during the process. Thanks to co-developments in molecular techniques that require ever smaller amounts of tissue, alongside increasing digitisation of the treasures held in natural history collections, it has never been easier to integrate genome data with temporal spatial information. Many of us hope that such datasets will not only teach us about the pressures that different populations have been under in the past, and how their genomes were shaped in the process, but also guide recovery efforts. However researchers are also beginning to appreciate that what sounds simple in practice, may not be quite so straightforward. This raises key questions about what we might need to start focusing on now, if we are to reach this goal?

Unlocking the temporal multi-omics potential of formalin-fixed museum specimens

Dr. Erin Hahn[1]
[1]CSIRO National Research Collections Australia

S37 - Museomics: Challenges and Possibilities

MEETING ROOM 120+121, August 21, 2025, 10:30 AM - 12:30 PM

Formalin-fixed museum specimens, once considered incompatible with molecular research, are now being recognised as a globally significant resource for recovering molecular data spanning the last century. For decades, chemical fixation was thought to prevent meaningful molecular analysis, effectively sidelining a large proportion of natural history collections from genomic research. Recent methodological advances have challenged this assumption. By establishing predictive specimen quality metrics and refining DNA extraction and sequencing workflows, reliable recovery of molecular data from century-old specimens has now been achieved. These advances have not only restored access to historical genomes but have also opened new avenues for investigating preserved patterns of gene regulation, providing critical insight into how organisms responded to past environments and how gene regulation has shifted during the Anthropocene.

At the Australian National Wildlife Collection, we have demonstrated that spirit-preserved vertebrates retain tissue-specific, sex-specific, and environmentally responsive chromatin architecture. By generating genome-wide chromatin profiles from specimens up to 117 years old, we revealed regulatory states preserved at the time of death. These findings show that formalin fixation captures not only morphology, but also the epigenomic landscape, enabling transcriptional snapshots of historical environmental responses. Building on this foundation, we are developing temporal multi-omics approaches that include RNA sequencing, historical viromics, and DNA methylation profiling. We are using these tools to investigate host-pathogen response dynamics over time and to disentangle environmentally responsive epigenetic variation from genetic background in clonal vertebrates. Together, they extend the power of museomics beyond genomics alone, offering new ways to examine how organisms responded to past pressures and how they may respond in the future.

This work builds on a strong foundation in phylogenomics and population genetics, broadening the scope of museomics to include functional and regulatory dimensions of biological change. Spirit collections are increasingly being repositioned as central to this emerging field, offering molecular insights that complement existing genomic data. Interdisciplinary collaboration is playing a key role in advancing this research, with protocols developed in recognition of both the precious nature of historical collections and the constraints of working with retrospective cohorts. By unlocking the molecular content of these specimens, we not only enrich the historical record but also develop tools to better understand and predict biological responses to environmental change.

The Earth BioGenome Project and its Impact on our Understanding of Chromosome Evolution in Mammals

Dr. Harris Lewin[1]
[1]Arizona State University, Tempe, United States

S38 - New Frontiers in Genome Diversity and Evolution: Exploring the 3D Organization and Function of Genomes

MEETING ROOM 118+119, August 19, 2025, 11:00 AM - 1:30 PM

My talk will focus on the progress of the Earth BioGenome Project (EBP) and how the chromosome-scale assemblies produced by the EBP are being utilized to understand chromosome evolution in mammals. EBP-affiliated projects have now generated genome assemblies for over 4,000 unique eukaryotic taxa, with nearly 2,800 meeting the EBP metrics for a reference-quality genome. These represent approximately 56% of the world's total output of reference-quality genomes and about 70% of the total at the family level. Such remarkable advances have been enabled by the rapid adoption of standards established by the EBP, which has extended to the international biodiversity genomics community. The EBP Phase I goal of sequencing and annotating the genomes of 10,000 species, representing at least half of the eukaryotic families, is now well within reach. Scaling up to EBP Phase II—the sequencing of 150,000 genomes over four years—will require more than a tenfold increase in current global production. The requirements for this scale-up will be discussed. Results of recent studies demonstrate how high-quality genomes have provided the resolution necessary to reveal the intricate evolutionary history of mammalian chromosomes, tracing the origins of chromosome breakpoints, conserved syntenic blocks, gene gains and losses, repetitive elements, 3D structure, and other genomic features over approximately 200 million years of mammalian evolution.

Structural Genomic Variants: Diversity, Functional Impact and Role in Evolution

Dr. Claire Mérot[1]
[1]CNRS ECOBIO- Université de Rennes, Rennes, France

S38 - New Frontiers in Genome Diversity and Evolution: Exploring the 3D Organization and Function of Genomes

MEETING ROOM 118+119, August 19, 2025, 11:00 AM - 1:30 PM

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 the evolution of biodiversity and adaptation, with suggestions to consider more systematically the role and function of SVs in adaptation genomics. We will support these ideas with empirical studies addressing the functional role of large rearrangement such as chromosomal inversions in seaweed flies.

A natural mechanism of eukaryotic horizontal gene transfer

Dr. Andrew Urquhart[1]
[1]School of BioSciences, University of Melbourne, Melbourne, Australia

S39 - Novel experimental and computational approaches to understand the prevalence of reticulate evolution in eukaryotes

MEETING ROOM 131 +132, August 21, 2025, 3:30 PM - 5:00 PM

Horizontal gene transfer (HGT) is well established as a major evolutionary force in prokaryotes, but its significance in eukaryotes has historically been controversial. Genomic studies are now uncovering growing evidence of HGT across diverse eukaryotic lineages, including plants, animals, protists, and fungi. However, it remains unclear whether these events are merely isolated chance occurrences or if active mechanisms exist to mediate gene exchanges between eukaryotic species.

We recently demonstrated that giant transposable elements, which we call Starships, can mediate active gene transfer between distantly related fungal species. In simple co-culture experiments involving fungi from different genera, we observed repeated Starship transfers between individuals. Using whole-genome sequencing, we confirmed that only Starship DNA is precisely transferred, thus excluding alternative hypotheses such as the random uptake of exogenous DNA or hybridisation. The transferred Starship elements total 500 kilobases in length (similar to the size of some fungal chromosomes) and mobilize approximately 150 genes with diverse biological functions as cargo. One transferred Starship carried genes for metal resistance. Following transfer, the recipient strain acquired a metal resistance phenotype.

Beyond our experimental results, bioinformatic analysis suggests that Starship-mediated HGT is a widespread and frequent natural phenomenon across filamentous fungi. We conclude that Starships represent an active mechanism of HGT between eukaryotic species. These findings challenge the traditional view that eukaryotic HGT is rare and passive, and open new avenues for understanding how fungal genomes evolve, adapt, and innovate through horizontal exchange.

Clarifying the origin of eukaryotic cells using new deep-time phylogenetic models.

Prof. Andrew Roger[1]
[1]Dalhousie University, Halifax, Canada

S40 - Phylogenomics methodology and the deep tree of life

MEETING ROOM 113, August 22, 2025, 10:30 AM - 12:30 PM

The origin of eukaryotic cells from prokaryotic ancestors remains one of the most enigmatic major transitions in the evolution of life on Earth. It is widely accepted that the nucleocytoplasmic lineage of eukaryotes is related to asgard Archaea and mitochondria evolved from endosymbionts related to Alphaproteobacteria. However, the precise phylogenetic positions of these two ancestral lineages, the nature of additional genetic contributors, the position of the root of the eukaryotic tree and the relative timing of events that occurred in eukaryogenesis have been difficult to resolve. This lack of clarity stems, in part, from artefacts induced by the inadequacy of standard phylogenetic models of amino acid sequence evolution to capture the dynamics of sequence change on the billion-year timescale. Here I will discuss new models of protein sequence evolution for deep-time phylogenetic estimation that account for: i) heterogeneity in the amino acid substitution process over sites, ii) functional shifts in molecules over splits, and iii) simultaneous across-site and -branch-heterogeneity in amino acid frequencies. We show how these methods were applied to robustly determine the root of the eukaryote tree and address other deep-time phylogenetic problems.

Deep roots and evolution of cellular life on Earth

Prof. Anja Spang[1]
[1]NOZ and UvA, 't Horntje, Texel , Netherlands

S40 - Phylogenomics methodology and the deep tree of life

MEETING ROOM 113, August 22, 2025, 10:30 AM - 12:30 PM

The tree of life (TOL) is a powerful framework to depict the evolutionary history of cellular organisms through time, from the last universal common ancestor, LUCA, to extant archaea, bacteria and eukaryotes shaping biodiversity on Earth today.
During the past decades, our perception of the TOL has fundamentally changed in part due to profound methodological advances which allowed a more objective approach to study organismal diversity and led to the discovery of major new branches in the TOL. For example, single cell and metagenomics approaches to reconstruct genomes of uncultivated microorganisms, has enabled the generation of a wealth of genomic data of previously unknown microbial such as the ubiquitous and diverse symbiotic DPANN archaea and CPR bacteria as well as shed new insights into the origin of the eukaryotic cell from a symbiosis between an Asgardarchaeon and alphaproteobacterial partner.
In this talk, I will present aspects of our research that have contributed to new key insights into the divergence of archaea and bacteria, the placement of genome-reduced symbionts in the TOL and the timing of major evolutionary transitions including the origin of the eukaryotic cell.

Animal Phylogenomics: Navigating Data, Paralogy, and Non-Tree-like Events

Prof. Mary O'connell
[1]University Of Nottingham, Nottingham, United Kingdom, [2]Natural History Museum, London, ,

S41 - Post-phylogenomics: new and evolving molecular methods to address challenging phylogenies

MEETING ROOM 131 +132, August 18, 2025, 10:30 AM - 12:30 PM

Reconstructing challenging phylogenies demands careful consideration of data and models. Using some examples from our work I will demonstrate the critical impact of dataset construction on phylogenetic inference, particularly concerning hidden paralogy. I will show how filtering for orthologous signal significantly improves model fit and can alter phylogenetic conclusions. Furthermore, while gene duplication is a well-established mechanism driving the evolution of novel phenotypes, non-tree like processes such as gene fusion offer a distinct perspective on emergence of novel and convergent phenotypes across animal life.

Using simulation to understand phylogenetic problems.

Prof. Max Telford[1], Dr Paschalia Kapli, Dr Paschalis Natsidis, Dr Irepan Salvador-Martinez
[1]UCL, London, UK

S41 - Post-phylogenomics: new and evolving molecular methods to address challenging phylogenies

MEETING ROOM 131 +132, August 18, 2025, 10:30 AM - 12:30 PM

I will present three very different case studies in which we have used simulation of data to help us to understand a phylogenetic problem.

In the first, we use simulation to produce sets of orthologs that experience no gains or losses. We show that errors in identifying orthologs increase with higher rates of evolution. We use the predicted sets of orthologs (with the errors just mentioned), to: reconstruct phylogenetic trees using gene presence/absence; to count gains and losses across a phylogeny; and for phylostratigraphy. Our simulated data, containing information only from errors in orthology prediction, nevertheless closely recapitulated findings from empirical data.

In the second we study the contentious issue of the affinities of the ctenophores or comb jellies. Using both empirical data and simulations, we show that the Ctenophora-first topology (but not Porifera-first topology) is supported by analyses affected by systematic errors.

Finally (time permitting) I will discuss the prospect of using artificially introduced mutations to reconstruct cell lineages. We use computer simulations to estimate the performance of different approaches under different conditions. We incorporate empirical data on CRISPR-induced mutation frequencies in Drosophila. We show significant impacts from multiple biological and technical parameters - variable cell division rates, skewed mutational outcomes, target dropouts and different sequencing strategies

Partitioning the phenotypic and genetic variances of reaction norms

Mr. Pierre de Villemereuil[1,2], Mr. Luis-Miguel Chevin[3]
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S42 - Predicting evolutionary change in ecologically relevant contexts

MEETING ROOM 114, August 21, 2025, 10:30 AM - 12:30 PM

Many traits show plastic phenotypic variation across environments, captured by their norms of reaction. These reaction norms may be discrete or continuous, and can substantially vary in shape across organisms and traits, making it difficult to compare amounts and types of plasticity among (or even within) studies. In addition, the evolutionary potential of phenotypic traits and their plasticity in heterogeneous environments critically depends on how reaction norms vary genetically, but there is no consensus on how this should be quantified.

I will present a partitioning of phenotypic variance across genotypes and environments that jointly address these challenges, implemented in the Reacnorm R package.

This partitioning starts by distinguishing the components of phenotypic variance arising from the average reaction norm across genotypes, genetic variation in reaction norms (with additive and non-additive components), and a residual that cannot be predicted from the genotype and the environment.

It then further partitions the genetic variance of the trait (additive or not) into an environment-blind component and a component arising from genetic variance in plasticity. The additive components can be expressed and further decomposed according to the relative contributions from each parameter of the reaction norm, using what we describe as the reaction norm gradient. This allows for a very general framework applicable from the character-state to curve-parameter approaches, including polynomial functions, or arbitrary non-linear models.

I will present simulations to illustrate how it is possible to efficiently partition variation in reaction norms for complex, non-linear cases. I will also illustrate how this framework for decomposing non-linear function-valued traits can be used to study growth curves using a case study on the common lizard.

Adaptation to climate change in wild bird populations: Variation in evolutionary potential and plasticity in blue and great tits populations across Europe

Dr. Céline Teplitsky[1]
[1]CEFE - CNRS, Montpellier, France

S42 - Predicting evolutionary change in ecologically relevant contexts

MEETING ROOM 114, August 21, 2025, 2:00 PM - 5:00 PM

Earlier phenology and decreased body size are among the most widespread reported trends in response to climate change in a large diversity of taxa. However, a large heterogeneity exists among populations and species in their plastic and/or evolutionary responses.

Our understanding of evolutionary trajectories relies notably on our estimates of evolutionary potential, and several questions need to be answered: How is evolutionary potential varying across a species distribution? Does it change under new environmental conditions? We addressed these questions using a comparative analysis of multivariate evolutionary potential (via the genetic variance–covariance matrix, or G-matrix) of 10 wild great tit populations (Parus major) distributed across Europe. For each population, detailed information about morphology, life history traits and a pedigree have been collected, allowing quantitative genetics analyses. We showed that G-matrices vary across the species range for both types of traits, but these differences are explained by climatic niche for life history traits only.

Plastic responses to temperature frequently explain a large part of recent phenotypic changes. However, we know very little about how these responses may be constrained by other components of global change such as habitat degradation. We evaluated how urbanisation and agriculture affected the expression of plasticity of phenology in great and blue tit (Cyanistes caeruleus) populations. Phenological plasticity of great tits was reduced in highly urbanised environments and blue tits were less plastic in agricultural landscapes, highlighting how combined environmental degradations may threaten populations' capacity of adaptation. Altogether, our results emphasise how integrating the impact of ecological conditions may affect global adaptive potential (evolution + plasticity), but much variation remains unexplained and further work is required to evaluate the extent to which it can affect populations persistence.

Exploring multi-level coevolution and evolutionary conflict in wild marine phage–bacteria systems

Mrs. Frederique Le Roux[1]
[1]Université de Montréal, MONTRÉAL, Canada

S43 - The dynamics and consequences of bacteria-bacteriophage interactions and co-evolution in complex communities

MEETING ROOM 120+121, August 19, 2025, 4:00 PM - 5:30 PM

Parasitism presents a fundamental evolutionary paradox: how do organisms that exploit and harm their hosts persist over evolutionary timescales? We investigate this question using a marine model system where coevolution occurs across multiple biological levels—between invertebrate hosts (oysters), their bacterial pathogens (Vibrio spp.), the bacteriophages that infect them, and satellite elements that parasitize those phages. By integrating time-series sampling from oyster farms with large-scale genomic analyses (>600 Vibrio genomes, >1000 phages), we examine how ecological context and evolutionary pressures shape host–parasite dynamics. We show that local adaptation, genome plasticity, and epigenetic defense systems drive ongoing coevolutionary arms races between phages and bacteria. Modular infection networks structured by mobile genetic elements reveal dynamic exchanges of genetic defense and counter-defense mechanisms, reminiscent of Red Queen dynamics. Strikingly, we also uncover broad-host-range phages (e.g., Schizotequatroviruses) whose ecological rarity—despite genomic versatility—suggests evolutionary trade-offs between generalism and fitness. Adding another layer of complexity, we describe minimalist phage satellites (PICMIs) that exploit virulent phage particles for transmission while protecting bacteria from secondary phage infections, exemplifying “hyperparasitism.” Together, these nested interactions illuminate how parasitism evolves, stabilizes, and diversifies in complex microbial ecosystems. Our findings highlight the evolutionary consequences of multi-level conflicts and position wild phage–bacteria systems as powerful models for understanding coevolution, genomic conflict, and the evolutionary ecology of parasitism.

Elevational variation in gametophytic thermal performance and its influence on floral thermoregulatory evolution

Dr. Matthew Koski[1]
[1]Clemson University, Clemson, United States

S44 - The ecological and evolutionary implications of climate change on reproduction

MEETING ROOM 115, August 20, 2025, 10:30 AM - 12:45 PM

Temperature is a key driver of natural selection, varying predictably across species' ranges and creating opportunities for local adaptation of thermal performance. In flowering plants, gametophytes are temperature sensitive, but several floral traits have evolved that can ameliorate thermal stress. However, few studies have tested whether gametophytic thermal performance or floral thermoregulation exhibit signatures of local adaptation. I present findings from studies of Argentina anserina, a widespread perennial, examining whether gametophytic thermal traits and floral thermoregulation are locally adapted across a 1000-meter elevation gradient in the Colorado Rockies. We first assessed thermal optima and tolerance breadth for pollen viability in low- and high-elevation populations, relating these metrics to long-term ambient and flower-level operative temperatures. Surprisingly, high-elevation populations exhibited pollen thermal optima ~4°C higher than low-elevation populations, despite experiencing cooler environments. We then evaluated: (1) whether populations differ in floral thermoregulation, (2) the mechanisms underlying thermoregulation, and (3) its fitness consequences. High-elevation populations warmed their floral microenvironments more effectively, driven by plasticity in petal angle—more cupped flowers enhanced solar radiation capture and interior warming. Pollinator-mediated selection favored floral warming at high elevation, as evidenced by increased seed production and pollen export. However, we found no selection for warming via pollen viability. In contrast, at low elevation, viability selection favored floral cooling. These results demonstrate that both gametophytic thermal performance and variation in operative temperature contribute to floral trait evolution, with distinct selective pressures across environments. Understanding the mechanisms and consequences of floral thermoregulation are critical for predicting evolutionary trajectories of floral traits under continued warming.

Can evolution and plasticity buffer fertility loss under climate change?

Dr. Belinda van Heerwaarden[1]
[1]University Of Melbourne, Melbourne, Australia

S44 - The ecological and evolutionary implications of climate change on reproduction

MEETING ROOM 115, August 21, 2025, 10:30 AM - 12:30 PM

Male fertility loss at high temperatures is emerging as a key trait underpinning species' vulnerability to climate change. Both high developmental temperatures and acute, sublethal heat stress can cause male sterility at temperatures well below critical thermal limits for survival or activity. These male fertility thermal limits are emerging as better predictors of current species distributions and laboratory extinction temperatures than lethal or knockdown thresholds. Consequently, many species may be more vulnerable to climate change than previously estimated. Despite this, we still know relatively little about the capacity of species to mitigate heat-induced male fertility loss. In this talk, I will explore the complex and sometimes species-specific nature of heat-induced male sterility. I will examine the potential for plasticity, evolution, and bacterial endosymbionts to mitigate heat-induced male fertility loss, and consider implications for predicting species persistence under climate warming.

Why do bacterial pangenomes vary across species?

Dr. Anna Dewar[1], Dr. Chunhui Hao[1], Dr. Laurence Belcher[1], Dr. Melanie Ghoul[1], Professor Stuart West[1]
[1]University Of Oxford, Oxford, United Kingdom

S45 - The evolution of microbial pangenomes

MEETING ROOM 113, August 22, 2025, 2:00 PM - 3:00 PM

Pangenomes vary across bacteria. Some species have fluid pangenomes, with a high proportion of genes varying between individual genomes. Other species have less fluid pangenomes, with different genomes tending to contain the same genes. Two main hypotheses have been suggested to explain this variation: differences in species' bacterial lifestyle and effective population size. However, previous studies have not been able to test between these hypotheses because the different features of lifestyle and effective population size are highly correlated with each other, and phylogenetically conserved, making it hard to disentangle their relative importance. We used phylogeny-based analyses, across 126 bacterial species, to tease apart the causal role of different factors. Our analyses suggest that bacterial lifestyle and ecology is the key factor causing variation in pangenome fluidity across species. In contrast, we found no support for the competing hypothesis that larger effective population sizes lead to more fluid pangenomes. Effective population size appears to correlate with pangenome variation because it is also driven by bacterial lifestyle, rather than because of a causal relationship. Our study illustrates the potential power of using comparative methods in combination with the ever-growing quantity of genomic data to address broad evolutionary questions.

Protein Structure before LUCA

Dr. Klara Hlouchova[1], Valerio G. Giacobelli[1], Mikhail Makarov[1], Robin Krystufek[1]
[1]Charles University, Prague, Czech Republic

S46 - The future meets the beginning: Synthetic biology, evolution, and the origin of life

MEETING ROOM 131 +132, August 18, 2025, 2:00 PM - 3:30 PM

All extant cells known to humankind build proteins from the same 20 coded amino acids. Is this canonical alphabet a prerequisite for life to be as successful as it has been on our planet or could protein structures and functions depend on a different/smaller set of amino acids?
We report structural and functional propensities of proteins and peptide libraries built from different subsets of both canonical and non-canonical amino acids, mimicking different hypothetical stages of the prebiotic-to-biological sequences. The study of origins of life implies that earlier cells functioned with a smaller alphabet, which was selected from a pool of prebiotically plausible (canonical and non-canonical) amino acids before the fixation of the Central Dogma. Our work implies that the "early" canonical amino acids that were selected from the prebiotic environment have a higher structure-forming propensity than possible alternatives. Despite lacking positively charged and aromatic residues, proteins composed from such "early" components would be prone to structure formation but also capable of interacting with organic and inorganic cofactors. On select examples, we observe that such binding can significantly assist with early protein folding as well as with catalytic and binding propensities.
Our work indicates that protein folding propensity was an important factor during the earliest stages of the genetic code evolution. A reduced acidic alphabet would be sufficient to build small proteins, sometimes capitalizing on interactions that are less frequent or rare in today's biology. These properties could nominate acidic peptides as early functional hubs.

Darwinian evolution of RNA replicators in artificial cell-like systems

Dr. Ryo Mizuuchi[1]
[1]Waseda University, Shinjuku, Japan

S46 - The future meets the beginning: Synthetic biology, evolution, and the origin of life

MEETING ROOM 131 +132, August 18, 2025, 2:00 PM - 3:30 PM

During the origins of life, molecular self-replicators such as RNA are thought to have evolved into complex biological systems. To explore possible evolutionary scenarios, we have developed artificial RNA replication systems and subjected them to experimental evolution. One such system consists of an RNA replicator encoding an RNA replicase, combined with a cell-free translation system, enabling the RNA to replicate using its encoded replicase. Through repeated replication, the RNA accumulates mutations and undergoes natural selection. Sustained RNA replication and Darwinian evolution were achieved in artificial cell-like compartments, which prevent the accumulation of deleterious mutations and the takeover by parasitic RNAs that exploit replicase-encoding “host” RNAs.

We have performed multiple evolution experiments using the system in a serial transfer format (i.e., repeated cycles of replication, dilution, and nutrient replenishment). In one experiment using water-in-oil emulsions, a clonal RNA replicator population diversified into quasi-stable, coexisting lineages, forming an ecosystem of up to five RNA species with diverse interactions (Mizuuchi et al., Nat. Commun., 2022). This ecosystem included a highly cooperative replicator that helped replicate all other members, along with parasitic RNAs, both of which appeared essential for maintaining the ecosystem. In another experimental evolution, two cooperating RNA replicators, each expressing either a replicase or a metabolic enzyme, integrated into a single, longer RNA, forming a primitive chromosome-like structure capable of independent replication (Ueda et al., PLOS Genet., 2023).

We are now extending these studies in two directions. One focuses on how novel functions could evolve in RNA replicators. The other explores more realistic primitive cell structures. We found that liquid–liquid phase-separated droplets, previously combined with the RNA replication system (Mizuuchi & Ichihashi, Chem. Commun., 2020), supported RNA evolution, at least in part. Overall, our studies demonstrate diverse evolutionary dynamics in simple molecular systems, providing insights into the emergence of living systems.

Adaptive architecture of complex traits in Drosophila

Dr. Neda Barghi[1]
[1]Max Planck Institute for Evolutionary Biology, Plön, Germany

S47 - The interplay between genetic architecture and the evolution of biodiversity

MEETING ROOM 117, August 19, 2025, 11:00 AM - 1:00 PM

Most traits are under natural selection, highly heritable and complex, with many underlying segregating loci, each with a small effect. It is therefore reasonable to assume that adaptation of these complex traits requires small changes in the frequencies of many of the underlying alleles, i.e. polygenic adaptation. There is ample theoretical work addressing the genomic and phenotypic responses of populations at the onset of environmental change. However, there is limited empirical evidence to confirm these predictions. Moreover, different populations can use different alleles to reach the same trait optimum. This is genetic redundancy, a characteristic of polygenic adaptation which could result in non-parallel signatures of adaptation across populations. First, I will demonstrate how phenotypic and time-series genomic data from experimental evolution in highly replicated Drosophila populations can be used to identify polygenic adaptation despite genetic redundancy. Next, I will describe evolution experiments under conditions similar to those assumed in theoretical models. Using time-series, high-throughput phenotypic data across replicated experimental populations we characterized the phases of polygenic adaptation empirically. The empirical inference of the directional and stabilizing phases of polygenic adaptation confirms the theoretical predictions and sheds light on characteristics of the loci that contribute to adaptive phenotypic evolution during different phases of adaptation, such as the degree of pleiotropy. Overall, evolution experiments can provide evidence of polygenic adaptation over short evolutionary timescales.

The Evolution of Polymorphic Mimicry and Supergenes in Butterflies

Prof. Krushnamegh Jagannath Kunte[1], Dr. Riddhi Deshmukh, Dr. Saurav Baral, Ms. Muktai Kuwalekar, Dr. Athulya Kizhakke
[1]National Centre For Biological Sciences TIFR, Bengaluru, India

S47 - The interplay between genetic architecture and the evolution of biodiversity

MEETING ROOM 117, August 20, 2025, 10:30 AM - 12:30 PM

Evolution of adaptive novelty is often facilitated by strong selection, a versatile genetic toolbox, and dynamic developmental genetic mechanisms that rapidly evolve to regulate new phenotypes. In this talk I will present a broad overview of Batesian mimicry as a key adaptation in a diverse model clade, the Papilio swallowtail butterflies. Using phylogenetic and genetic analysis, I will specifically provide detailed insights into the evolution of genetic (allelic) variants, genetic dominance, gene networks, and genotype-phenotype relationships that underpin the complex mimicry found in the Oriental Papilio polytes species group. A large inversion around doublesex, the mimicry gene, acts as a partial supergene, producing a protective and constraining genetic architecture that allows non-mimetic and mimetic forms to co-exist, without producing many maladaptive intermediates. The allelic variants of the supergene employ different gene networks to produce alternative mimetic and non-mimetic wing colour patterns. Thus, this work will provide a comprehensive understanding of how strong selection for mimicry, genetic architecture, genetic dominance, and developmental flexibility, produce a complex ecological polymorphism.

The maintenance and detection of sexually antagonistic genetic variation

Dr. Karl Grieshop[1]
[1]University of East Anglia, Norwich, United Kingdom

S48 - The maintenance of adaptive polymorphisms

MEETING ROOM 122+123, August 20, 2025, 10:30 AM - 12:30 PM

The modern debate over the maintenance of genetic variance in fitness is often framed around the relative contribution of mutation-selection balance versus balancing selection. In this talk I aim to encourage a more nuanced framework for this debate. I show that polymorphisms under antagonistic mutation-selection balance (e.g. sexual antagonism) will yield higher allele frequencies, greater fitness variance, and longer transit times to fixation than those under simple mutation-selection balance. Such genetic trade-offs can result in stable polymorphism but may or may not result in long-term balancing selection. I present genomic and transcriptomic evidence from Drosophila melanogaster that supports this notion, and I point out areas of needed theoretical and empirical work. I conclude that the concept of long-term balancing selection has been an unsuitably high bar for assessing whether genetic trade-offs can maintain genetic variance in fitness. I suggest this classic debate be reframed around the relative contribution of i) simple mutation-selection balance with ubiquitously deleterious alleles, ii) antagonistic mutation selection balance where alleles have context-dependent fitness effects, and iii) long-term balancing selection owing to various mechanisms (of which genetic trade-offs are one). I argue that antagonistic mutation selection balance is the most plausible and widespread of these.

How does plant chemodiversity evolve? Testing five hypotheses in one population genetic model

Prof. Meike Wittmann[1], Prof. Andrea Bräutigam
[1]Bielefeld University

S48 - The maintenance of adaptive polymorphisms

MEETING ROOM 122+123, August 21, 2025, 10:30 AM - 12:30 PM

Plant chemodiversity, the diversity of plant specialized metabolites, is an important dimension of biodiversity. One aspect of chemodiversity is that in many plant species, individuals produce different sets of metabolites and in different quantities. In many cases, such polymorphisms have a genetic basis. So far, there are few mathematical models to test verbal hypotheses on how this chemodiversity evolved. Here we develop such a model to test predictions of five hypotheses: the "fluctuating selection hypothesis", the "dominance reversal hypothesis", the interaction diversity hypothesis, the synergy hypothesis, and the screening hypothesis. We build a population genetic model of a plant population attacked by herbivore species whose occurrence fluctuates over time. We study the model using mathematical analysis and individual-based simulations. As predicted by the "dominance reversal hypothesis", chemodiversity can be maintained if alleles conferring a defense metabolite are dominant with respect to the benefits, but recessive with respect to costs. However, even smaller changes in dominance can maintain polymorphism. Moreover, our results underpin and elaborate predictions of the synergy and interaction diversity hypotheses, and, to the extent that our model can address it, the screening hypotheses. By contrast, we found only partial support for the "fluctuating selection hypothesis". In summary, we have developed a flexible model and tested various verbal models for the evolution of chemodiversity. Next, more mechanistic models are needed that explicitly consider the organization of metabolic pathways.

Noise leads to the perceived increase in evolutionary rates over short time scales

Dr. Jeremy Michael Beaulieu[1], Dr. Brian O'Meara[1]
[1]University Of Arkansas, Fayetteville, United States

S49 - Time-dependency in micro- and macroevolutionary rates

MEETING ROOM 122+123, August 19, 2025, 11:00 AM - 1:15 PM

Across a variety of biological datasets, from genomes to conservation to the fossil record, evolutionary rates appear to increase toward the present or over short time scales. This has long been seen as an indication of processes operating differently at different time scales, even potentially as an indicator of a need for new theory connecting macroevolution and microevolution. Here we introduce a set of models that assess the relationship between rate and time and demonstrate that these patterns are statistical artifacts of time-independent errors present across ecological and evolutionary datasets, which produce hyperbolic patterns of rates through time. We will show that plotting a noisy numerator divided by time versus time leads to the observed hyperbolic pattern; in fact, randomizing the amount of change over time generates patterns functionally identical to observed patterns. Ignoring noise can not only obscure true patterns but create novel patterns that have long misled scientists. We will also briefly discuss the need for a broader term for noise (i.e., tip fog), and then present new methods for dealing with tip fog in a variety of phylogenetic comparative methods, even when the underlying variation is not actually measured.

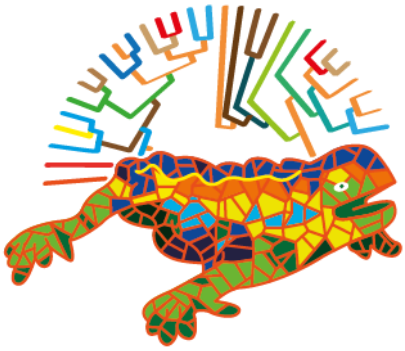
The symbiotic origin of the eukaryotic cell

Dr. Puri Lopez-Garcia[1]
[1]CNRS & Université Paris-Saclay, Gif-sur-Yvette, France

S50 - Unraveling the origin of eukaryotes: integrating prokaryotic and eukaryotic perspectives

MEETING ROOM 129+130, August 21, 2025, 3:30 PM - 5:00 PM

The origin of the eukaryotic cell, eukaryogenesis, was a unique evolutionary event that led to the emergence of complex cells from simpler ancestors. Eukaryotes radiated from their heterotrophic Last Eukaryotic Common Ancestor (LECA), colonizing newly available ecological niches and acquiring diverse specific lifestyles. Current knowledge allows inferring a complex LECA, fully comparable to modern heterotrophic flagellated protists. How did it evolve? Although the endosymbiotic origin of mitochondria and chloroplasts from, respectively, Alphaproteobacteria and Cyanobacteria was clearly established more than four decades ago, the origin of the host to those bacteria remained elusive for a long time. Until recently, the most accepted scenario involved the evolution of an independent lineage of proto-eukaryotes sister to archaea and endowed with an endomembrane system, including a nuclear compartment, a developed cytoskeleton and phagocytosis, as the host for the alphaproteobacterial ancestor of mitochondria. However, the discovery by metagenomic and cultural approaches of Asgard archaea, which harbor many genes in common with eukaryotes and are their closest relatives in phylogenomic trees, supports scenarios based on the symbiosis of one Asgard-like archaeon and one or more bacteria at the origin of the eukaryotic cell. Environmental information, cultural evidence and genomic inferences suggest that these symbioses between Asgard archaea and their bacterial partner(s) were based on syntrophic interactions. Here, I will briefly review the discoveries that led to this conceptual shift, evoking current models and the challenges ahead to establish a detailed, plausible scenario of eukaryogenesis.



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JMS Prize and EUEA Award and Stearns Prize Winners Presentation Summaries

Correlated genomic patterns of introgression across space despite contrasting hybridization histories.

Dr. Matthew Farnitano[1,2], Dr. V. Alex Sotola[2,3], Dr. Keith Karoly[4], Dr. Andrea Sweigart[1]
[1]University Of California San Deigo, La Jolla, United States, [2]University of Georgia, Athens, United States, [3]SUNY Oneonta, Oneonta, United States, [4]Reed College, Portland, United States

Stearns Prize Symposium

MEETING ROOM 117, August 21, 2025, 10:30 AM - 12:30 PM

When lineages hybridize, the extent of introgression varies across time, across populations, and across genomic loci. Yet, we still know little about the ecological, demographic, and selective forces that shape this variation. Through a comparison of geographically disparate contact zones, we investigate the scope of parallelism in patterns of genomic ancestry within the model species pair Mimulus guttatus and Mimulus nasutus. In addition, we take advantage of known candidate loci and QTL for premating and postmating reproductive barriers between these species to ask how well trait mapping approaches predict patterns of ancestry in wild hybridizing populations. We find that the extent and timing of introgression varies considerably both among and within geographic areas. Parallelism in patterns of genomic ancestry is strongest for geographically proximal groups but remains significant even for populations separated by ~1000km. We find evidence for the selective filtering of introgressed alleles from more admixed to less admixed groups, providing a window into the adaptive introgression process. Finally, we see mixed evidence for a correspondence between known reproductive isolation candidate loci and introgression outliers. We discuss reasons for this lack of strong correspondence, including intra- and interpopulation variation and fluctuating selection pressures. Overall, our findings highlight the complexity of factors shaping hybridization patterns, and argue for the complementarity of different approaches to studying reproductive isolation.

Why do closely related species that live together differ in colour?: Experimental examinations of the drivers of signal divergence and the forces that influence signal efficacy

Dr. Haley Kenyon[1]
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Stearns Prize Symposium

MEETING ROOM 117, August 21, 2025, 10:30 AM - 12:30 PM

Signals like colour patterns mediate interactions among animals that live together. Specifically, colour pattern divergence is widespread among closely related species that co-occur; this pattern is commonly thought to result from the role that this signal plays in species recognition, enabling individuals to distinguish members of their own species (conspecifics) from other species (heterospecifics). We still, however, have much to learn about the selective pressures that drive this pattern and how they interact with other forces that influence signal efficacy. Specifically, the importance of signal divergence for coexistence remains controversial due to the idea that species recognition can be enhanced in the absence of selection for signal divergence, simply through learned responses to heterospecifics or the evolution of refined species discrimination in areas of co-occurrence. Here, I present a suite of field experiments designed to test whether colour pattern divergence reduces costly interactions between closely related bird species, chickadees (genus: Poecile), where sympatric species differ more in colour pattern than allopatric species. I examine the influence of colour differences on the responses of naïve, allopatric birds to their congeners in both aggressive and mating interactions, and subsequently compare these responses to those of birds with experience with heterospecifics (i.e., in sympatry). I show that while colour pattern differences alone can reduce certain costly interactions in ways that could drive signal evolution, experience with heterospecifics is necessary for colour pattern divergence to effectively reduce costly interactions in other contexts.

Genetic architecture of multiple mutualisms and mating system in Turnera ulmifolia

Dr. Jason Laurich[1,2], Christopher Reid[2], Caroline Biel[2], Tianbi Wu[2], Christopher Knox[2], Dr. Megan Frederickson[2]
[1]University Of Guelph, Guelph, Canada, [2]University of Toronto, Toronto, Canada

Stearns Prize Symposium

MEETING ROOM 117, August 21, 2025, 10:30 AM - 12:30 PM

Plants often associate with multiple arthropod mutualists. These partners provide important services to their hosts, but multiple interactions can constrain a plant's ability to respond to complex, multivariate selection. Here, we quantified patterns of genetic variance and covariance among rewards for pollination, biotic defence and seed dispersal mutualisms in multiple populations of Turnera ulmifolia to better understand how the genetic architecture of multiple mutualisms might influence their evolution. We phenotyped plants cultivated from 17 Jamaican populations for several mutualism and mating system-related traits. We then fit genetic variance-covariance (G) matrices for the island metapopulation and the five largest individual populations. At the metapopulation level, we observed significant positive genetic correlations among stigma-anther separation, floral nectar production and extrafloral nectar production. These correlations have the potential to significantly constrain or facilitate the evolution of multiple mutualisms in T. ulmifolia and suggest that pollination, seed dispersal and defence mutualisms do not evolve independently. In particular, we found that positive genetic correlations between floral and extrafloral nectar production may help explain their stable coexistence in the face of physiological trade-offs and negative interactions between pollinators and ant bodyguards. Locally, we found only small differences in G among our T. ulmifolia populations, suggesting that geographic variation in G may not shape the evolution of multiple mutualisms.

Evolution of intraspecific floral variation in a generalist–specialist pollination system

Dr. Marion Leménager[1], John L. Clark[2], Silvana Martén-Rodríguez[3], Abel Almarales-Castro[4], Simon Joly[1,5]
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Stearns Prize Symposium

MEETING ROOM 117, August 21, 2025, 10:30 AM - 12:30 PM

Intraspecific processes influence macroevolutionary patterns through individual variation, selection, and ecological strategies. The niche variation hypothesis suggests that generalist species exhibit greater morphological variation due to either relaxed selection or the presence of diverse specialists within a species.
To test this, we examined floral morphology in Antillean Gesneriaceae, a tropical plant group that has repeatedly transitioned between hummingbird-specialist and generalist pollination systems. We used geometric morphometrics to quantify corolla shape and compared intraspecific variance between specialists and generalists within a phylogenetic framework.
Three analytical approaches were applied, each accounting for the high dimensionality of morphological traits, the evolutionary history, and variance estimation error in different ways.
Results partially support the niche variation hypothesis: generalists tend to show more variation in corolla tubularity, but not in curvature. Accounting for sampling error reduced support for the hypothesis, underscoring the need for larger datasets.
This study highlights how pollination strategy shapes intraspecific morphological variation, and how such variation contributes to macroevolutionary patterns. It also emphasizes the reciprocal influence between plant morphology and pollinator interactions across biodiversity scales.

Pronounced differentiation on the Z chromosome and parts of the autosomes in crowned sparrows contrasts with mitochondrial paraphyly: implications for speciation

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Stearns Prize Symposium

MEETING ROOM 117, August 21, 2025, 10:30 AM - 12:30 PM

When a single species evolves into multiple descendent species, some parts of the genome can play a key role in the evolution of reproductive isolation while other parts flow between the evolving species via interbreeding. Genomic evolution during the speciation process is particularly interesting when major components of the genome—for instance sex chromosomes vs. autosomes vs. mitochondrial DNA—show widely differing patterns of relationships between three diverging populations. The golden-crowned sparrow (Zonotrichia atricapilla) and the white-crowned sparrow (Zonotrichia leucophrys) are phenotypically differentiated sister species that are largely reproductively isolated despite possessing similar mitochondrial genomes, likely due to recent introgression. We assessed variation in more than 45,000 single nucleotide polymorphisms (SNPs) to determine the structure of nuclear genomic differentiation between these species and between two hybridizing subspecies of Z. leucophrys. The two Z. leucophrys subspecies showed moderate levels of relative differentiation and patterns consistent with a history of recurrent selection in both ancestral and daughter populations, with much of the sex chromosome Z and a large region on the autosome 1A showing increased differentiation compared to the rest of the genome. The two species, Z. leucophrys and Z. atricapilla, show high relative differentiation and strong heterogeneity in the level of differentiation among various chromosomal regions, with a large portion of the sex chromosome (Z) showing highly divergent haplotypes between these species. Studies of speciation often emphasize mitochondrial DNA differentiation, but speciation between Z. atricapilla and Z. leucophrys appears primarily associated with Z chromosome divergence and more moderately associated with autosomal differentiation, whereas mitochondria appear highly similar due apparently to recent introgression. These results add to the growing body of evidence for highly heterogeneous patterns of genomic differentiation during speciation, with some genomic regions showing lack of gene flow between populations many hundreds of thousands of years before other genomic regions.

Single cells to microbiome perspective of bacterial adaptations

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Stearns Prize Symposium

MEETING ROOM 117, August 21, 2025, 10:30 AM - 12:30 PM

Bacteria indulge in complex social behaviours such as cooperation, competition, biofilm formation, chemotaxis, swarming motility, predation, colonisation resistance and niche differentiation etc. Behaviours are often mediated by secretion of molecules either extracellularly or intracellularly, that act as toxins, metabolites for nutrient uptake, antimicrobials for competition, and signalling etc. Bacteria adapt their behaviours in response to chemical cues, like signals from neighbours and competitors, nutrients, and their intrinsic metabolic state. Firstly, I investigated whether differences in microenvironment can spur phenotypic heterogeneity within populations. For this I studied metabolite gene expression in Pseudomonas aeruginosa at the single cell level. Our results revealed that individual cells synchronise their behaviour as signalling increases in the environment. Subsequently, adaptations can be phenotypic as well as genotypic. In the clinical context, antimicrobial resistance is one such adaptation, that is a public health problem. In search for alternatives, I investigated the potential of predatory bacterium Bdellovibrio bacteriovorus against Escherichia coli as prey, using experimental evolution. Our results revealed that prey adapts in the presence of predator by acquiring resistance via genetic mutations, that primarily affect the outer membrane of individual cells. Ultimately, bacteria often reside in complex communities called microbiomes where interactions between species and host functions, drive bacterial adaptations. A diverse microbiome is considered healthy and can be leveraged to cure diseases. I am using faecal microbiota transplantation to establish colonisation resistance to eliminate the human enteric pathogen Clostridioides difficile. To further understand the adaptations of this pathogen in a diseased state, I performed an in-vivo experimental evolution in mice. Our results reveal that long-term pathogen survival is driven by mutations in the nutrient uptake pathways. Altogether, my research explores the phenotypic and genotypic adaptations of bacterial behaviours, and underlines that a single cell to microbiome approach is key towards understanding its complexities.

Challenging a host–pathogen paradigm: Susceptibility to chytridiomycosis is decoupled from genetic erosion

Dr. Donal Smith[1]
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Stearns Prize Symposium

MEETING ROOM 117, August 21, 2025, 10:30 AM - 12:30 PM

The putatively positive association between host genetic diversity and the ability to defend against pathogens has long attracted the attention of evolutionary biologists. Chytridiomycosis, a disease caused by the chytrid fungus Batrachochytrium dendrobatidis (Bd), has emerged in recent decades as a cause of dramatic declines and extinctions across the amphibian clade. Bd susceptibility can vary widely across populations of the same species, but the relationship between standing genetic diversity and susceptibility has remained notably underexplored so far. Here, we focus on a putatively Bd-naive system of two mainland and two island populations of the common toad (Bufo bufo) at the edge of the species' range and use controlled infection experiments and dd-RAD sequencing of >10 000 SNPs across 95 individuals to characterize the role of host population identity, genetic variation and individual body mass in mediating host response to the pathogen. We found strong genetic differentiation between populations and marked variation in their susceptibility to Bd. This variation was not, however, governed by isolation-mediated genetic erosion, and individual heterozygosity was even found to be negatively correlated with survival. Individual survival during infection experiments was strongly positively related to body mass, which itself was unrelated to population of origin or heterozygosity. Our findings underscore the general importance of context-dependency when assessing the role of host genetic variation for the ability of defence against pathogens.

Reproductive isolation via divergent genital morphology due to cascade reinforcement in Ohomopterus ground beetles

Dr. Tian Xia[1]
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Stearns Prize Symposium

MEETING ROOM 117, August 21, 2025, 10:30 AM - 12:30 PM

Secondary contact between incipient species and selection against maladaptive hybridization can drive reinforcement between populations in contact and result in reproductive character displacement (RCD). Resultant divergence in mating traits within a species may generate downstream reproductive isolation between populations with displaced and non-displaced traits, referred to as the cascade reinforcement hypothesis. We examined this hypothesis using three allopatric populations of the ground beetle Carabus maiyasanus with a genital lock-and-key system. This species shows RCD in male and female genital morphologies in populations in contact with the sister species C. iwawakianus. In a reciprocal mating experiment using three allopatric populations with differences in male and female genital sizes, insemination failure increased as the difference in genital size increased. Based on the reproductive isolation index, insemination failure was the major postmating-prezygotic isolation barrier, at least in one population pair with comparable total isolation to those of other species pairs. By contrast, there was only incomplete premating isolation among populations.
These results suggest that RCD in genital morphologies drives incipient allopatric speciation, supporting the cascade reinforcement hypothesis. These findings provide insight into the roles of interspecific interactions and subsequent trait diversification in speciation processes.

Evolutionary interplay between male-killing symbionts and insects

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JMS Prize and EUEA Award Winners Symposium

PLENARY SESSION (114-117), August 22, 2025, 10:30 AM - 12:30 PM

Symbiosis represents a transformational agent of evolutionary change that lies at the very root of all eukaryotic life. Whilst symbioses are conceptualised as interactions arising during a host's lifetime, arthropods, such as insects, frequently harbour microbial symbionts that are passed from mother to offspring. These maternally inherited symbionts are selected for their mutualistic contributions, as a healthy host ensures successful transmission. However, such symbionts can also act parasitically. Parasitic phenotypes are driven by the maternal transmission of these symbionts, which makes male hosts a 'dead end'. This lack of transmission through males often leads to the evolution of reproductive parasitism, wherein symbionts manipulate host reproduction to favour the production and survival of female hosts.

One common outcome is the male-killing (MK) phenotype, in which male offspring of infected mothers die during development. Remarkably, heritable male killers are widespread among insects, yet the mechanistic basis of MK and its evolutionary consequences have remained largely unresolved.

Here, I present three key findings:

1. MK mechanisms vary across divergent symbiont and host lineages, providing evidence of convergent evolution.

2. MK phenotypes induced by the endosymbiotic bacterium Wolbachia are mediated by multiple genes located in prophage WO regions, indicating that MK can represent an extended phenotype arising from complex interactions between bacteriophage, bacterium, and host.

3. The interplay between MK symbionts and their hosts exhibits features of an evolutionary arms race: while hosts evolve suppressors to silence symbiont-induced MK, symbionts in turn acquire novel strategies to evade suppression and re-establish MK.

Building on these findings, I discuss how MK has diversified mechanistically and how insect biology is, in many elements, shaped by their evolutionary interactions with MK symbionts.

From chromosomal inversions to sex chromosomes: how deleterious mutations shape recombination landscapes

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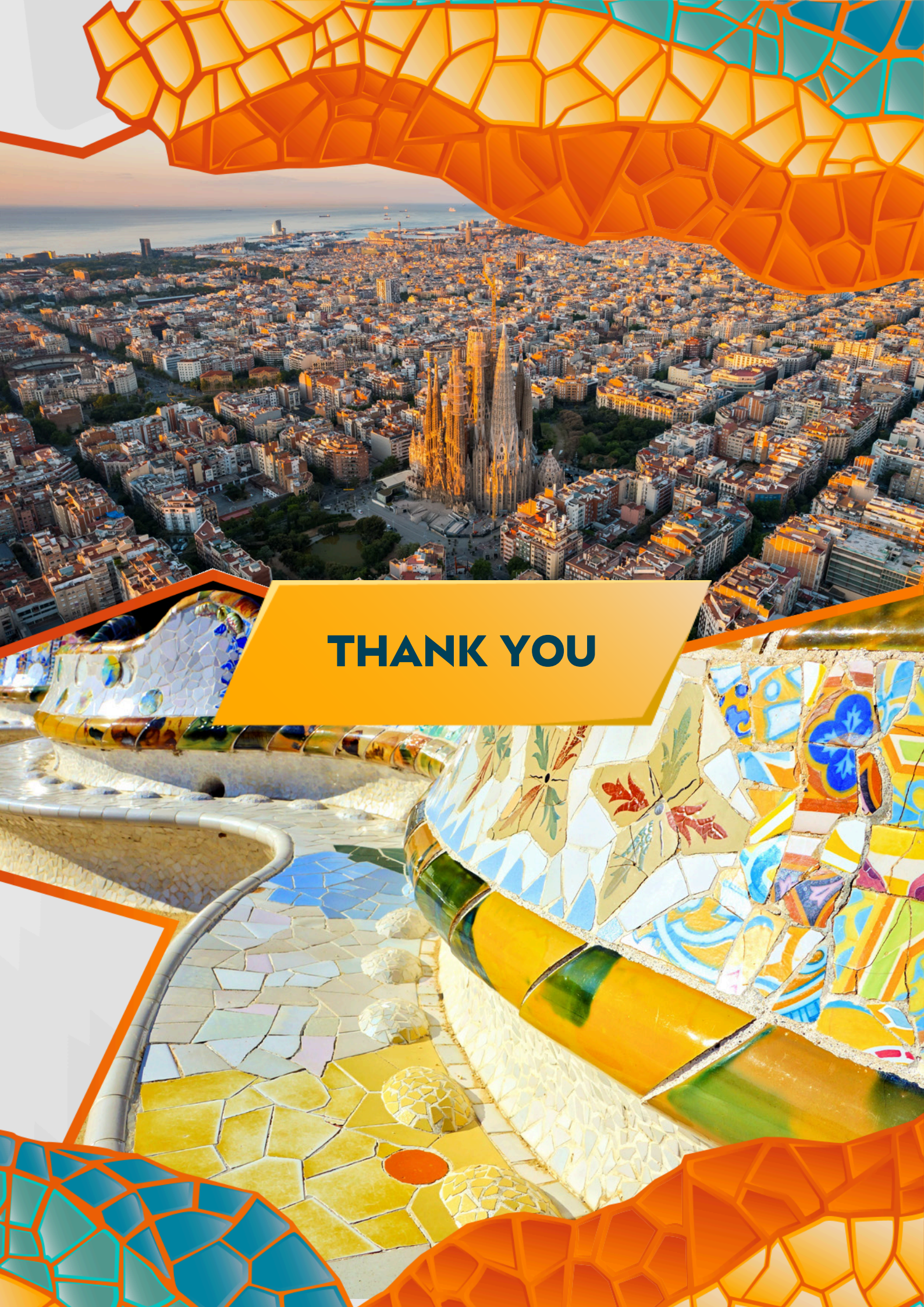
Recombination is a ubiquitous and fundamental evolutionary force, long theorized to facilitate the purging of deleterious mutations and the formation of beneficial allele combinations. Yet across the tree of life, some of the most intriguing genomic regions consistently defy this norm by exhibiting recombination suppression, either entirely or between specific haplotypes. Textbook examples notably include centromeres, sex chromosomes, supergenes, major histocompatibility loci, self-incompatibility loci, and mating-type chromosomes. Why does this happen, and what are the evolutionary consequences? In this talk, I will explore recent theoretical models revealing how deleterious mutations can drive the evolution of recombination suppression, particularly in sex chromosomes and around loci under balancing selection. I will then turn to empirical evidence from Heliconius butterflies, fungi, and humans, showing how mutation load shapes the long-term fate of non-recombining regions. Together, these findings shed new light on why recombination varies across genomes—and how this variation may influence the evolutionary trajectories of species.



THANK YOU