European Society for Evolutionary Biology

ORAL PRESENTATION ABSTRACTS AND LIST OF POSTERS

12th Congress, Turin, Italy, 24 -29 August 2009

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Symposia

Plenary Lectures

Location: Aula Magna

1. Tuesday August 25
   Hanna Kokko, University of Helsinky, Finland
   "From individuals to populations... and back"
2. Wednesday August 26
   Massimo Pigliucci, Stony Brook University, New York, United States
   "Is there a coming new evolutionary synthesis?"
3. Thursday August 27
   Ian Tattersall, American Museum of Natural History, New York, United States
   "Human evolution and the human biological future"
4. Friday August 28
   Cristina Vieira, CNRS, Université Lyon 1, France
   "Transposable elements and genome evolution"
5. Saturday August 29
   John N. Thompson, University of California at Santa Cruz, United States
   "Coevolution on our rapidly changing earth"

JOHN MAYNARD SMITH PRIZE LECTURE

Wednesday August 26
Tanja Schwander, Simon Fraser University, Burnaby, Canada
"Evolution of genetic caste determination in social insects"

FROM INDIVIDUALS TO POPULATIONS... AND BACK

Hanna Kokko [1,2], Michael Jennions [2], Andrés López-Sepulcre [3], Ken Norris [4], Daniel J. Rankin [5], Katja U. Heubel [1]

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[3]University of California, Department of Biology, Riverside, United States
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This ESEB conference hosts a total of nine symposia that mention the word ‘ecology’ in their title or topic description, and this figure probably rises further when all their abstracts are taken into account. Nevertheless, I will argue that ecology is all too often ignored, or treated in a superficial way, when explaining evolutionary phenomena, and that this can lead to misleading arguments or conclusions. I will discuss three case studies — one theoretical, and two empirical — where proper understanding of evolutionary ecology either sheds new light on old questions or raises new exciting issues. The key theme is that if we consider selectively important traits they should show up in the life history of a population, thus evolutionary change is probably reflected in population dynamics too. Changed dynamics in turn can select for different behaviours or life-history traits (ecogenetic feedback).

As my first example I will consider sex roles and parental care evolution, where recent theoretical work has highlighted that old explanations may have been jumping to conclusions too quickly, and evolving population-wide sex ratios may have more explanatory power than previously thought.

Thereafter, I will discuss competition for breeding sites in an endangered bird species (the Seychelles magpie robin) and show that individual-level selection may promote behaviours that are detrimental enough for species-level survival that they should be taken into account in conservation management.

My final example is an extreme case of ‘unintelligent design’: a gynogenetic, asexual fish, the Amazon molly. This species reproduces asexually (and hence produces no males) but still requires sperm to trigger embryogenesis. As a consequence, it can only live in sympatry with sexual ‘host’ species, which it however tends to replace ecologically, thus promoting its own local extinction. This leads to very complicated dynamics that eventually raises an intriguing question from the host species point of view: can mate choice ever be group selected?

IS THERE A COMING NEW EVOLUTIONARY SYNTHESIS?

Massimo Pigliucci [1]

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Modern evolutionary biology began with the publication of Charles Darwin's Origin of Species in 1859. Since then, two major reassessments of the theory have taken place: the neo-Darwinian turn at the end of the 19th century (which definitely excluded Lamarckism), and the Modern Synthesis of the 1930s and '40s (which reconciled Mendelism, statistical genetics and Darwinism). For years now scholars have been hinting at the necessity of a new Extended Synthesis, building on the conceptual framework laid out during the middle of the 20th century while incorporating new empirical findings and theoretical advances that have occurred since. In this talk I sketch how the Extended Synthesis is beginning to shape, with contributions from fields such as evo-devo, genomics, ecology and complexity theory, and with the incorporation of new concepts like phenotypic plasticity, modularity and evolvability. There is much intellectual ferment in the field, and this is an exciting time to be an evolutionary biologist!

HUMAN EVOLUTION AND THE HUMAN BIOLOGICAL FUTURE

Ian Tattersall [1]

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Major innovations in hominid biology and culture have been highly sporadic, conflicting with the received notion that human evolution, and particularly the attainment of the unique human symbolic mind, was essentially a matter of long-term, generation-by generation burnishing by natural selection. Natural selection can only operate on entire integrated individuals, and brain size increase in human evolution may well reflect the preferential success of larger-brained species in a diverse hominid family rather than generation-by-generation augmentation of intelligence in a single central lineage. This makes it both necessary and possible to suggest a more plausible mechanism than simple selective pressure for the unprecedented transition of *Homo sapiens* from a nonsymbolic and nonlinguistic precursor condition to its unprecedented cognitive status today: a mechanism involving both exaptation and emergence, the process whereby a new and unanticipated level of complexity may be achieved through a random coincidence of acquisitions. Not only does this change our view of the past, but it also has implications for the human biological future.

Keynote

TRANSPOSABLE ELEMENTS AND GENOME EVOLUTION

Cristina Vieira [1]

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We learned recently that the human genome is very poor in genes, with almost the same number as in fly. What is still more surprising is that most of our genetic material is considered as junk. How is it possible to spend so much energy to maintain this system? Maybe this "junk DNA" is in fact important, in different ways, to the genome evolution of species and populations? Transposable elements (TEs), which were initially called "jumping genes", belong to the class of non-genic DNA. These DNA sequences have the ability to jump (to transpose) inside genomes and represent an important part of these genomes. Although Barbara McClintock discovered them in the '50, it is only now that we are beginning to understand their effects. We know that they have a major role on gene regulation and on the stability of the chromatin (DNA and proteins). Moreover, since they are able to move, they are powerful mutagenic agents, which contribute to the variability and evolution of a genome. Increasing our knowledge on how the TEs are regulated within genomes and populations is thus fundamental to understand the impact of the environment on an individual genotype expression, and thus on the phenotype.

COEVOLUTION ON OUR RAPIDLY CHANGING EARTH

John N. Thompson [1]

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In recent years we have learned that coevolution is a much more dynamic and ongoing process than we previously suspected. Interacting species coevolve in ways that create constantly changing geographic mosaics of adaptation and counter-adaptation. These coevolutionary mosaics develop in laboratory microcosms within hundreds of generations, and they have now been observed to develop across natural communities within thousands of years, and sometimes within only a few hundred years. As we continue to alter all the major ecosystems on earth, we are creating the conditions for novel coevolutionary dynamics. We are only beginning to understand how coevolution during the early stages of coevolving interactions may differ from that observed in interactions that have coevolved for millions of years.

EVOLUTION OF GENETIC CASTE DETERMINATION IN SOCIAL INSECTS

Tanja Schwander [1]

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Understanding how a single genome can produce a variety of different phenotypes is of fundamental importance in genetics and developmental biology. One of the most striking examples of phenotypic plasticity is the female caste system found in ants and other eusocial insects, where different phenotypes are associated with reproduction (queen caste) or helping behaviour (worker castes).

A long-standing paradigm for caste determination was that female eggs are always totipotent with the important morphological and physiological differences between queens and workers stemming solely from a developmental switch during the larval stage under the control of nutritional and other environmental factors. However, there are an increasing number of examples showing genetic components to caste determination as well as maternal effects influencing the developmental fate of females.

I will present a broad overview of the studies providing strong direct and indirect evidence for a genetic component to caste differentiation and discuss factors that may have led to the evolution of genetically hardwired caste systems. In addition, I will argue that a purely environment- controlled caste system is very difficult to demonstrate and probably unlikely to occur. Detailed molecular analyses are likely to uncover additional cases of genetically-determined queen and worker determination and various degrees of genetic predispositions towards a particular caste.

Evolutionary systems biology

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Program

Tuesday August 25 - **Symposium 1**

Location: Room 1

Evolutionary systems biology

Organizers:	*Laurence Loewe, University of Edinburgh, United Kingdom* *Balazs Papp, Biological Research Center, Szeged, Hungary*

9.45 - 10.15	**LAURENCE D. HURST** (invited) “The EMBO Lecture” Noise abatement and genome evolution
10.15 - 10.45	**ROY KISHONY** (invited) Evolution of resistance in multi-drug space
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**RYSZARD KORONA** Genetic and environmental factors of fitness variation in yeast gene-deletion strains
11.35 - 11.55	**IVANA GUDELJ** Quantifying fitness in a public goods game
11.55 - 12.15	**CRAIG MACLEAN** The distribution of fitness effects of beneficial mutations in *Pseudomonas aeruginosa*
12.15 - 12.35	**PIERRICK LABBÉ** Resistance gene replacement in the mosquito *Culex pipiens*
12.35 - 13.35	*Lunch*
13.35 - 13.55	**STEPHEN S. FONG** Integration of Metabolic Modeling and Laboratory Evolution
13.55 - 14.15	**STEFAN SCHUSTER** Has molar yield in metabolic networks been maximized during evolution?
14.15 - 14.35	**STEFAN RICHTER** Exploring relatedness of proteins based on electrostatic properties - application to estimation of enzyme kinetic parameters
14.35 - 14.55	**JOHN F. BROOKFIELD** Statistical Properties of Evolved Gene Regulatory Networks- Feed Forward Loops in *Escherichia coli*
14.55 - 15.25	*Coffee break*

1-1 Oral

NOISE ABATEMENT AND GENOME EVOLUTION

Laurence D. Hurst [1], Nizar N. Batada [2], Balazs Papp [3], Karoly Kovacs [3], Araxi O. Urrutia [1]

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Noise in gene expression is inevitable, but is it selectively important? Here I approach the issue by asking whether genomes adapt to modify expression in noise. In particular I will show how clustering of essential genes in yeast into domains of open chromatin and co-linearity of metabolic genes in bacterial operons both are expected as noise abatement mechanisms. Both models have striking predictive ability. The operon model uniquely explains why co-linearity is strongest for lowly expressed operons and the essential gene noise minimization model correctly predicts the dearth of sub-telomeric essential genes and that noise levels should be predicted by the local density of essential genes. If selection to modify noise can determine gene order, noise must itself be selectively important.

1-2 Oral

EVOLUTION OF RESISTANCE IN MULTI-DRUG SPACE

Roy Kishony [1]

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The emergence of resistance during multi-drug chemotherapy impedes the treatment of many human diseases, including malaria, TB, HIV, and cancer. While certain combination therapies have long been known to be more effective in curing patients than single drugs, the impact of such treatments on the evolution of drug resistance is unclear. In particular, very little is known about how the evolution of resistance is affected by the nature of the interactions—synergy or antagonism—between the drugs. I will describe a combined theoretical-experimental approach to study the effect of antibiotic combinations on the evolution of resistance in bacteria. Our results indicate that synergistic drug pairs, typically preferred in clinical settings, actually accelerate bacterial adaptation. Drug antagonism, on the other hand, can generate selection against resistant bacteria, thereby slowing down the evolution of resistance. These results suggest a tradeoff in drug-combination therapy between immediate inhibition of growth and long-term inhibition of resistance.

1-3 Oral

GENETIC AND ENVIRONMENTAL FACTORS OF FITNESS VARIATION IN YEAST GENE-DELETION STRAINS

Ryszard Korona [1]

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Quantification and comprehension of phenotypic variation in terms of an interplay between genetic and environmental factors has been pursued for decades. This goal is no less important in the (post)genomics era because any analysis of genetic systems needs to take into account that they were shaped by natural selection evaluating fitness, an overall performance of phenotypes. We use a collection of yeast gene-deletions to determine distribution of fitness effects caused by single and multiple deletions in different laboratory environments. Our results show that beneficial mutations are much rarer and smaller in effect than deleterious ones confirming observations made previously with mutations of spontaneous origin and unknown nature. Deleterious mutations form bimodal distribution in which lethal and slightly negative effects greatly outnumber those of intermediate strength. The bimodality applies not only to an entire organism but also to particular cellular components and thus should be counted among basic features of genetic systems. Considering multiple factors, there is no evidence that environmental stress enlarges negative effects of mutations. Neither interactions between mutations aggravate fitness losses. On the contrary, interactions between genes and between genes and environment have a general alleviating effect. This is because an impairment inflicted upon the metabolism of a growing cell appears most harmful when growth is fastest irrespective whether the insult originates from a decline in quality of the external environment or from the deregulation of the internal environment. Theoretical models and empirical tests are needed to explain how this pattern is produced.

1-4 Oral

QUANTIFYING FITNESS IN A PUBLIC GOODS GAME

Ivana Gudelj [1], Ayari Fuentes-Hernandez [2], Craig MacLean [3], Duncan Greig [4], Laurence Hurst [2]

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The conditions favouring co-operation is one of the central problems in evolutionary biology. Hamiltonian framework is often used to explain when co-operation might or might not be favoured. However due to the difficulty associated with calculating the relevant parameters, it is difficult to use this approach to make quantitative predictions. Given advances in systems biology in yeast we propose that a next-generation quantitative modelling approach for studying evolution of cooperation may now be feasible.

Here we put forward a model approach that brings together systems biology and population genetics. Then we ask whether this model can make accurate quantitative predictions of fitness in a public goods game. Our system consist of two yeast strains, with only one strain secreting the enzyme invertase to catalyze the hydrolysis of the sucrose into glucose, the prefer carbon source of yeast. We use prior data on the biochemistry of the two yeast strains to parametrise the mathematical model and make numerous predictions regarding both absolute and relative fitness of invertase producers and non-producers under a variety of spatially structured experimental environments. Subsequently by performing experiments we show that the model has both strong qualitative and quantitative accuracy.

While Hamilton's rule has enormous impact in enabling predictions of general trends, we here show that an alternative framework can provide a next generation model that is suitable for quantitation of co-operation.

1-5 Oral

THE DISTRIBUTION OF FITNESS EFFECTS OF BENEFICIAL MUTATIONS IN *PSEUDOMONAS AERUGINOSA*

Craig MacLean [1], Angus Buckling [1]

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The distribution of fitness effects of spontaneous beneficial mutations is crucial to our understanding of adaptation by natural selection. Population genetic theory predicts that this distribution is exponential whenever fitness is high, suggesting that a mechanistic understanding of the fitness effects of beneficial mutations derived from systems biology may contribute little to our understanding of the properties of beneficial mutations. To test this idea, we used an experimental evolution approach involving adaptation to the antibiotic rifampicin in the opportunistic human pathogen *Pseudomonas aeruginosa*. As predicted by population genetic theory, the fitness effects of beneficial mutations are exponentially distributed when the fitness of the wild-type is high. However, when the fitness of the wild type is low, the fitness effects of beneficial mutations are no longer exponentially distributed because of a bias towards mutations of large effect. We show that this non-exponential distribution can be explained by a detailed structural understanding of the interactions that occur between rifampicin and RNA polymerase. This work shows how a detailed mechanistic understanding of genes under selection, in this case derived from structural biology, can be integrated with statistical population genetics to understand how beneficial mutations impact fitness. At a more applied level, our results suggest that systems biology approaches are critical for being able to predict the evolution of antibiotic resistance.

1-6 Oral

RESISTANCE GENE REPLACEMENT IN THE MOSQUITO *CULEX PIPIENS*

Pierrick Labbé [1], Michel Raymond [2], Mylène Weill [2], Nicolas Sidos [3], Thomas Lenormand [4]

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[2]CNRS, Université de Montpellier II, ISEM, Montpellier, France
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How adaptation appears and is later refined by natural selection has been the object of intense theoretical work. However the testing of these theories is limited by our ability to estimate the strength of natural selection in nature and to identify precisely its target at the molecular level. For some particular adaptations such as resistance to insecticide, it is now possible to bridge the knowledge from the genes implied in the adaptation to the dynamics observed in natural populations.

We will present here how we estimated the selection coefficients acting on different alleles at the same locus using long-term cline series. We specifically analysed the allele replacements observed in the insecticide resistance genes Ester and ace-1 in the mosquito *Culex pipiens* in the Montpellier area, southern France. Several alleles have been identified for both genes and the effect of these genes on the fitness of mosquitoes have been measured in the lab. More recently we managed to measure the fitness coefficients associated with the different alleles in natural populations. At the Ester locus, a first resistance allele appeared early, which was replaced by a second resistance allele providing the same advantage but at a lower cost, itself being replaced by a third resistance allele with both higher advantage and cost. At the ace-1 locus a different path has been followed which implies duplication of the gene.

More generally, we will discuss how the systemic understanding of the insecticide resistance, from the molecular mechanisms at the gene level to precise estimates of the strength of selection obtained from field data, help to understand more fully the process of adaptation.

1-7 Oral

INTEGRATION OF METABOLIC MODELING AND LABORATORY EVOLUTION

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One of the interesting and challenging aspects of biology is the fact that various biological components (genes, proteins, metabolites) are highly interconnected where small changes in a single component can influence many other components. This attribute of biology poses a particular challenge to understanding evolutionary biology where mechanistic changes can occur anywhere within the system to give rise to new phenotypes. One tool that can potentially facilitate the analysis of mechanistic changes occurring during biological evolution is a large-scale metabolic model of the system. This talk will cover the conceptual framework for constraint-based metabolic models, their relevance to evolutionary biology, and applications to studying laboratory evolution. Specifically, the benefits and limitations of using a large-scale metabolic model of *Escherichia coli* to study laboratory evolution and to analyze gene expression, metabolic flux, and genome re-sequencing data will be discussed. In addition, the combination of modeling, high-throughput data, and laboratory evolution to prospectively modify organism function for metabolic engineering applications will be presented.

1-8 Oral

HAS MOLAR YIELD IN METABOLIC NETWORKS BEEN MAXIMIZED DURING EVOLUTION?

Stefan Schuster [1]

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It is often been assumed that, during evolution, the network structure and kinetic properties of metabolic systems have changed so as to maximize the molar yield of biotransformations, that is, the conversion ratio between product (e.g. ATP or biomass) and substrate. This assumption underlies an approach to computing unknown fluxes, frequently called Flux Balance Analysis. Here, the relevance and applicability of that assumption are critically examined, and it is compared with the principle of maximizing pathway flux. We discuss diverse experimental evidence showing that, often, those biochemical pathways are operative that allow fast but low-yield synthesis of important products. Examples are provided by fermentation in *S. cerevisiae* and several other yeast species, as well as homolactic fermentation in *Lactobacillus plantarum*. Moreover, evolutionary game theory shows that organisms can be trapped in a Tragedy of the Commons, in which resources are not utilized economically. All this this leads us to the conclusion that maximization of molar yield is by no means a universal principle.

1-9 Oral

EXPLORING RELATEDNESS OF PROTEINS BASED ON ELECTROSTATIC PROPERTIES - APPLICATION TO ESTIMATION OF ENZYME KINETIC PARAMETERS

Stefan Richter [1], Matthias Stein [1], Razif R. Gabdoulline [1,2], Rebecca C. Wade [1]

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Protein molecular interaction fields like electrostatic potentials are key determinants of protein function. PIPSA (Protein Interaction Property Similarity Analysis) is a procedure to compare and analyze protein molecular interaction fields. For the calculation of protein similarity, first the protein electrostatic potential is calculated from the protein structure. From all-pairwise comparisons of the electrostatic potentials, similarity indices are calculated. These indices can then be used for clustering and visualization of proteins as epograms (tree-like diagrams showing electrostatic potential differences) or heat maps. This procedure is automated and can be used via the webPIPSA webserver (pipsa.eml.org).

PIPSA may assist in protein functional assignment, classification of proteins, the comparison of binding properties and the estimation of enzyme kinetic parameters. Depending on the rate limiting step of the enzyme reaction, the enzyme kinetic parameters can be correlated with differences in molecular interaction fields within a set of enzymes sharing the same structural fold. This allows the estimation of unknown kinetic parameters for proteins where the structure is known or can be modeled using comparative modeling approaches.

1-10 Oral

STATISTICAL PROPERTIES OF EVOLVED GENE REGULATORY NETWORKS - FEED FORWARD LOOPS IN *ESCHERICHIA COLI*

Max B. Cooper [1], John F. Brookfield [2], Matthew Loose [3]

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We present an approach to modelling the evolution of small gene regulation networks. When there is a need to convert an input gene expression pattern to an output gene expression pattern, populations can evolve many qualitatively different ways (different network architectures) to solve the same underlying problem. The relative frequencies with which these different network architectures are used constitute testable evolutionary predictions. This principle is illustrated through examination of Feed Forward Loops (FFLs) which are simple three-gene regulatory network motifs. They exist in different types, defined by the signs of the effects of genes in the motif on one another. We examine 36 feed forward loops in *Escherichia coli*, using evolutionary simulations to predict the forms of FFL expected to evolve to generate the pattern of expression of the output gene. These predictions are tested using likelihood ratios, comparing likelihoods of the observed FFL structures with their likelihoods under null models. The very high likelihood ratios generated, of over 1011, suggest that evolutionary simulation is a valuable component in the explanation of FFL structure.

1-1 Poster

A framework for evolutionary systems biology

LAURENCE LOEWE
University of Edinburgh, Centre for Systems Biology at Edinburgh, Edinburgh, United Kingdom

1-2 Poster

Systems biology of genetic interactions in yeast

BALAZS PAPP, BALAZS SZAPPANOS, CSABA PAL
Biological Research Center, Institute of Biochemistry, Szeged, Hungary

1-3 Poster

Within-species genetic and environmental variability of enzymatic kinetic parameters and concentrations

VICTOR SABARLY[1], CHRISTINE DILLMANN[2], ODILE BOUVET[3], ERICK DENAMUR[3], DOMINIQUE DE VIENNE[2]
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[3]*Université Paris 7 Denis Diderot INSERM U722, Faculté de Médecine, Paris, France*

1-4 Poster

A modular genomic architecture facilitates the repeated re-evolution of an adaptive phenotype in *Pseudomonas fluorescens*

CHRISTIAN KOST[1], ANDREW D. FARR[2], CAROLINE ROSE[2], GAYLE C. FERGUSON[2], HUBERTUS J. E. BEAUMONT[3], PAUL B. RAINEY[2]
[1]*Max Planck Institute for Chemical Ecology, Department of Bioorganic Chemistry, Jena, Germany*
[2]*Massey University New Zealand Institute for Advanced Study and Allan Wilson Centre for Molecular Ecology & Evolution, Auckland, New Zealand*
[3]*Leiden University, Institute of Biology Leiden, Leiden, The Netherlands*

1-5 Poster

Stochasticity in protein levels drives colinearity of gene order and enzymatic steps in metabolic operons of *Escherichia coli*

KÁROLY KOVÁCS[1], LAURENCE D. HURST[2], BALÁZS PAPP[1]
[1]*Biological Research Center Institute of Biochemistry, Szeged, Hungary*
[2]*University of Bath, Department of Biology and Biochemistry, Bath, United Kingdom*

1-6 Poster

Impact of hierarchical structure of transcriptional regulatory networks on the evolution of drug resistance

BALAZS BOGOS, ORSOLYA MÉHI, CSABA PÁL
HAS BRC, Institute of Biochemistry, Szeged, Hungary

1-7 Poster

Controlling the evolution of antimicrobial resistance in a single host

RAFAEL PENA-MILLER[1], ROBERT E. BEARDMORE[1], MARTIN ACKERMANN[2]
[1]*Imperial College, Mathematics, London, United Kingdom*
[2]*ETH-Zentrum, Theoretical Biology, Zurich, Switzerland*

1-8 Poster

Epistasis Between Antibiotic Resistance Mutations

SANDRA TRINDADE[1,2], ANA SOUSA[1], FRANCISCO DIONÍSIO[2], ISABEL GORDO[1]
[1]*Instituto Gulbenkian de Ciência, Oeiras, Portugal*
[2]*Faculdade de Ciências da Universidade de Lisboa, Departamento de Biologia Vegetal & Centro de Biologia Ambiental, Lisboa, Portugal*

1-9 Poster

Tempo and mode of compensatory evolution

ANA SOUSA, ISABEL GORDO
Instituto Gulbenkian de Ciencia, Oeiras, Portugal

1-10 Poster **Rule Based Modelling of Biochemical Networks**

ELAINE MURPHY, VINCENT DANOS
University of Edinburgh School of Informatics, Edinburgh, United Kingdom

1-11 Poster **Quantifying the robustness and evolvability of a developmental system**

CHRISTIAN BRAENDLE[1], CHARLIE BAER[2], MARIE-ANNE FELIX[3]
[1]University of Nice Sophia-Antipolis, Institute of Developmental Biology and Cancer, CNRS, Nice, France
[2]University of Florida, Department of Botany and Zoology, Gainesville, United States
[3]Universities of Paris 6/7, Institut Jacques Monod, CNRS, Paris, France

1-12 Poster **Canine genomics and the rapid generation of phenotypic diversity**

VIOLETA MUNOZ-FUENTES[1], CARLES VILA[2]
[1]Uppsala University, Department of Evolutionary Biology, Uppsala, Sweden
[2]Estacion Biologica de Donana-CSIC, Sevilla, Spain

1-13 Poster **Adaptive functions of melanin-based coloration, the role of melanocortins**

GUILLAUME EMARESI, ANNE-LYSE DUCREST, CÉLINE SIMON, ALEXANDRE ROULIN
University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

1-14 Poster **Robustness of Alternate Coding Tables - A Statistical Analysis**

TUGCE BILGIN[1], LEVENT M. KURNAZ[2], ISIL AKSAN KURNAZ[1]
[1]Yeditepe University, Department of Genetics and Bioengineering, Istanbul, Turkey
[2]Bogazici University, Physics Department, Istanbul, Turkey

1-15 Poster **New Paradigms for Modeling Long Term Evolution and Adaptations in Varying Selection Regimes: the elusive concepts of equiblibrium and optimality**

DAN COHEN
The Hebrew University in Jerusalem, Department of Evolution Systematics and Ecology E.S.E., Jerusalem, Israel

1-16 Poster **Fauceir Theory**

MATO NAGEL
Center for Nephrology and Metabolic Disorders, Molecular Genetic Laboratory, Weisswasser, Germany

1-17 Poster **Systems evolutionary analysis on the putative Hox transcriptional networks**

SOICHI OGISHIMA, HIROSHI TANAKA
Tokyo Medical and Dental University, Systems Biology and Evolution Group, Department of Bioinformatics, Tokyo, Japan

1-18 Poster **Phylogenetic analysis of genus *Salix***

JAROSLAV MRÁČEK, LUBOŠ ÚRADNÍČEK, SOŇA TICHÁ
Mendel University of Agriculture and Forestry in Brno, Department of Forest Botany, Dendrology and Geobiocoenology, Brno, Czech Republic

1-19 Poster **Nitrogen removal from landfill leachate by nitrification and denitrification**

TIBELA LANDEKA DRAGIČEVIĆ[1], MARIJANA ZANOŠKI HREN[1], ANA RUDE[1], JASMINA IBRAHIMPAŠIĆ[2]
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From the selfish gene to species extinction: levels of selection in evolution

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Program

Tuesday August 25 - **Symposium 2**

Location: Room 2

From the selfish gene to species extinction: levels of selection in evolution

Organizers:	*Daniel J. Rankin, University of Bern, Switzerland* *Kevin R. Foster, Harvard University, Cambridge, United States*

9.45 - 10.15	**SAMIR OKASHA** (invited) The Levels of Selection Question: some Philosophical Perspectives
10.15 - 10.45	**DAVID S. WILSON** (invited) Truth and reconciliation for group selection
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**JAN ENGELSTÄDTER** Quantifying species-level selection for sexual reproduction in aphids
11.35 - 11.55	**LISELOTTE SUNDSTRÖM** Are you my mother? Kin recognition in the ant *Formica fusca*
11.55 - 12.15	**DAVID R. NASH** Levels of selection across the mutualism-parasitism border
12.15 - 12.35	**LEONARD NUNNEY** Levels of selection in the age of genomics
12.35 - 13.35	*Lunch*
13.35 - 13.55	**HYWEL T.P. WILLIAMS** Community-level selection in simulated microbial ecosystems
13.55 - 14.15	**HENRIK H. DE FINE LICHT** From so simple a beginning: Enzymatic innovation in fungus-growing ants involved a transition from individual symbiont selection to colony-level selection
14.15 - 14.35	**LOUISE J. JOHNSON** Selfish genetic elements in animal development
14.35 - 14.55	**DANIEL J. RANKIN** Is species level selection a major force in evolution?
14.55 - 15.25	*Coffee break*

2-1 Oral

THE LEVELS OF SELECTION QUESTION: SOME PHILOSOPHICAL PERSPECTIVES

Samir Okasha [1]

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This paper addresses certain conceptual and philosophical issues that have arisen in the debate over levels of selection in evolution, which have caused confusion in the literature. My starting point is that for natural selection to occur at any given level of the biological hierarchy, there must exist a covariance between character and fitness at that level. However, this condition is not sufficient: it fails to distinguish 'genuine' selection at the level in question, i.e. a causal link between character and fitness, from character-fitness covariance that is a side effect of selection at a different level. I argue that this distinction provides the key to the levels of selection problem. A number of proposals for how to draw the distinction are critically examined, including an appeal to 'emergent properties'. I illustrate my ideas with examples drawn from a number of different areas of the levels of selection discussion.

2-2 Oral

TRUTH AND RECONCILIATION FOR GROUP SELECTION

David S. Wilson [1]

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Next year will mark the 35th anniversary of my involvement with the group selection controversy, which began much earlier. Why does a controversy such as this drag on so endlessly? To answer this question, we must examine the scientific process in addition to the narrow scientific issues. I am attempting to do this in a series of blogs on the Huffington Post titled "Truth and Reconciliation for Group Selection" (http://www.huffingtonpost.com/david-sloan-wilson/#blogger_bio). The blog format should not disguise my serious intent. I encourage audience members to read the blogs in preparation for a searching examination of the group selection controversy.

2-3 Oral

QUANTIFYING SPECIES-LEVEL SELECTION FOR SEXUAL REPRODUCTION IN APHIDS

Jan Engelstädter [1], Tanja Stadler [1]

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Despite the severe fitness costs it entails, sexual reproduction is almost ubiquitous in higher-level organisms. One class of hypotheses to explain this apparent paradox seeks to identify advantages of recombination that prevent asexual reproduction from spreading in a population. Alternatively, sex may be maintained in the long term through species-level selection. According to this view, genes conferring asexual reproduction may often be favored in the short term, spread and replace sexual reproduction within a species. However, because of long-term disadvantages, asexual species may suffer from a higher extinction rate than sexuals and are therefore rarely observed.

Support for this hypothesis comes from the 'twiggy' distribution of asexual species within clades of predominantly sexual species, but this has rarely been analyzed in detail. Here, we try to quantify species-level selection for sexual reproduction in aphids. Most aphid species (the "sexuals") reproduce through cyclic parthenogenesis (several asexual generations followed by round one sexual reproduction), but some species (the "asexuals") have lost the sexual part of the life-cycle. We constructed molecular phylogenies of several groups of aphids that contain species with both modes of reproduction. We then employed recently developed statistical methods to estimate extinction and speciation rates of sexuals and asexuals as well as transition rates from sex to asex and vice versa.

2-4 Oral

ARE YOU MY MOTHER? KIN RECOGNITION IN THE ANT *FORMICA FUSCA*

Sedeer El-Showk [1], Jelle van Zweden [2], Patrizia d'Ettorre [2], Liselotte Sundström [1]

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Interactions between members of cooperative groups often entail helping behaviour at a direct fitness cost to the helper. In social insects, helping is taken to its extreme, as workers trade personal reproduction for inclusive fitness returns from helping their mother rear collateral kin. Helping can only be directed towards kin if a mechanism for discriminating between kin and non-kin exists. Colony membership is generally used as a proxy for such recognition, but the question remains whether recognition also entails a genetic component, which would allow workers to discriminate between kin and non-kin regardless of colony affiliation. We investigated whether workers of *Formica fusca* can identify their mother in a cross-fostering design where workers were fostered with their mother, con-colonial workers, hetero-colonial queens, or hetero-colonial workers. We found that workers fostered with an unrelated queen or workers favoured their mother and their foster queen over an unfamiliar hetero-colonial queen, which suggests that recognition cues entail both environmental and genetic components. The cuticular chemistry supports this view, as workers maintain their colony integrity regardless of fostering regime, yet show moderations to their chemical profiles when exposed to different colony environments.

2-5 Oral

LEVELS OF SELECTION ACROSS THE MUTUALISM-PARASITISM BORDER

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Many butterflies in the family Lycaenidae have intimate associations with ants that range from facultative mutualism to obligate parasitism. The majority of species engage in apparently mutualistic interactions, but selection on individuals is expected to maximize the benefits that they gain from their association with ants, and to minimize the costs they pay, or in other words, to select for more parasitic interactions. However, very few interactions are overtly parasitic, and those lineages in which parasitism has evolved have arisen relatively recently, are mostly threatened with extinction, and have interactions that appear to be very inefficient. It is far from clear why efficient parasites do not appear frequently and persist over evolutionary time. I will argue that this pattern can be explained by a change in the importance of different levels of selection as the mutualism/parasitism border is traversed. Strong negative impacts on host populations are likely to lead to interdemic selection favouring mutualistic populations and selecting against efficient parasitism, so counteracting the direction of individual level selection. Levels of genetic viscosity of both ant and butterfly populations will be important in this process, leading to associations between dispersal and virulence. I will support my argument with comparative data on a range of lycaenids, concentrating on recent work on the parasitic large blue butterflies.

2-6 Oral

LEVELS OF SELECTION IN THE AGE OF GENOMICS

Leonard Nunney [1]

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Natural selection can act at any level of biological organization; however, we often distinguish three levels of selection: gametic; individual; plus some higher group level such as family or species. At the gametic (or gene) level the success of a gene copy can be increased through transmission distortion, at the individual level the success of a collection of interacting genes is mediated through the fitness of an individual phenotype, and at the group level the success is determined by the emergent properties of the group. Of these, gametic selection is generally the most efficient form of selection and this has important implications for genome evolution. Success of elements in the genome can be detrimental at the individual and group level, a process that can result in extinction unless limited by lineage selection driving the evolution of genome defense. Here I consider the potential contributions of individual and species level selection in this process.

2-7 Oral

COMMUNITY-LEVEL SELECTION IN SIMULATED MICROBIAL ECOSYSTEMS

Hywel T.P. Williams [1], Timothy M. Lenton [1]

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Here we use an abstract individual-based model of an evolving microbial ecosystem to explore community-level selection in artificial and natural selection scenarios. We perform artificial selection experiments on model ecosystems and observe a robust response, similar to that reported elsewhere for real microbial communities. The mechanisms of this response and the level at which adaptation occurred were unclear for the real communities — did the community-level selection process act implicitly on traits of individual species, or were higher-level traits genuinely being selected? Careful analysis allows us to elucidate the level of adaptation in our model system. We find that genuine community-level adaptation occurs in a significant fraction of cases. However, when the ecological problem posed by the artificial selection process can be easily solved by a single dominant species, it often is. In another series of experiments, we show that spatial structure and environmental feedbacks on growth can create conditions for a limited form of community-level natural selection to operate. Local communities that improve their environmental conditions achieve larger populations and are better colonizers of available space, whereas local communities that degrade their environment shrink and become susceptible to invasion. The spread of environment-improving communities has a genetic basis in environment-altering traits of individuals, even though these traits are neutral at the individual level. Overall, our modelling work shows that under certain conditions selection at the level of the community can be an important evolutionary mechanism.

2-8 Oral

FROM SO SIMPLE A BEGINNING: ENZYMATIC INNOVATION IN FUNGUS-GROWING ANTS INVOLVED A TRANSITION FROM INDIVIDUAL SYMBIONT SELECTION TO COLONY-LEVEL SELECTION

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Obligate mutualistic relationships are often inferred to be the result of higher levels of selection. However, because such mutualists consist of separate gene pools, innovative group-selected traits can only become established when they first provide a decisive fitness advantage to one of the partner species. Here we document such a sequence that was connected to a major evolutionary transition in the fungus-growing ants, when the ancestor of the derived leaf-cutting ants shifted from a diet of dry vegetative material to the almost exclusive use of freshly cut leaves. This shift generated visible adaptations in the host ants, such as increased worker dimorphism allowing large workers to cut fresh leaves, but comparative studies of the specific fungal adaptations that accompanied the transition have not been done. Here we report the first large comparative data set on enzymatic fungus garden profiles and focus on one of these enzymes, a laccase that is believed to oxidize phenols in defensive secondary plant compounds. We show that this laccase is exclusively found in the gardens of leaf-cutting ants where it can be inferred to have arisen by selection at the individual level when the ants increased the share of fresh leaves in their forage. However, once in place, this novel enzyme function gave the entire mutualism a significant colony-level advantage, which allowed the leaf-cutting ants to evolve very large long-lived colonies and to become one of the most important and widespread herbivores in neotropical ecosystems.

2-9 Oral

SELFISH GENETIC ELEMENTS IN ANIMAL DEVELOPMENT

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Many multicellular organisms have evolved a dedicated germline. This can benefit the whole organism, but also benefits genetic parasites as it allows them to tailor their replication rate in different host tissues to maximise transmission to gametes. Using modeling and simulations, I examine the fate of selfish elements able to influence host development, and consider what features of animal development may be the result of genetic conflicts in animal evolution.

2-10 Oral

IS SPECIES LEVEL SELECTION A MAJOR FORCE IN EVOLUTION?

Daniel J. Rankin [1], Joao B. Xavier [2], Kevin R. Foster [2]

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Natural selection fundamentally acts at the level of the gene. However, it is acknowledged that traits which are beneficial to a gene or an individual may have a detrimental effect at the level of the population or the species. While most of the levels-of-selection debate has focused on selection at the group level, selection at the species level has often been neglected in this debate. Species-level selection can manifest itself through two simple processes: differential extinction or differential rates of speciation among species. Here we introduce simple models to explore the link between selection at the individual level and its effects on selection at the species level. We find that net speciation and extinction rates can influence the final distribution of traits among species. While simple, our analysis allows us to address the relevant forces involved in species-level selection, and to start to define the conditions under which species-level selection becomes a major part of the evolutionary process. Our results should apply to a wide range of scenarios where the forces of individual-level selection and species-level selection are opposed. We discuss a number of systems where species level selection may play a key role, including the evolution of sex, transposable element evolution and the evolution of specialist, versus generalist, ecologies.

2-1 Poster

Group selection, kin selection, altruism and cooperation: when inclusive fitness is right and when it can be wrong

MATTHIJS VAN VEELEN
Universiteit van Amsterdam, Department of Experimental Economics (CREED), Amsterdam, Netherlands

2-2 Poster

Evolution of chemical disguise in a social parasite

VOLKER NEHRING, JACOBUS J. BOOMSMA, PATRIZIA D'ETTORRE
University of Copenhagen, Department of Biology, Copenhagen, Denmark

2-3 Poster

The R2 element in *Triops cancriformis* (Bosc, 1801): characterization, analyses of its dynamics and effects on the concerted evolution

VALENTINA MINGAZZINI, ANDREA LUCHETTI, BARBARA MANTOVANI
Università di Bologna, Dipartimento di Biologia Evoluzionistica Sperimentale, Bologna, Italy

2-4 Poster

SINEs evolutionary dynamics & inbred genomes: the eusocial model of *Reticulitermes termites* (Isoptera, Rhinotermitidae)

ANDREA LUCHETTI, BARBARA MANTOVANI
Università di Bologna, Dipartimento di Biologia Evoluzionistica Sperimentale, Bologna, Italy

2-5 Poster

The maintenance of sex by species level selection

DANAE THIVAIOU[1,2], PIERRE-HENRI GOUYON[3], TATIANA GIRAUD[4]
[1] *Museum National d'Histoire Naturelle, Paris, France*
[2] *Université d'Orsay Paris XI, Paris, France*
[3] *Muséum de Botanics, Paris, France*
[4] *Université de Systematics and Evolution, Orsay, France*

2-6 Poster

Selfish Plasmids and Community Sex

DUSAN MISEVIC, FRANÇOIS TADDEI
Descartes Faculty of Medicine, INSERM U571, Paris, France

2-7 Poster

An evolutionary ecology approach to the evolution of multicellularity

CRISTIAN A. SOLARI
Universidad de Buenos Aires, Facultad de Ciencias Exactas y Naturales, Departamento de Biodiversidad y Biologia Experimental, Buenos Aires, Argentina

2-8 Poster

Evidence for purifiying selection among genetically different nuclei in one individual of the symbiotic fungus *Glomus intraradices*

DANIEL CROLL, IAN R. SANDERS
University of Lausanne, Department of Ecology & Evolution, Lausanne, Switzerland

2-9 Poster

Sexual selection at the colony level in army ants

BENJAMIN M. BARTH, ROBIN F. A. MORITZ
Martin-Luther-Universität Halle-Wittenberg, Department of Biology, Halle (Saale), Germany

2-10 Poster

Sex and Selfishness: Virulence Evolution In A Genetic Parasite

ELLIE HARRISON[1], VASSILIKI KOUFOPANOU[1], CRAIG MACLEAN[2]
[1] *Imperial College, Center for Population Biology, London, United Kingdom*
[2] *University of Oxford, Department of Zoology, Oxford, United Kingdom*

2-11 Poster

Aging as a consequence of re-emergent conflicts between two levels. Insights from the combination of levels of selection and physiology

GREGORY PAUL[1], FRANÇOIS TADDEI[2]
[1]*ETHZ, Department of Computer Science, Zurich, Switzerland*
[2]*INSERM, Paris, France*

2-12 Poster

Where do selfish genes go? Levels of selection in dispersal evolution

JOSTEIN STARRFELT
University of Helsinki, Department of Biological and Environmental Science, Helsinki, Finland

2-13 Poster

Evolution of MHC class II B exon 2 diversity in the bluethroat (*Luscinia svecica*): local adaptation or ancestral polymorphism?

JARL A. ANMARKRUD, ARILD JOHNSEN, JAN T. LIFJELD
University of Oslo, National Centre for Biosystematics, Natural History Museum, Oslo, Norway

Are ”good genes” theories of sexual selection finally sinking into the sunset?

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12th Congress
Turin 2009

3

Program

Tuesday August 25 - **Symposium 3**

Location: Room 3

Are ”good genes” theories of sexual selection finally sinking into the sunset?

Organizers:	*Mike Ritchie, University of St Andrews, United Kingdom* *Nathan Bailey, University of California at Riverside, United States*
9.45 - 10.15	**ADAM CHIPPINDALE** (invited) The ecological genetics of good genes. On the plasticity of the intersex genetic correlation
10.15 - 10.45	**ANNA QVARNSTRÖM** (invited) Testing the genetics underlying the co-evolution of mate choice and ornament in the wild
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**ESA KOSKELA** Sexually antagonistic alleles oppose good genes in the bank vole, *Myodes glareolus*
11.35 - 11.55	**TRINE BILDE** Postmating sexual selection favours males that sire offspring with low fitness
11.55 - 12.15	**JENNY BOUGHMAN** Context dependent genetic benefits to mate choice contribute to divergent mate preferences and sexual isolation in sticklebacks
12.15 - 12.35	**ZOFIA M. PROKOP** Does sexual ornament size signal mutation load in stalk-eyed fly *Teleopsis dalmanni*?
12.35 - 13.35	*Lunch*
13.35 - 13.55	**PIM EDELAAR** Sexual selection on good genes is promoted and maintained by local adaptation, and can even lead to speciation with gene flow
13.55 - 14.15	**CHRISTOPHE EIZAGUIRRE** MHC-based mate choice combines good genes and maintenance of MHC polymorphism
14.15 - 14.35	**ANDREW POMIANKOWSKI** Do male fertility benefits contribute to the evolution of mate preference in stalk-eyed flies?
14.35 - 14.55	**LOCKE ROWE** Good genes, bad genes and the role of condition-dependence in the co-evolution of the sexes
14.55 - 15.25	*Coffee break*

3-1 Oral

THE ECOLOGICAL GENETICS OF GOOD GENES. ON THE PLASTICITY OF THE INTERSEX GENETIC CORRELATION

Adam Chippindale [1]

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Good genes theories of sexual selection are built upon the reliable transmission of fitness from parent to offspring. My lab's data from *Drosophila* show that a combination of sexually antagonistic genes and X-linkage will subvert potential good genes benefits, and can produce a net negative relationship between parent and offspring fitness. However, the intersexual genetic correlation for the viability component of fitness tends to be positive. Hence, the use of viability as a proxy for fitness would promote unwarranted support for indirect benefits to mate choice. When mutations are experimentally allowed to accumulate, the intersexual correlation for fitness becomes more positive because of deleterious effects on both sexes. These results point to a role for genetic architecture, mutational input, and ecology in determining the potential benefits of sexual selection. The strengths and limitations of inference from laboratory model systems are discussed.

3-2 Oral

TESTING THE GENETICS UNDERLYING THE CO-EVOLUTION OF MATE CHOICE AND ORNAMENT IN THE WILD

Anna Qvarnström [1]

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One of the most debated questions in evolutionary biology is whether female choice of males with exaggerated sexual displays can evolve as a correlated response to selection acting on genes coding for male attractiveness or high overall viability. Empirical studies have provided support for parts of this scenario, but we provide the first test of all the key genetic requirements of both Fisherian and good-genes models on sexual selection in the wild. We used an animal-model quantitative genetic analysis on data from over 8,500 collared flycatchers *(Ficedula albicollis)* in a population followed for 24 years. We found significant additive genetic variances of all the main components: male ornament (forehead patch size), female mate choice for this ornament, male fitness and female fitness. However, when the necessary genetic correlations between these components were taken into account the estimated strength of indirect sexual selection on female mate choice was negligible. Our results show that the combined effect of environmental influences on several components reduced the potential for indirect sexual selection. In addition, further analysis showed that female choice was not only influenced by environmental conditions but is also subjected to gene-environment interactions. I conclude that in general, comparatively little is known about the genes coding for mate choice but that we should expect such genes to most often evolve by their own pathways rather than hitchhiking with genes coding for the ornament.

3-3 Oral

SEXUALLY ANTAGONISTIC ALLELES OPPOSE GOOD GENES IN THE BANK VOLE, *MYODES GLAREOLUS*

Esa Koskela [1], Tapio Mappes [2], Suzanne C. Mills [3], Mikael Mokkonen [1]

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‘Good genes’ theories of sexual selection hypothesise that in the absence of direct benefits, females receive indirect genetic benefits via offspring fitness. However, these models may be complicated by the presence of sexually antagonistic genes that arise when males and females inherit the same alleles that have have differential fitness effects on the two sexes. We created selection lines divergent for male testosterone (T), the main determinant of male mating and reproductive success in polygynandrous bank voles. Males were selected based on T levels (High and Low) and females based on the mean T levels of their brothers; homozygous (male x female crosses: High x High T or Low x Low T) and heterozygous (High x Low T or Low x High T) selection lines were produced. Female reproductive success was determined from female-female competition for a sexually active male; male reproductive success was determined from two measures: male-male competition for an oestrus female and microsatellite paternity analyses following mating trials. Our results reveal a significant negative intersexual correlation for reproductive success using brother-sister averages within each litter. Therefore, ‘good genes’ in this system may be highly gender specific, such that whilst a female mating with the fittest male may produce fit sons, daughters may only show average fitness.

3-4 Oral

POSTMATING SEXUAL SELECTION FAVOURS MALES THAT SIRE OFFSPRING WITH LOW FITNESS

Trine Bilde [1,2], Goran Arnqvist [2]

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Despite the sizeable costs of mating, females of most taxa mate with more than one male. It is commonly believed that polyandrous females gain genetic benefits for their offspring, but this assumes paternity bias in favour of male genotypes that enhance offspring viability. However, evidence for such paternity bias is limited outside the context of inbreeding avoidance. Using discrete genotypes of a seed beetle, we determined net male genetic effects on female lifetime offspring production and the reproductive fitness of daughters for a variety of combinations of maternal and paternal genotypes. We used this information to rank males according to their genetic quality, defined as the net additive (good genes) and nonadditive (epistatic interactions) genetic effects. In double mating experiments, females were mated to a high and a low quality male, testing whether fertilization success was biased in favour of high quality male genotypes. Contrary to expectations, high quality male genotypes consistently had a lower postmating fertilization success in two independent assays. Our results suggest the presence of antagonistic male sperm competition adaptations, or of antagonistic genes that confer advantage in sperm competition while depressing fitness in daughters. In light of these results, it is unlikely that evolution of polyandry is generally driven by postmating female choice for males of high genetic quality, and any female benefits of polyandry should be sought for elsewhere than in the paternal genetic contribution to offspring.

3-5 Oral

CONTEXT DEPENDENT GENETIC BENEFITS TO MATE CHOICE CONTRIBUTE TO DIVERGENT MATE PREFERENCES AND SEXUAL ISOLATION IN STICKLEBACKS

Jenny Boughman [1]

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Ecological conditions can alter the value of indirect benefits that females acquire from their mates. Such context dependent genetic benefits are typically viewed as a mechanism to maintain genetic variation. But if environments differ consistently between populations, context dependence will exert consistently different selection which can lead to divergence in female preferences and male traits. Such differences can cause reproductive isolation. We tested whether two species of stickleback fish that are adapted to distinct niches differ in the genetic benefits provided by attractive colorful males, and whether these benefits depend on their different ecologies. We generated maternal half sibs by crossing each female to both an attractive and an unattractive male. Each sibship was split and raised on diets that mimic the typical resources exploited by each species in nature. We then measured total fitness on native and alternate diets for offspring of attractive and unattractive fathers. This design allowed us to isolate paternal genetic effects, to partition genetic and environmental variance, and to detect tradeoffs among fitness components and between the sexes. We found pervasive evidence for context dependence on the fitness of sons and daughters. We detected indirect genetic benefits on attractiveness and mating success of sons and on survival of both sexes. We found interactions with diet for many fitness components indicating substantial GxE. Effects differed for sons and daughters. These results highlight that which genes are ‘good’ depends on ecological context. Moreover, responses differed between the two species, revealing that adaptation to divergent niches alters indirect benefits in a manner that would lead to divergence in mate preferences. Our work shows that context dependence is likely to contribute to the strong sexual isolation between these species.

3-6 Oral

DOES SEXUAL ORNAMENT SIZE SIGNAL MUTATION LOAD IN STALK-EYED FLY *TELEOPSIS DALMANNI?*

Zofia M. Prokop [1], Łukasz Michalczyk [2], Joanna E. Leś [1], Andrew Pomiankowski [3], Jacek Radwan [1]

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Genic capture hypothesis of sexual selection predicts that male sexual ornaments are costly to produce and hence depend on numerous genes affecting resource acquisition and use, providing a large target for mutations. If this is the case, then ornaments should provide an honest estimate of male genome-wide mutation load.

We test this hypothesis using a stalk-eyed fly *Teleopsis dalmanni*. We apply ionizing radiation to induce mutations, enabling direct comparison of ornament size between groups of flies differing in mutation load. After irradiating adult males, we screen their progeny for the effects on male ornament (eyespan), non-sexual morphometric traits and life-history traits. According to genic capture hypothesis, the ornament should be affected by mutagenesis more than non-sexual morphological characters, and similarly to life-history traits, which are known to depend on numerous loci. Our preliminary results indicate that male eyespan does indeed decrease under mutagenesis more than non-sexual morphometric traits.

3-7 Oral

SEXUAL SELECTION ON GOOD GENES IS PROMOTED AND MAINTAINED BY LOCAL ADAPTATION, AND CAN EVEN LEAD TO SPECIATION WITH GENE FLOW

Pim Edelaar [1], Sander Van Doorn [2], Franz J. Weissing [3]

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Classical good genes models are based on direction selection, which should lead to the exhaustion of genetic variation in good genes. We show how a spatially structured environment with selection for local adaptation prevents the depletion of genetic variation by sexual selection. We simulated an environment with two kinds of habitat patches providing divergent natural selection for local adaptation. Surviving natural selection, individuals mate within their patch, and a fraction of their offspring migrate to random patches. We next allowed for the evolution of a male ornament whose expression is determined by environment-dependent condition, and its allocation of available resources. We also allowed for the evolution of costly female choice. Male signalling and female choice are observed to evolve from scratch, because females benefit from mating with locally adapted males. Sexual selection indirectly increases divergence of the ecological traits, favouring stronger female preference for locally adapted males, and higher male signalling investment. Thus sexual selection based on indicators of good genes and divergent natural selection reinforce each other. Because of local adaptation, the variation in good genes of potential mates is never depleted, as long as some migrating individuals end up in suboptimal habitat. We find that the increased specialisation and assortative mating caused by sexual selection can even facilitate speciation across the continuum of allopatry to sympatry. The ubiquity of condition-dependence of sexual ornamentation and local adaptation of populations suggests that maintenance of good genes and their contribution to local adaptation and speciation should have a high generality.

3-8 Oral

MHC-BASED MATE CHOICE COMBINES GOOD GENES AND MAINTENANCE OF MHC POLYMORPHISM

Christophe Eizaguirre [1,2], Sarah E. Yeates [3], Tobias L. Lenz [2], Martin Kalbe [2], Manfred Milinski [2]

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Polymorphic genes of the major histocompatibility complex (MHC) are regarded as essential genes for individual fitness under conditions of natural and sexual selection. To test this hypothesis, we investigated the ultimate individual fitness trait- that of reproductive success. We used three-spined sticklebacks *(Gasterosteus aculeatus)* in semi natural enclosures, located in natural breeding areas where the experimental fish had been caught. During their reproductive period, fish were exposed continuously to their natural sympatric parasites. By genotyping almost 4000 eggs with 9 microsatellites, we determined parenthood and inferred female mating decision. We found that with reference to their own MHC profile, female sticklebacks preferred to mate with males sharing an intermediate MHC diversity. In addition, males with a specific MHC haplotype were bigger and better at fighting a common parasite (*Gyrodactylus* sp.). This translated directly into Darwinian fitness since fish harboring this specific MHC haplotype were more likely to be chosen and had a higher reproductive output. We conclude that females based their mating decision also on a specific MHC haplotype conferring resistance against a common parasite. This identifies and supports “good genes”. We argue that such interaction between host and parasite driving assortative mating is not only a pre-requisite for negative-frequency-dependent selection - a potential mechanism to explain the maintenance of MHC polymorphism, but also potentially speciation.

3-9 Oral

DO MALE FERTILITY BENEFITS CONTRIBUTE TO THE EVOLUTION OF MATE PREFERENCE IN STALK-EYED FLIES?

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Stalk-eyed flies are a classic textbook example of exaggerated sexual ornaments evolving through the action of female mate preference. Putative genetic benefits are genes which confer higher condition and suppressors of meiotic drive. Female stalk-eyed flies also show low fertility. Males transfer very small ejaculates and very few sperm per mating. Females need to mate multiply in order to raise their fertility. Here we investigate whether preference for larger male eyespan (the sexual ornament) could confer fertility benefits on females. Theory suggests that the conditions under which this can occur are limited. This view is supported by many of our findings in two stalk-eyed fly species. However, the nature of the stalk-eyed fly mating system points to natural conditions under which females gain fertility benefits. The contribution of fertility and genetic benefits to the evolution of mate preference will then be compared.

3-10 Oral

GOOD GENES, BAD GENES AND THE ROLE OF CONDITION-DEPENDENCE IN THE CO-EVOLUTION OF THE SEXES

Locke Rowe [1]

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A renewed focus on condition-dependent expression in studies of sexual selection has reinvigorated interest in the so-called good genes theory of preference evolution. This focus on condition-dependence, has also led us to a better understanding of the evolution of sexual dimorphism, the evolution of sex, and adaptation under natural selection. For example, recent theory suggests that sex-limited condition-dependence can facilitate the evolution of sexual dimorphism independent of the source of sex-biased selection. In this talk I will review recent evidence suggesting that sex-biased selection has led to widespread condition-dependence, observable from studies of specific exaggerated phenotypic traits to broad scans of the transcriptome. I will then discuss the role of condition-dependence in the good genes theory of preference evolution, as well as alternative theories for the evolution of mating biases. These data suggest that good genes remains a viable theory, but point to some limits on its efficacy. Specifically, we need to know much more about the magnitude and nature of genetic variance in fitness residing in natural populations. Without this knowledge, the results of many tests of the good genes theory will remain difficult to interpret.

3-1 Poster **Acquiring and maintaining parasitoid resistance: the roles of natural and sexual selection**

FEMMIE J.L. KRAAIJEVELD-SMIT, JACQUES J.M. VAN ALPHEN

Leiden University, Department of Animal Ecology, Leiden, Netherlands

3-2 Poster **MHC class I genes and extra-pair mating in a socially monogamous songbird, the Scarlet rosefinch (*Carpodacus erythrinus*)**

MARTA PROMEROVA[1], JAN SCHNITZER[2], JOSEF BRYJA[1], MICHAL VINKLER[2], PAVEL MUNCLINGER[2], TOMAS ALBRECHT[2]

[1]*Institute of Vertebrate Biology AS CR, Department of Population Biology, Studenec, Czech Republic*
[2] *Charles University, Biodiversity Research Group, Department of Zoology, Prague, Czech Republic*

3-3 Poster **Introduction of a novel male signal trait in a sensory exploitation system**

MIRJAM AMCOFF, NICLAS KOLM

Uppsala University, Department of Animal Ecology, Uppsala, Sweden

3-4 Poster **MHC and mate choice in polygynous ungulate: the reindeer**

NATASA DJAKOVIC[1,2], KNUT H. RØED[2], ØYSTEIN HOLAND[1]

[1]*Norwegian University of Life Sciences, Department of Animal and Aquacultural Sciences, Aas, Norway*
[2]*Norwegian School of Veterinary Science, Department of Basic Sciences and Aquatic Medicine, Oslo, Norway*

3-5 Poster **Quantitative genetic basis of female mate preferences across two environments**

MATTHIEU DELCOURT[1], MARK W. BLOWS[2], HOWARD D. RUNDLE[1]

[1]*University of Ottawa, Department of Biology, Ottawa, Canada*
[2]*University of Queensland, School of Integrative Biology, St. Lucia, Australia*

3-6 Poster **Male and female influences on the sperm phenotype**

KLAUS REINHARDT

University of Sheffield, Department of Animal & Plant Sciences, Sheffield, United Kingdom

3-7 Poster **Sexual selection against deleterious mutations via variable male search effort**

KELSIE MACLELLAN[1], MICHAEL C. WHITLOCK[2], HOWARD D. RUNDLE[1]

[1]*University of Ottawa, Department of Biology, Ottawa, Canada*
[2]*University of British Columbia, Department of Zoology, Vancouver, Canada*

3-8 Poster **Attractive amplifiers in sexual selection: where efficacy meets honesty**

SERGIO CASTELLANO[1], PAOLO CERMELLI[2]

[1]*University of Turin, Department of Animal and Human biology, Turin, Italy*
[2]*University of Turin, Department of Mathematics, Turin, Italy*

3-9 Poster **Does male genital size and shape influence male success during cooperative matings in the guppy?**

CLELIA GASPARINI[1], ANDREA PILASTRO[1], JONATHAN P. EVANS[2]

[1]*University of Padova, Department of Biology, Padova, Italy*
[2]*University of Western Australia, Centre for Evolutionary Biology, Perth, Australia*

3-10 Poster **Costs and benfits of mating in *Drosophila melanogaster***

CLAUDIA FRICKE, TRACEY CHAPMAN
University of East Anglia, School of Biological Sciences, Norwich, United Kingdom

3-11 Poster **Wounding leads to the growth of larger sexual signals in the stalk-eyed fly, *Teleopsis dalmanni***

LEEANN T. REANEY[1], IAN WARREN[2], ROBERT J. KNELL[1]
[1]Queen Mary University of London, School of Biological and Chemical Sciences, London, United Kingdom
[2]University College of London, Department of Biology, London, United Kingdom

3-12 Poster **Genetic incompatibility: how do females make a post-copulatory choice?**

AMANDA BRETMAN, TOM TREGENZA, DEVI NEWCOMBE
University of Exeter, Cornwall Campus, School of Biosciences, Penryn, United Kingdom

3-13 Poster **Movements of oestrous females: more to the rut than male competition?**

KATIE V. STOPHER[1,2], DANIEL N. NUSSEY[1], TIM H. CLUTTON-BROCK[3], ALISON MORRIS[1], JOSEPHINE M. PEMBERTON[1]
[1]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom
[2]Macaulay Institute, Aberdeen, United Kingdom
[3]University of Cambridge, Department of Zoology , Cambridge, United Kingdom

3-14 Poster **Function and selection response of egg-spots in *Astatotilapia burtoni***

FREDERICO HENNING[1], TOPI LEHTONEN[2], AXEL MEYER[1]
[1]Universität Konstanz, Fachbereich Biologie, Konstanz, Germany
[2]Monash University, School of Biological Sciences, Victoria, Australia

3-15 Poster **Field crickets change mating preferences using remembered social information**

NATHAN W. BAILEY, MARLENE ZUK
University of California, Department of Biology, Riverside, United States

3-16 Poster **A beginning of signal divergence in *Enchenopa* treehoppers**

RAFAEL L. RODRIGUEZ
University of Wisconsin, Department of Biological Sciences, Milwaukee, United States

3-17 Poster **Do female promiscuity promote male cooperation in predator defense and division of resources?**

SIGRUNN ELIASSEN, CHRISTIAN JØRGENSEN
University of Bergen, Department of Biology, Bergen, Norway

3-18 Poster **Antagonistic evolution: reduction of foraging efficiency as a consequence of sensory exploitation**

YOLITZI SALDIVAR LEMUS, CONSTANTINO MACIAS GARCIA
Universidad Nacional Autonoma de Mexico, Instituto de Ecologia, Mexico

3-19 Poster **Cryptic fertilisation bias for MHC similar males in red junglefowl, *Gallus gallus***

KIRSTY WORLEY[1,2], DAVID S. RICHARDSON[2], TOMMASO PIZZARI[1]
[1]University of Oxford, Edward Grey Institute, Department of Zoology, Oxford, United Kingdom
[2]University of East Anglia, Department Of Biological Sciences, Norwich, United Kingdom

3-20 Poster **Divorce in monogamous mammals: example of the Alpine marmot *Marmota marmota***

SOPHIE LARDY, DOMINIQUE ALLAINÉ
University Lyon1, CNRS-UMR 5558 Laboratoire de Biométrie et Biologie Evolutive, Villeurbanne, France

3-21 Poster **Genetic benefits are unlikely to compensate direct costs of polyandry in a partially inbreeding spider**

CRISTINA TUNI, TRINE BILDE
Aarhus University, Department of Biological Sciences, Aarhus, Denmark

3-22 Poster **Responses to inbreeding depend on sex and context in the red junglefowl**

HANNE LØVLIE, TOMMASO PIZZARI
University of Oxford, Edward Grey Institute, Department of Zoology, Oxford, United Kingdom

3-23 Poster **Paternal effects on egg size variation and egg survival in blackfin pearl killifish (*Austrolebias nigripinnis)***

MAHMOUD MOSHGANI, TOM JM VAN DOOREN
Leiden University, Institute of Biology, Leiden, Netherlands

3-24 Poster **Is Mate Choice in Humans MHC-Dependent?**

RAPHAELLE CHAIX[1], CHEN CAO[2], PETER DONNELLY[3,4]
[1]CNRS-MNHN, Department of Hommes, Natures, Sociétés, Paris, France
[2]CAS-MPG Partner Institute for Computational Biology, Shanghai, China
[3]The Wellcome Trust Centre for Human Genetics, Oxford, United Kingdom
[4]University of Oxford, Oxford, United Kingdom

3-25 Poster **Why is the role of developmental instability in sexual selection so variable? A potential resolution**

MICHAL POLAK
University of Cincinnati, Department of Biological Sciences, Cincinnati, United States

3-26 Poster **The Role of Good Genes and Genetic Compatibility in Multiply Mating Horseshoe Crabs**

SHERI JOHNSON, H. JANE BROCKMANN
University of Florida, Department of Biology, Gainesville, United States

3-27 Poster **Courtship display reliably signals fertilization power in a lekking species**

REMI CHARGE[1,2], MICHEL SAINT JALME[1], FREDERIC LACROIX[2], ADELINE CADET[2], GABRIELE SORCI[3]

[1]MNHN, Department of Ecologie et gestion de la biodiversite, Paris, France
[2]ECWP , Missour, Morroco
[3]CNRS, Department of Biogeosciences, Dijon, France

3-28 Poster **Inbreeding depression in a sexual trait in the stalk-eyed fly *Teleopsis dalmanni* - weak evidence for genic capture**

JOANNA E. LES, ZOFIA M. PROKOP, PAULINA K. BANAS, PAWEL KOTEJA, JACEK RADWAN

Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland

3-29 Poster **Evolution of mate choice for genome-wide heterozygosity**

LUTZ FROMHAGE[1], HANNA KOKKO[2], JANE M. REID[3]

[1]University of Hamburg, Department of Ethology, Hamburg, Germany
[2]University of Helsinki, Department of Biological and Environmental Science, Helsinki, Finland
[3]University of Aberdeen, School of Biological Sciences, Aberdeen, United Kingdom

3-30 Poster **Male choice is influenced by the attractiveness of potential competitors**

ANDREA PILASTRO, CLELIA GASPARINI, CHIARA OGNIBEN

Università di Padova, Dipartimento di Biologia, Padova, Italy

3-31 Poster **Genetic variation in paternity success in a flatworm**

PETER SANDNER, LUKAS SCHÄRER

University of Basel, Zoological Institute, Basel, Switzerland

The evolution of threshold, inducible and polyphenic traits

eseb •
12th Congress
Turin 2009

4

Program

Tuesday August 25 - **Symposium 4**

Location: Room 4

The evolution of threshold, inducible and polyphenic traits

Organizers: *Derek Roff, University of California at Riverside, United States*
Wade Hazel, DePauw University, Greencastle, United States

9.45 - 10.15	**KATHLEEN DONOHUE** (invited) Life history and the seasonal induction of phenotypes: development in natural environments
10.15 - 10.45	**BRADLEY R. ANHOLT** (invited) The evolution of inducible anti-predator defenses
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**DIRK J. MIKOLAJEWSKI** Integrating antipredator traits: multiple predators and shifts in selection
11.35 - 11.55	**MICHAEL KOPP** Predator-prey cycles and the evolution of inducible defenses
11.55 - 12.15	**JEFFREY A. HUTCHINGS** Genetic variation in threshold reaction norms for alternative reproductive tactics in male Atlantic salmon
12.15 - 12.35	**FABIEN HALKETT** Evolution of trade-offs between sexual and asexual phases and the role of reproductive plasticity in the genetic architecture of aphid life histories
12.35 - 13.35	*Lunch*
13.35 - 13.55	**KARL GOTTHARD** Developmental plasticity for optimal size in a butterfly
13.55 - 14.15	**HUBERTUS J. E. BEAUMONT** Experimental evolution of a bet-hedging strategy
14.15 - 14.35	**EMILIE SNELL-ROOD** Developmental reprogramming in the evolution of polyphenisms: a case study of morph- and sex-specific gene expression in horned beetles
14.35 - 14.55	**REINMAR HAGER** The plasticity of the epigenome: genomic imprinting effects on complex traits can be modified by maternal environment
14.55 - 15.25	*Coffee break*

4-1 Oral

LIFE HISTORY AND THE SEASONAL INDUCTION OF PHENOTYPES: DEVELOPMENT IN NATURAL ENVIRONMENTS

Kathleen Donohue [1]

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A life cycle is a sequence of developmental events. Notably, this temporal sequence of development occurs within a temporal sequence of seasons. Because seasons are not completely predictable, adaptive life histories frequently require a continuous assessment of seasonal changes and appropriate developmental responses to those seasonal changes. That is, adaptive life histories require matching the appropriate life stage with the appropriate season. In this sense, phenotypic plasticity—and specifically developmental responses to external seasonal environments—becomes important for understanding adaptive life histories of organisms in nature. I will discuss mechanisms of seasonal assessment and responses in plants, and illustrate how sequences of seasonal cues and developmental responses to such sequences result in particular angiosperm life cycles and life-history variation, with special reference to germination and flowering in annual plants.

4-2 Oral

THE EVOLUTION OF INDUCIBLE ANTI-PREDATOR DEFENSES

Bradley R. Anholt [1,2]

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2Bamfield Marine Sciences Centre, Bamfield, Canada

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The canonical model for inducible defenses requires that predation risk is temporally variable, a reliable cue for changes in risk is available to prey, and defenses have a cost. Hundreds of examples abound of inducible defenses in organisms from protists to vertebrates. Defense varies among species whose preferred habitats harbour different predators. The level of defense also varies among strains. Prey often fail to induce defenses in response to novel predators. Thus introduced predators can have unexpectedly large conservation consequences. The benefits of a defense are usually easy to demonstrate but costs are more subtle. This is partly because it is easy to overestimate the size of the benefit. An alternative approach is to use experimental evolution to demonstrate costs and I present an example from the hypotrich ciliate *Euplotes* where costs have led to the evolutionary reduction in the ability to induce.

4-3 Oral

INTEGRATING ANTIPREDATOR TRAITS: MULTIPLE PREDATORS AND SHIFTS IN SELECTION

Dirk J. Mikolajewski [1], Andrew P. Beckerman [1]

[1]*University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom*

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Predation is known to be heterogeneous in space and time and prey often experience threats by multiple predator species rather than a single predator. Current theory suggests that to avoid and repel predators, prey apply sets of integrated antipredator traits by altering morphology, behaviour and life history simultaneously. Predator species differ qualitatively in their foraging characteristics suggesting that the magnitude and direction – the integration - of trait changes will be predator specific. Here, we studied the integration of antipredator traits among genotypes of the waterflea *Daphnia pulex* facing antagonistic selection regimes by predatory fish (*Gasterosteus aculeatus*; stickleback) and an insect predator (*Chaoborus* spec.; phantom midge larvae). These two predators select for opposite pattern in size and age at maturity, in morphology and in behavioural antipredator traits. By studying the covariance of antipredator traits along a gradient of both predators, we show that anti-predator responses are sensitive to specific predators, but that the integration of traits is a graded multivariate response governed by levels of risk.

4-4 Oral

PREDATOR-PREY CYCLES AND THE EVOLUTION OF INDUCIBLE DEFENSES

Michael Kopp [1]

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Inducible defenses are examples of phenotypic plasticity that allow prey organisms to adjust their investment in defense to the current risk of predation. They are wide-spread in species facing temporally of spatially variable predation pressure. A number of models have shown that inducible defenses have the potential to stabilize predator-prey interactions. In contrast, no studies to date have investigated how unstable population dynamics, such as predator-prey cycles, influence the evolution of inducible defenses. Here, I use the so-called environmental threshold model to study the evolution of induction thresholds in a dynamic predator-prey model with an inducible defense. Prey build up the defense if predator density exceeds a threshold, but the value of this threshold varies between individuals and is subject to selection. In the model, threshold evolution tends to destabilize initially stable equilibria and induces predator-prey cycles. In the course of these cycles, selection on the thresholds is reversed, and the result is a steady state characterized by fluctuations in both population densities and mean threshold values. I also investigate how predator-prey dynamics influence the evolution of inducible versus genetically fixed defenses.

4-5 Oral

GENETIC VARIATION IN THRESHOLD REACTION NORMS FOR ALTERNATIVE REPRODUCTIVE TACTICS IN MALE ATLANTIC SALMON

Jeffrey A. Hutchings [1], Jacinthe Piché [1], Wade Blanchard [2]

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[2]*Dalhousie University, Department of Mathematics and Statistics, Halifax, Canada*

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Alternative reproductive tactics may be a product of adaptive phenotypic plasticity, such that discontinuous variation in life history depends on both genotype and the environment. Phenotypes that fall below a genetically-determined threshold adopt one tactic, while those exceeding the threshold adopt the alternative tactic. We report evidence of genetic variability in maturation thresholds for male Atlantic salmon *(Salmo salar)* which mature either as large (>1 kg) anadromous males or as small (10-150g) parr. Using a common-garden experimental protocol, we find that the growth rate at which the sneaker parr phenotype is expressed differs among pure and mixed population crosses. Maturation thresholds of hybrids were intermediate to those of pure crosses, consistent with the hypothesis that the life-history switch-points are heritable. Our work provides evidence, for a vertebrate, that thresholds for alternative reproductive tactics differ genetically among populations and can be modelled as discontinuous reaction norms for age and size at maturity.

4-6 Oral

EVOLUTION OF TRADE-OFFS BETWEEN SEXUAL AND ASEXUAL PHASES AND THE ROLE OF REPRODUCTIVE PLASTICITY IN THE GENETIC ARCHITECTURE OF APHID LIFE HISTORIES

Roberto Nespolo [1], Fabien Halkett [2], Christian C. Figueroa [1], Manuel Plantegenest [3], Jean-Christophe Simon [4]

[1]*Universidad Austral de Chile, Instituto de Ecologia y Evolución, Valdivia, Chile*
[2]*INRA, UMR 1136 Interactions Arbres-Microorganismes, Nancy, France*
[3]*Agrocampus Ouest, UMR 1099 BiO3P , Rennes, France*
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Life-history theory postulates that evolution is constrained by trade-offs. However, in organisms with complex life-cycles, trade-offs may drastically differ between phases, putatively leading to different evolutionary trajectories. Here, we tested this possibility by examining changes in life-history traits in an aphid species that alternates asexual and sexual reproduction in its life-cycle. Aphids are characterized by intense phenotypic plasticity and they can produce a wide variety of environmentally-induced morphs, encompassing sexual and asexual forms plus, among the latter, sedentary (apterous) or migratory (winged) forms. Besides, aphids can show strong lineage specialization but it is not clear to what extent the production of these different forms is genetically determined. Here, we found large and significant heritabilities (broad-sense) for all traits and several negative genetic correlations between traits, suggesting that these aphid lineages are specialized both in reproductive and dispersal strategies. In addition, we found important differences in the structure of genetic variance-covariance matrices (**G**) between sexual and asexual phases. These differences were due to two large, negative genetic correlations detected during the asexual phase only: (1) between fecundity and age at maturity and (2) between the production of wingless and winged parthenogenetic females. We propose that this differential expression in genetic architecture results from a re-allocation scheme during the asexual phase, when sexual morphs are not produced. Our results reveal a rather unique situation in which the same population and even the same genotypes exhibit different **G**-matrices under different environmental conditions and because of greater costs to produce sexual forms.

4-7 Oral

DEVELOPMENTAL PLASTICITY FOR OPTIMAL SIZE IN A BUTTERFLY

Karl Gotthard [1], David Berger [1,2]

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[2]*University of Zürich, Zoological Museum of Zürich-Irchel, Zürich, Switzerland*

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The diapause decision in insects is a threshold trait that leads to the presence of alternative developmental pathways. As a consequence, individuals within a given population will develop and reproduce during different parts of the year that may present substantially different selection pressures. In southern Sweden the butterfly *Pararge aegeria* has two alternative developmental pathways producing two non-overlapping adult cohorts that fly in early May or in June. Life history modeling of this situation predicts that optimal size is lower in May than in June because of a stronger thermally induced time-limitation on female oviposition rates in May than in June. We tested this prediction by producing adults of both developmental pathways and estimating female oviposition rates of both types in typical thermal conditions of May and June. As predicted, individuals following the developmental pathway that predestine them for reproduction in June grow larger than individuals of the May cohort. Moreover, "June"-females could only realize their higher potential fecundity under typical June conditions and not in typical May conditions. A rearing experiment on a more northern population of *P. aegeria* that only expresses one of the developmental pathways in nature indicates that, when experimentally manipulated to use both pathways, there is no difference in adult size between the two developmental types. We conclude that local selection in southern Sweden has led to a coordination of development downstream of the diapause threshold that allows the development of two types of adults adapted to the typical conditions of their expected reproductive period.

4-8 Oral

EXPERIMENTAL EVOLUTION OF A BET-HEDGING STRATEGY

Hubertus J. E. Beaumont [1], Jenna Gallie [2], Christian Kost [3], Paul B. Rainey [2]

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[2]*New Zealand Institute for Advanced Study and Allan Wilson Centre for Molecular Ecology & Evolution, Auckland, New Zealand*
[3]*Max Planck Institute for Chemical Ecology, Department of Bioorganic Chemistry, Jena, Germany*

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Bet-hedging – stochastic phenotype variation – is a canonical example of an evolutionary adaptation that facilitates persistence in the face of fluctuating environmental conditions. While bet-hedging is found in organisms ranging from pathogenic bacteria to humans, evidence for the adaptive origin of this behaviour is indirect. We selected experimental bacterial populations under conditions that mimic the host immune system to gain mechanistic insight into the evolution of adaptations to fluctuating environments. The trait under fluctuating selection was the morphology of the bacterial colonies. Initially, all populations adapted to rounds of selection by mutation; however, in two (of twelve) populations this trend was broken by the *de novo* evolution of bet-hedging genotypes, which persisted on account of stochastic phenotype switching. Bet-hedging involved the stochastic expression of different colony morphologies. Sequencing of the complete genome of one of these switching types showed that it differed from the ancestor by nine mutations. The final mutation was both necessary and sufficient to cause switching; nonetheless, the evolution of bet-hedging was contingent upon earlier mutations that altered the relative fitness effect of the final mutation. Our findings represent an empirical account of the evolutionary emergence of bet-hedging, and shed light on the underlying molecular, physiological, and ecological causes.

4-9 Oral

DEVELOPMENTAL REPROGRAMMING IN THE EVOLUTION OF POLYPHENISMS: A CASE STUDY OF MORPH- AND SEX-SPECIFIC GENE EXPRESSION IN HORNED BEETLES

Emilie Snell-Rood [1], Amy Cash [1], Teiya Kijimoto [1], Justen Andrews [1], Armin Moczek [1]

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Polyphenisms are often assumed to involve a large degree of "developmental reprogramming," whereby an environmental cue triggers one of several independent, alternative developmental pathways. This assumption is rarely tested at a genome-wide level, in particular with reference to other instances of presumed developmental reprogramming. In this study, we use microarrays to survey gene expression in male morphs in the horned beetles, *Onthophagus*, and compare morph-specific expression to sex-specific expression, a hallmark of reprogramming. Depending on larval nutrition, males of these beetles emerge as either large, horned individuals that fight for access to females, or small, hornless males that sneak copulations. We investigated gene expression in the developing horns and brains of beetles, relative to a reference tissue (either abdominal epidermis or thoracic ganglia, respectively), a design which allowed us to quantify both differences and similarites in gene expression between morphs and sexes. This approach was replicated across two species that differ in horn placement: *O. taurus* (head horns) and *O. nigriventris* (thoracic horns). Overall, we found that similarites in gene expression far outweighed differences, however, magnitudes of gene expression differences across morphs were congruent with those across sexes. Intriguingly, in *O. nigriventris*, gene expression in hornless males was more similar to expression patterns in females than in horned males. Lastly, we found evidence that differences in morph-specificity of expression may affect the evolution of these genes through relaxed selection. In conclusion, this study emphasizes the importance of quantifying developmental reprogramming in the study of phenotypic plasticity.

4-10 Oral

THE PLASTICITY OF THE EPIGENOME: GENOMIC IMPRINTING EFFECTS ON COMPLEX TRAITS CAN BE MODIFIED BY MATERNAL ENVIRONMENT

Reinmar Hager [1], James M. Cheverud [2], Jason B. Wolf [1]

[1]*University of Manchester, Faculty of Life Sciences, Manchester, United Kingdom*
[2]*Washington University, School of Medicine, Department of Anatomy and Neurobiology, St Louis, United States*

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Recent research has demonstrated that variation in complex traits is not only due to genetic and epigenetic variation but that epigenetic effects may be subject to modifications by the maternal environment with important implications for individual development and fitness. Genomic imprinting resulting in parent-of-origin dependent gene expression is among the best studied epigenetic effects. We currently know very little about the degree to which genomic imprinting effects can be modified by the maternally provided. We addressed this unresolved issue using a cross-fostering design in mice in which pups were nursed by either their own or an unrelated mother. We scanned the entire genome to search for quantitative trait loci whose effects depend on cross-fostering and detected seven of such loci. Cross-fostering had a much larger impact on epigenetic than on genetic effects and in most cases, the interaction effect was due to the presence of an effect in either cross-fostered or non-cross-fostered animals. Our results demonstrate that such environmental interactions with epigenotype can affect key fitness-related traits and suggest a greater plasticity of the epigenome than previously assumed.

4-1 Poster **Maternal manipulation of offspring performance**

MARJO PIHLAJA, RAUNO V. ALATALO, MIKAEL PUURTINEN, HELI SIITARI
University of Jyväskylä, Department of Biological and Environmental Sciences, Jyväskylä, Finland

4-2 Poster **Parental control over offspring characteristics in a polyembryonic parasitoid wasp via maternal effects**

NA'AMA MORAG[1], AMOS BOUSKILA[1], ALLY R. HARARI[2], MICHAL SEGOLI[1], TAMAR KEASAR[3]
[1]*Ben Gurion University, Department of Life Sciences, Be'er Sheva, Israel*
[2]*Volcani Center, Department of Entomology, Bet Dagan, Israel*
[3]*University of Haifa – Oranim Department of Science Education - Biology, Tivon , Israel*

4-3 Poster **Evolution of Phenotype Determination - Stochastic simulations of adaptation in time-varying environments**

HANNES SVARDAL[1], CLAUS RUEFFLER[1], PETER A. ABRAMS[2]
[1]*University of Vienna, Faculty of Mathematics, Vienna, Austria*
[2]*University of Toronto, Department of Ecology and Evolutionary Biology, Canada*

4-4 Poster **Spatially heterogeneous stochasticity and the adaptive diversification of dormancy**

ETIENNE RAJON, SAMUEL VENNER, FRÉDÉRIC MENU
Université Lyon 1, Laboratoire de Biométrie et Biologie Evolutive, Villeurbanne, France

4-5 Poster **Sex-specific fitness consequences of dispersal in a house sparrow metapopulation**

HENRIK PÄRN, HENRIK JENSEN, THOR HARALD RINGSBY, BERNT-ERIK SÆTHER
Norwegian University of Science and Technology, Centre for Conservation Biology, Department of Biology, Trondheim, Norway

4-6 Poster **The evolution of dispersal kernels: do short and long distance dispersal evolve independently?**

BONTE DRIES
Ghent University, Department of Biology - Research group Terrestrial Ecology, Gent, Belgium

4-7 Poster **Can phenotypic plasticity explain fire melanism in pygmy grasshoppers?**

MAGNUS KARLSSON, ANDERS FORSMAN, SOFIA CAESAR, JENNY JOHANSSON
University of Kalmar, School of pure and applied natural sciences, Kalmar, Sweden

4-8 Poster **Adaptive and environmentally induced variation in life-history traits between latitudinal populations of a lichen-feeding moth *Eilema depressum***

HEIKKI PÖYKKÖ[1], TOOMAS TAMMARU[2]
[1]*University of Oulu, Biology, Oulu, Finland*
[2]*University of Tartu, Institute of Ecology and Earth Sciences, Tartu, Estonia*

4-9 Poster **Population differences in growth and in the incidence of alternative reproductive tactics: local adaptation or phenotypic plasticity?**

DAVID J. PAEZ[1,2], LOUIS BERNATCHEZ[1,2], JULIAN J. DODSON[1,2]
[1]*Universtite Laval, Department of Biology, Quebec, Canada*
[2]*Quebec Ocean, Quebec, Canada*

4-10 Poster **Hormonal control of adaptive polyphenism in a tropical butterfly**

VICENCIO OOSTRA[1], MAAIKE A. DE JONG[1], BRANDON M. INVERGO[1], FANJA KESBEKE[1], FRANZISKA WENDE[2], BAS J. ZWAAN[1]

[1]Leiden University, Institute of Biology, Department of Evolutionary Biology, Leiden, Netherlands
[2]University of Bayreuth, Department of Animal Ecology I, Bayreuth, Germany

4-11 Poster **Laboratory evolution of a male dimorphic threshold trait in response to habitat complexity**

JOSEPH L. TOMKINS[1], WADE N. HAZEL[2], MARISSA A. PENROSE[1], JACEK RADWAN[3], NATASHA R. LEBAS[1]

[1]The University of Western Australia, School of Animal Biology, Crawley, Australia
[2]DePauw University, Department of Biology, Greencastle, United States
[3]Jagiellonian University, Institute for Ecology, Krakow, Poland

4-12 Poster **Using quantitative genetic models of plasticity to understand the evolution of the genetic variance underlying environmentally-cued threshold traits**

RICHARD SMOCK[1], WADE HAZEL[2]

[1]DePauw University, Department of Mathematics, Greencastle, United States
[2]DePauw University, Department of Biology, Greencastle, United States

4-13 Poster **What to do first: Grow or reproduce? Evolutionary dilemma of indeterminate growers in the seasonal environment**

MACIEJ J. EJSMOND, MARCIN CZARNOŁĘSKI, FILIP KAPUSTKA, JAN KOZŁOWSKI

Jagiellonian University, Institute of Environmental Sciences, Cracow, Poland

4-14 Poster **The energetic cost of thermotolerance in *Drosophila melanogaster***

LUKE A. HOEKSTRA, KRISTI L. MONTOOTH

Indiana University, Department of Biology, Bloomington, United States

4-15 Poster **Reproductive Character Displacement in Female Green Tree Frogs - Reinforcement or Behavioral Plasticity?**

GERLINDE HOEBEL

University of Wisconsin, Department of Biological Sciences, Milwaukee, United States

4-16 Poster **Bumblebee offspring carry a cost with trans-generational immune priming**

BEN M. SADD, PAUL SCHMID-HEMPEL

ETH Zurich, Institute of Integrative Biology, Zurich, Switzerland

4-17 Poster **Reversible phenotypic plasticity and population extinction risk**

JOUNI LAAKSO[1], TARMO KETOLA[2], VEIJO KAITALA[1]

[1]University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland
[2]University of Jyväskylä, Department of Biological and Environmental Sciences, Jyväskylä, Finland

4-18 Poster **Polyphenism in the mouth forms of *Pristionchus pacificus***

GILBERTO BENTO, AKIRA OGAWA, CHRISTOPH DIETERICH, RALF J. SOMMER

Max Planck Institute for Developmental Biology, Department of Evolutionary Biology, Tuebingen, Germany

4-19 Poster **Probing the limits of plasticity: quantitative genetic analyses of risk-induced hatching**

IVAN GOMEZ-MESTRE[1,2], JUSTIN C. TOUCHON[2], VICTORIA L. SACCOCCIO[2], KAREN M. WARKENTIN[2]

[1]Donana Biological Station, Wetland Ecology, CSIC, Spain
[2]Boston University, Department of Biology, Boston, United States

4-20 Poster **Antagonistic inducible polyphenism in a cannibalism population**

KINYA NISHIMURA[1], OSAMU KISHIDA[2], TAKUYA IKAWA[1]

[1]Hokkaido University, Graduate School of Fisheries Sciences, Hakodate, Japan
[2]Kyoto University, Center for Ecological Research, Shiga, Japan

4-21 Poster **Inducible defences: reaction norms or threshold traits?**

THOMAS O. SVENNUNGSEN[1], ØISTEIN H. HOLEN[1], OLOF LEIMAR[2]

[1]University of Oslo, CEES, Department of Biology, Oslo, Norway
[2]Stockholm University, Department of Zoology, Stockholm, Sweden

4-22 Poster **Population differentiation and phenotypic plasticity in a polymorphic sperm storage organ**

MARTIN A. SCHÄFER, DAVID BERGER, STEPHANIE S. BAUERFEIND, WOLF U. BLANCKENHORN

University of Zurich, Zoological Museum, Zurich, Switzerland

4-23 Poster **Variation in survival and rates of development in *Austrolebias* annual killifish**

TOM J.M. VAN DOOREN

Leiden University, Institute of Biology, Leiden, Netherlands

4-24 Poster **Independent, repeated evolution of an ‘insular’ phenotype of nine-spined stickleback**

GABOR HERCZEG, ABIGÉL GONDA, JUHA MERILÄ

University of Helsinki, Ecological Genetics Research Unit, Department of Biological and Environmental Sciences, Helsinki, Finland

4-25 Poster **Dynamics of sex determination systems**

CHRISTINE GROSSEN, SAMUEL NEUENSCHWANDER, NICOLAS PERRIN

University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

Diversity of host-microbe symbioses

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Turin 2009

5

Program

Tuesday August 25 - **Symposium 5**

Location: Room 6

Diversity of host-microbe symbioses

Organizers:
Maurizio Casiraghi, Università degli Studi Milano Bicocca, Italy
Hinrich Schulenburg, University of Tuebingen, Germany
Telmo Pievani,Università degli Studi Milano Bicocca, Italy
Christian Braendle, Centre d'Immunologie de Marseille, France

9.45 - 10.15	**THOMAS C. G. BOSCH** (invited) Host-microbe communication in the Basal Metazoan *Hydra*
10.15 - 10.45	**CLAUDIO BANDI** (invited) Conflicts and cooperation in the evolution of host-symbiont interactions
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**MATHIEU SICARD** Reinforcement speciation in terrestrial isopods infected by *Wolbachia*
11.35 - 11.55	**LAUREN B. CARRINGTON** Ongoing evolution of the interaction between a bacterial endosymbiont and its *Drosophila* host
11.55 - 12.15	**PHILIPPE GAYRAL** Phylogeny of Banana streak virus reveals recent and repetitive endogenization in the genome of its banana host (*Musa* sp.)
12.15 - 12.35	**STÉPHANE DE MITA** Evolution of Nod factor perception
12.35 - 13.35	*Lunch*
13.35 - 13.55	**MARIO X. RUIZ-GONZALEZ** Three eukaryotic kingdoms of life interacting in a novel and highly specialised mutualism
13.55 - 14.15	**MARIO FARES** Antagonistic mutations mediate the survival of endosymbiotic bacterial genomes
14.15 - 14.35	**MARGRIET VAN ASCH** Facultative symbionts affects fitness, parasitoid resistance and host plant specialisation in the pea aphid
14.35 - 14.55	**CHRISTOPH VORBURGER** Symbiont-mediated coevolution in aphid host-parasitoid systems
14.55 - 15.25	*Coffee break*

5-1 Oral

HOST-MICROBE COMMUNICATION IN THE BASAL METAZOAN *HYDRA*

Thomas C. G. Bosch [1], Sebastian Fraune [1]

[1]*Christian-Albrechts-University of Kiel, Zoological Institute, Kiel, Germany*

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Epithelia are colonized by complex communities of microbes. Although a topic of long-standing interest, understanding the evolution of microbial communities has resisted analysis. Cnidaria are amongst the simplest animals at the tissue grade of organization. In order to systematically uncover the components of host defense in the complex interaction of host and microbiota, we study the freshwater cnidarian *Hydra*. Previous work has identified receptors, signal transduction cascades and effector molecules involved in *Hydra´*s epithelial defense (Bosch et al., 2009). We previously have also shown (Fraune & Bosch, 2007) that the *Hydra* epithelium actively selects and shapes its microbial community indicating distinct selective pressures imposed on the epithelium. Here, we present two observations which may have profound impact on understanding the maintenance of tissue homeostasis and the host´s interaction with its microenvironment: (i) *Hydra* in which tissue homeostasis was experimentally disturbed by eliminating distinct cell types from the epithelium display significant differences in the microbial communities. (ii) Overexpression of an antimicrobial peptide in ectodermal epithelial cells has drastic effects on the bacterial community resulting in reduced bacterial load and changes in the composition of the colonizing microbiota. Together, these insights indicate a link between host tissue and microbiota, and promise to unveil ancient mechanisms derived from the in vivo context of a whole epithelial organism that control tissue and host-microbe homeostasis.

5-2 Oral

CONFLICTS AND COOPERATION IN THE EVOLUTION OF HOST-SYMBIONT INTERACTIONS

Claudio Bandi [1], Chouaia Bessem [1], Sara Epis [1], Dario Pistone [1], Davide Sassera [1]

[1]Università degli Studi di Milano, DIPAV, Sezione di Patologia Generale e Parassitologia, Milano, Italy

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There are forms of symbiosis that dramatically emphasize the ‘power’ of natural selection. This is the case of a number of symbiotic microorganisms of insects and other arthropods, that are vertically transmitted to the progeny of the host through the female. This uniparental transmission implies a conflict between the interests of the symbionts (whose reproductive success is linked to the success of females, or even to the success of those particular females that harbor them), and the interests of the hosts as a whole (where males, or even uninfected females, are not useful to the symbiotic microorganisms). In these form of symbiosis, natural selection displays its strong power. Indeed, characteristics that would appear ununderstandable (e.g. the appearance of sterilized females, or the death of male embryos) can found an explanation if we focus our attention on the interests of the symbionts, rather than on the interest of the hosts. On the other side, other forms of symbiosis emphasize the role of ‘cooperation’ between organisms belonging to different species, perhaps in contradiction with selection-centered evolutionary views, and providing new insights into how macromutations might have occurred during evolution. Charles Darwin was obviously not aware of the discoveries in symbiosis of the last half of the XXth century, and he was certainly not aware of the existence of microorganisms capable of sterilizing hosts not useful for their own transmission to the progeny. However, Darwin insights can be re-interpreted and re-evaluated on the basis on novel discoveries, in symbiosis as well as in other fields.

5-3 Oral

REINFORCEMENT SPECIATION IN TERRESTRIAL ISOPODS INFECTED BY *WOLBACHIA*

Mathieu Sicard [1], Yves Caubet [1], Roland Raimond [1], Laura Ceyrac [1], Monique Johnson [1],
Didier Bouchon [1], Pierre Greve [1]

[1]*Université de Poitiers-CNRS, LEES, Poitiers, France*

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The reinforcement theory states that postmating isolation between populations should induce a selection pressure promoting premating isolation and thus reinforceisolation between populations. Reinforcement speciation relies on postmating incompatibilities from various nuclear and cytoplasmic origins. The cytoplasmic incompatibility (CI) caused by the maternally transmitted bacteria of the genus *Wolbachia* is one factor that could catalyze reinforcement speciation in arthropods. Such incompatibility is observed when the sperm originates from infected males fertilizes either (i) not infected females (i.e. unidirectional CI) or (ii) females infected with a different *Wolbachia* strain (i.e. bidirectional CI). Because CI leads to reduced gene flows between individuals that differ in infection status, *Wolbachia* could be regarded as promoting speciation. In particular, recent theoretical and empirical studies have shown that *Wolbachia*-induced CI can generate reinforcement between populations in conjunction with nuclear factors. In this talk, we will present how *Wolbachia* promotes postmating isolation between two subspecies of *Porcellio dilatatus* by cytoplamic incompatibility. Such isolation is also shown as reinforced by premating avoidance of incompatible partners. This core of data suggests that *P. dilatatus* is undergoing a reinforcement speciation process influenced by *Wolbachia.*

5-4 Oral

ONGOING EVOLUTION OF THE INTERACTION BETWEEN A BACTERIAL ENDOSYMBIONT AND ITS *DROSOPHILA* HOST

Lauren B. Carrington [1], Andrew R. Weeks [1], Ary A. Hoffmann [1], Michael Turelli [2]

[1]*University of Melbourne, Department of Genetics, Melbourne, Australia*
[2]*University of California at Davis, Section of Evolution and Ecology, Davis, United States*

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It is rare to observe interactions between a symbiont and its host evolve in nature over a period of decades. However, in California, USA, the interaction between *Drosophila simulans* and the *Wolbachia* variant, *w*Ri, which induces cytoplasmic incompatibility (CI) between infected males and uninfected females, has evolved significantly in the last 20 years. Theoretical predictions were made ~15 years ago about the expected paths of coevolution. Data from the early 2000s demonstrated that, consistent with these predictions, the *Wolbachia* in these populations evolved to increase (rather than decrease) the fecundity of infected females. Field data from 2008 indicate the levels and patterns of maternal transmission and cytoplasmic incompatibility are similar to what was observed in nature in the mid-1990s. However, as predicted, the level of CI has significantly declined in some lines. This effect could be caused by evolution of either *w*Ri or *D. simulans*. By combining backcrossing of the maternally inherited *Wolbachia* with curing of infected isofemale lines, the relative contributions of host and *Wolbachia* evolution can be determined.

5-5 Oral

PHYLOGENY OF BANANA STREAK VIRUS REVEALS RECENT AND REPETITIVE ENDOGENIZATION IN THE GENOME OF ITS BANANA HOST (*MUSA* SP.)

Philippe Gayral [1], Marie-Line Caruana [1]

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Banana streak virus (BSV) is a plant dsDNA pararetrovirus that possess hallmarks of typical viral parasites: it infects banana plants (*Musa* sp.) and causes Banana Streak Disease in tropical crops. Although integration is not required in the replication cycle of BSV, the genome of banana (*Musa* sp.) contains numerous BSV endogenous pararetrovirus sequences (EPRVs). This unusual interaction may benefit to both partners. On the one hand, infectious BSV EPRVs are able to release a functional viral genome in interspecific banana hybrids only. On the other hand, banana might use BSV EPRVs for virus resistance via homology-dependant gene-silencing mechanisms. BSV-banana may therefore be shifting from parasitic to symbiotic interaction. Recent studies revesaled a large molecular diversity of non-integrated BSV, while other focused on BSV EPRV sequences only. The present study investigates the evolutionary history of BSV integration in banana, inferred from phylogenetic relationships between BSV and BSV EPRVs. We compared the relative evolution rates and selective pressures between endogenous and non-integrated viral sequences. At least 27 recent independent integration events occurred after the divergence of three banana species, indicating that viral integration is a recent and frequent phenomenon. We observed a strong relaxation of selective pressure when integrated in the plant genome. Additionally, we observed a significant decrease in EPRV evolution rate compared to BSV, reflecting the difference in evolution rate between non-integrated BSV and plant genome. The comparison of our results with the evolution rate of *Musa* genome suggested that EPRVs played an active role in BSV diversity and evolution.

5-6 Oral

EVOLUTION OF NOD FACTOR PERCEPTION

Stéphane De Mita [1], Arend Streng [1], René Geurts [1], Ton Bisseling [1]

[1]*Wageningen University, Laboratory of Molecular Biology, Wageningen, Netherlands*

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Approximately 90% of the species of the legume family form a symbiosis with nitrogen-fixing bacteria (rhizobia). The interaction requires mutual recognition between both partners and the growth of specific organs, root nodules. The perception of Nod factors released by rhizobia plays a central role in both recognition and nodule growth initiation. Variation of the structure of Nod factors mediates a strict host specificity. They are perceived by two genes belonging to the LysM-receptor kinase protein family, named LYK3 and NFP in *Medicago truncatula*. All responses to rhizobia require both of these genes. We aim to understand the role of evolution of these genes at the molecular level with respect to the evolution of symbiosis. While NFP is a single-copy gene in all studies species so far, LYK3 has undergone a number of duplications. In *M. truncatula* LYK3 belong to a cluster of six genes, plus an unlinked gene LYK9. We find that all LYK3 copies in *M. truncatula* and other legumes originate from two duplications that occurred shortly before the most recent common ancestor of legumes. Non-legume species have one homolog that controls defense responses against pathogenic fungi. The pattern of evolution of LYK3 and NFP is examined through the pattern of nucleotide substitution rates. Our results suggest that initial duplications may have allowed uncoupling the initial defense function of LYK3 and the new symbiotic function (neofunctionalization) while later coevolution of signalling molecules has driven rapid evolution of specific binding sites in both LYK3 and NFP.

5-7 Oral

THREE EUKARYOTIC KINGDOMS OF LIFE INTERACTING IN A NOVEL AND HIGHLY SPECIALISED MUTUALISM

Mario X. Ruiz-Gonzalez [1], Celine Leroy [2], Herve Gryta [1], Patricia Jargeat [1], Alain Dejean [2], Jerome Orivel [1]

[1]Université Paul Sabatier, Laboratoire Evolution et Diversité Biologique, Toulouse, France
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Mutualistic interactions between ants and plants or fungus led to the evolution of complex symbioses and evolutionary innovations such as agriculture. We study a system involving three different partners: a myrmecophytic plant hosting two ant species of the genus *Allomerus* that manipulate a fungus for purposes other than nutrition. First, we explore the ants' use or exploitation of the fungus to build a robust trap strengthened by the mycelium of the fungus to capture prey. Second, through molecular analysis we are able to describe the phylogenetic position of the fungus. Thirdly, we discovered that the fungus and the plant have developed a new kind of interaction in which the fungus provides the plant with nitrogen that is possibly absorbed by its mycelium while the ants feed on the prey that they capture in the trap. Finally, we studied the population genetic structure of the fungi in the traps of different ant populations in French Guiana both spatially and in terms of transmission mode by the ants. Our results point to an extreme evolutionary output in the field of interactions among different species.

5-8 Oral

ANTAGONISTIC MUTATIONS MEDIATE THE SURVIVAL OF ENDOSYMBIOTIC BACTERIAL GENOMES

Mario Fares [1], Christina Toft [1]

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Identification of interaction between mutations' effects is crucial to the understanding of the emergence of sex, evolution of ploidy, reproductive isolation and fixation of deleterious mutations in small populations. In endosymbiotic bacteria of insects, the rate of fixation of slightly deleterious mutations is accelerated due to genetic drift, lack of molecular repair mechanisms and clonal intergenerational transmission. Despite this, endosymbiotic bacteria have persisted for tens to hundreds of millions of years. Several studies have proposed that the over-produced chaperonin GroEL can abate the fitness cost of accumulated deleterious mutations in these bacteria. Here we perform an exhaustive genome analysis of the distribution of slightly deleterious mutations in endosymbionts of aphids and carpenter ants. We show that antagonistic intra- and inter-protein mutations assist GroEL in ameliorating the effects of slightly deleterious mutations and in precluding the demise of endosymbiotic bacterial lineages. We also identify a mutational threshold beyond which GroEL proofs inefficient in buffering structurally destabilizing mutations. Our results underpin biological innovation in these bacteria mediated by the emergence of genomic and proteomic mechanisms that synergize to overcome the cross-organism biological barriers.

5-9 Oral

FACULTATIVE SYMBIONTS AFFECTS FITNESS, PARASITOID RESISTANCE AND HOST PLANT SPECIALISATION IN THE PEA APHID

Margriet van Asch [1], Ailsa H.C. McLean [1], Charles H.J. Godfray [1], Julia Ferrari [2]

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The biology of many insects is strongly influenced by mutualisms with symbiotic bacteria. These bacteria shape many aspects of their hosts' life histories. We use the pea aphid (*Acyrthosiphon pisum*) as a model system to explore the effects of symbionts on their hosts. In addition to an obligate symbiont (*Buchnera*), pea aphids also carry several facultative symbionts. These have been associated with resistance to natural enemies and with resistance to abiotic stress. The presence of bacteria is also linked to host plant use, and may thus play a role in host plant specialisation, and ultimately speciation.

We look here at the effects of symbionts on aphid performance, using aphids artificially infected with different strains of *Hamiltonella insecticola.* In addition, we also look at aphids cured from their symbiont. We investigate the effect of the symbionts on interactions between the aphid hosts and one of their parasitoids, *Aphidius ervi*, as well as general aphid performance on both the original host plants and on *Vicia faba*.

The results will help us to understand the variation in effects between facultative symbionts occurring in different pea aphid populations and demonstrate the importance of bacterial symbionts in shaping the biological interactions of pea aphids.

5-10 Oral

SYMBIONT-MEDIATED COEVOLUTION IN APHID HOST-PARASITOID SYSTEMS

Christoph Vorburger [1], Christoph Sandrock [1], Alexandre Gouskov [1], Lukas Gehrer [1], Paula Rodriguez [1]

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The present understanding of host-parasite coevolution is largely derived from models based on interaction loci, i.e. polymorphic genes in host and parasite that interact to determine the outcome of infection. In aphids, however, much of the variation in resistance to parasitoids and pathogens is due to endosymbiotic bacteria rather than genetic differences among hosts. We provide evidence (1) that the symbiont's ability to protect hosts against parasitoids evolves readily as it occurs in even more bacteria than previously thought, (2) that parasitoid populations exhibit genetic variation in the ability to overcome symbiont-conferred resistance, and (3) that the benefits of harbouring defensive symbionts may be reduced by high induced costs of symbiont-derived defenses. Based on these findings, we argue that aphid-parasitoid systems represent a case of symbiont-mediated coevolution that can only be understood by accounting for the complex interactions among host, symbiont and parasitoid genotypes, and we highlight promising avenues of future research towards this goal.

5-1 Poster **Serpentine soils do not limit ectomycorrhizal fungal diversity**

SARA BRANCO

University of Chicago, Committe on Evolutionary Biology, Chicago, United States

5-2 Poster **Plasticity and adaptation in symbiosis: Depth differentiation in the Mediterranean sea whip *Eunicella singularis* (Esper 1791)**

JEROME CATANEO, DIDIER FORCIOLI, PAOLA FURLA

Universite de Nice - Sophia Antipolis E.A. 4228, Nice, France

5-3 Poster **The direct fitness effects of male-killer infection on female hosts**

SHERIF M. ELNAGDY[1,2], MIKE N. MAJERUS[2]

[1]Cairo University, Department of Botany, Cairo, Egypt
[2]University of Cambridge, Department of Genetics, Cambridge, United Kingdom

5-4 Poster **Cell division in the endosymbiont bacterium of the trypanosomatid protozoan *Crithidia deanei***

ROSANA E.G. GONÇALVES[1], LUCÍA YIM[2], CHRISTIAN PROBST[1], LEONARDO FOTI[1], ADRIANA C.S. UMAKI[1], MARIA C.M. MOTTA[3], WANDERLEY DE SOUZA[3], MARCO A. KRIEGER[1], SAMUEL GOLDENBERG[1], STENIO P. FRAGOSO[1]

[1]Instituto Carlos Chagas, Curitiba, Brazi
[2]Facultad de Medicina de Montevideo, Departamento de Desarrollo Biotecnológico, Montevideo, Uruguayl
[3]Universidade Federal do Rio de Janeiro, Instituto de Biofísica Carlos Chagas Filho, Rio de Janeiro, Brazil

5-5 Poster **Coevolution mtDNA of *Drosophila melanogaster* and its primary endosymbiont *Wolbachia***

YURIY Y. ILINSKY

Institute of Cytology and Genetics, Laboratory of Populations Genetics, Novosibirsk, Russia

5-6 Poster **Microbial Diversity in Bumble Bee Hosts**

HAUKE KOCH, PAUL SCHMID-HEMPEL

ETH Zürich, Institute of Integrative Biology, Zürich, Switzerland

5-7 Poster **Evolution of dependence upon *Wolbachia* symbiosis in two parasitoid wasps**

NATACHA KREMER, EDWIGE RANCÈS, DELPHINE CHARIF, HÉLÈNE HENRI, FABRICE VAVRE

Université Lyon 1, Laboratoire de Biométrie et Biologie Evolutive, Lyon, France

5-8 Poster **Intraspecific genetic variation of *Abies alba* Mill. has an effect on the associated ectomycorrhiza community**

SASCHA LIEPELT[1], EVA CREMER[1,2], KATHRIN DONGES[3], KARL-HEINZ REXER[3], GERHARD KOST[3], BIRGIT ZIEGENHAGEN[1]

[1]Philipps-University of Marburg, Department of Conservation Biology, Marburg, Germany
[2]ASP, Teisendorf, Germany
[3]Philipps-University of Marburg, Department of Mycology, Marburg, Germany

5-9 Poster **A Host-Parasite Model: *Daphnia-Caullerya mesnili***

JENNIFER N. LOHR, JUSTYNA WOLINSKA

Ludwig-Maximilians-Universitaet-Muenchen, Department of Biology II, Munich, Germany

5-10 Poster **Simple genetics underlie highly specific host × parasite genotypic interactions in the *Daphnia Pasteuria* system**

PEPIJN LUIJCKX, DIETER EBERT, FRIDA BEN-AMI, HARRIS FIENBERG, LOUIS DU PASQUIER
University Basel, Zoologisches Institut , Basel, Switzerland

5-11 Poster ***Wolbachia* dynamics through host evolutionary radiation: a case study in endemic Fijian damselflies**

PATRÍCIA MARTINS SIMÕES[1], CHRISTOPHER BEATTY[2], HANS VAN GOSSUM[3], MARIE-FRANCE SAGOT[4], TOM SHERRATT[5], SYLVAIN CHARLAT[1]
[1]Université Claude Bernard Lyon1, LBBE, VILLEURBANNE cedex, France
[2]Universidade de Vigo, Grupo de Ecoloxía Evolutiva, Departamento de Ecoloxía e Bioloía Animal, EUET Forestal, Pontevedra, Spain
[3]University of Antwerp Groenenborgerlaan 171, Evolutionary Biology Group, Antwrep, Belgium
[4]Université Claude Bernard Lyon1, UMR CNRS 5558 LBB, VILLEURBANNE cedex, France
[5]Carleton University, Department of Biology, Ottawa, Canada

5-12 Poster **Facultative symbionts influence host plant use in the pea aphid**

AILSA H.C. McLEAN[1], JULIA FERRARI[2], CHARLES J.H. GODFRAY[1], MARGRIET VAN ASCH[1]
[1]University of Oxford, Department of Zoology, Oxford, United Kingdom
[2]University of York, Department of Biology, York, United Kingdom

5-13 Poster **High prevalence of a virus manipulating its insect host behaviour and consequence on host community structure**

SABINE PATOT, JULIEN VARALDI, FRÉDÉRIC FLEURY
Université de Lyon - Lyon 1, Laboratory of Biometry and Evolutive Biology, Lyon, France

5-14 Poster **The endosymbionts of scale insects: Does it matter who they are and where they came from?**

LAURA ROSS[1,3], GREG COLBY[2], BENJAMIN B. NORMARK[2], IDO PEN[1], DAVID M. SHUKER[3]
[1]University of Groningen, Centre for Ecological and Evolutionary Studies, Haren, Netherlands
[2]University of Massachusetts, Department of Plant Soil & Insect Sciences, Amherst, United States
[3]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom

5-15 Poster **Asexual grass endophyte symbiosis – mutual exploitation or reciprocal cooperation?**

KARI SAIKKONEN
MTT Agrifood Research Finland, Plant Production Research and Plant Protection, Jokioinen, Finland

5-16 Poster **Identification of proteins found in fungus-growing ant fecal material**

MORTEN SCHIOETT, HENRIK H. DE FINE LICHT, JACOBUS J. BOOMSMA
University of Copenhagen, Department of Biology, Copengahen, Denmark

5-17 Poster **48 generations of real-time covolution between *C. elegans* and its microparasite *Bacillus thuringiensis***

REBECCA D. SCHULTE[1], CARSTEN MAKUS[2], BARBARA HASERT[2], NICO K. MICHIELS[3], HINRICH SCHULENBURG[4]
[1]University of Osnabrueck, Department of Behavioural Biology, Osnabrueck, Germany
[2]University of Muenster, Institute for Evolution and Biodiversity, Muenster, Germany
[3]University of Tuebingen, Department of Animal Evolutionary Ecology, Tuebingen, Germany
[4]Christian-Albrechts-Universitaet zu Kie, Zoological Institute, Kiel, Germany

5-18 Poster **Consequences of feminizing cytoplasmic factors on host genetic structure: the case of *Armadillidium vulgare* and *Wolbachia***

SEBASTIEN VERNE, MONIQUE JOHNSON, DIDIER BOUCHON, FREDERIC GRANDJEAN
Université de Poitiers, UMR 6556, Laboratoire Ecologie Evolution Symbiose, Poitiers, France

5-19 Poster **Different habitats select endophyte-fine fescue symbioses with different characters**

PIIPPA R. WALI[1], RIITTA AHONEN[1], KALLE HELLSTRÖM[1], MARJO HELANDER[2], KARI SAIKKONEN[3]
[1]University of Oulu, Department of Biology, Oulu, Finland
[2]University of Turku, Department of Biology, Turku, Finland
[3]MTT Agrifood Research Finland Plant Production, Jokioinen, Finland

5-20 Poster **Sexual transmission of cloacal bacteria in a monogamous seabird: Effects on fitness and role in the evolution of mating strategies**

JOËL WHITE[1,2], ETIENNE DANCHIN[2], HERVÉ MULARD[3], PASCAL MIRLEAU[4], PHILIPP HEEB[2], RICHARD WAGNER[5]
[1]Konrad Lorenz Institute for Ethology, Austrian Academy of Sciences, Vienna, Austria
[2]Université Paul Sabatier, Laboratoire Evolution et Diversité Biologique, Toulouse, France
[3]ENES Université Jean Monnet, St Etienne, France
[4]IMEP Université Paul Cézanne, Marseille, France
[5]KLIVV, Austrian Academy of Sciences, Vienna, Austria

The evolution of conflict and cooperation: when theory meets data

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6

Program

Wednesday August 26 - **Symposium 6**

Location: Room 1

The evolution of conflict and cooperation: when theory meets data

Organizers:	*Suzanne Alonzo, Yale University, New Haven, United States* *Stuart West, University of Edinburgh, United Kingdom*
9.45 - 10.15	**ALLEN J. MOORE** (invited) Cooperation and conflict in the evolution of biparental care
10.15 - 10.45	**MICHAEL CANT** (invited) Threats and cooperation in animal societies: the case of the banded mongoose
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**REBECCA FEATHERSTON** Female Control: evidence for trait evolution via maternal/paternal genome conflict over progeny sex ratio
11.35 - 11.55	**HANNAH L. DUGDALE** Fitness consequences and heritability of helping behaviour in the Seychelles warbler *Acrocephalus sechellensis*
11.55 - 12.15	**FREYA HARRISON** Cooperation over care: do parents compensate for reduced partner effort?
12.15 - 12.35	**CLARE P. ANDREWS** The resolution of parent-offspring conflict over parental care: distinguishing between alternative models for the evolution of offspring begging
12.35 - 12.55	**FRANCISCO UBEDA** Evolution of Genomic Imprinting with Bi-parental Care: Implications for Prader-Willi and Angelman Syndromes
12.55 - 13.55	*Lunch*
13.55 - 14.25	**ANDY GARDNER** (invited) Inclusive fitness: theory and practice
14.25 - 14.45	**LUKE HOLMAN** Do queen pheromones facilitate cooperation or create conflict?
14.45 - 15.05	**ANIEK. B. F. IVENS** Conflict resolution in mutualisms: the role of dispersal and partner diversity in theoretical and empirical model systems

15.05 - 15.35	*Coffee break*
15.35 - 15.55	**NEIL J. BUTTERY** What is cheating? Self-promotion and social-repression in a social amoeba
15.55 - 16.15	**R. FREDRIK INGLIS** Spite and Virulence in *Pseudomonas aeruginosa*
16.15 - 16.35	**ROLF KUEMMERLI** Repression of competition and the evolution of cooperation: an experimental test with bacteria
16.35 - 16.55	**AMMOTZ ZAHAVI** Cooperation Competition and the Handicap principle

6-1 Oral

COOPERATION AND CONFLICT IN THE EVOLUTION OF BIPARENTAL CARE

Allen J. Moore [1]

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Classically, shared parental care has been viewed as cooperation, where parents cooperate in care that benefits their offspring. More recently, biparental care has been viewed from the perspective of sexual conflict, with each parent attempting to have the other provide the bulk of the care. Both of these perspectives reflect perspectives based on costs and benefits, and therefore selection. Does information on the genetic basis of care help us reconcile these perspectives? If we consider the entire evolutionary process – that is, both genetics and selection – does this provide the information necessary to understand how conflict and cooperation can coexist in species with biparental care? I this talk I will explore how conflict and cooperation might coexist in the evolution of biparental care, and argue that allowing a single view to dominate limits our understanding of how complex social behaviour might evolve.

6-2 Oral

THREATS AND COOPERATION IN ANIMAL SOCIETIES: THE CASE OF THE BANDED MONGOOSE

Michael Cant [1]

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Cooperative animal societies are rife with internal conflict over the distribution of direct fitness among group members. In many species dominant individuals exert direct control over reproduction, for example by killing the offspring of subordinates that reproduce. Where such forms of control are ineffective current theory suggests that dominants will use eviction from the group to limit reproductive competition, and that subordinates will respond to the threat of eviction by exercising reproductive restraint. Here I present data from a thirteen-year study of wild banded mongooses aimed at testing this model, and discuss more generally the role of threats in social evolution. The data confirm that eviction is an effective means of limiting subordinate reproduction, but also suggest that eviction threats are ineffective to induce pre-emptive cooperation among multiple subordinates. The results help to identify general circumstances where threats will be effective at inducing compliance or cooperation in animal societies, and when by contrast enforcement will usually require overt intervention. Identifying hidden threats may require innovative experimental approaches; the potential reward is a much-improved understanding of the full range of forces shaping social evolution.

6-3 Oral

FEMALE CONTROL: EVIDENCE FOR TRAIT EVOLUTION VIA MATERNAL/PATERNAL GENOME CONFLICT OVER PROGENY SEX RATIO

Rebecca Featherston [1], Theresa Jones [1], Mark Elgar [1]

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Variation in the operational sex ratio may have a dramatic impact on the potential for sexual conflict within a population because it changes the frequency of interactions between the sexes. No study has tested explicitly whether maternal and paternal sex-determining genes can be in conflict over progeny sex-ratio. Moreover, the possible evolution of traits aiding the avoidance of costs associated with such a conflict has not been explored. In monogenic sciarid species, females are genetically predisposed to produce single-sex progeny, whilst in digenic species females have full control over progeny sex ratio. In both groups, males display paternal genome loss in the germline. Conflict between the sexes may arise because males transfer their genome only if their female produces daughters, and females transfer a significantly larger proportion of their genome by producing sons. We used two species from the genus *Bradysia*, one monogenic and one digenic, to explore whether females have evolved conflict avoidance strategies. First, we tested experimentally whether monogenic daughter-producing females were choosier selecting mates than monogenic son-producing females, by comparing female mate-rejection behaviours. We then tested whether monogenic daughter-producing mothers biased the proportion of daughter-producing and son-producing daughters in a progeny, depending on their mate's fitness. Finally, we tested whether digenic females producing female-biased progeny were similarly choosier selecting mates and whether progeny sex ratio was modified depending on their mate's fitness. Combined, our results indicate that sciarid females have evolved traits potentially selected to avoid the costs associated with maternal/paternal genome conflict over progeny sex ratio.

6-4 Oral

FITNESS CONSEQUENCES AND HERITABILITY OF HELPING BEHAVIOUR IN THE SEYCHELLES WARBLER *ACROCEPHALUS SECHELLENSIS*

Hannah L. Dugdale [1], David S. Richardson [2], Jan Komdeur [3], Terry Burke [1]

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Individuals are selected to maximise their fitness. In cooperatively-breeding species, individuals may forgo breeding in order to help raise offspring that are not their own. Why individuals breed cooperatively has therefore been the focal question of many studies. Microevolution may occur when selection acts on heritable traits; however, both the strength of selection and the heritability of traits may be influenced by environmental conditions. Understanding how all of these factors interact is vital for a complete understanding of evolutionary processes. Nevertheless, studies of cooperative breeding have tended to focus on the environmental factors that lead to the evolution of helping, with few studies investigating the heritability of helping behaviour. We use a novel Bayesian method to construct a multi-generation pedigree, based on a 14–year dataset of ca 1,250 Seychelles warblers that have been genotyped at 30 microsatellite loci. We then use this pedigree to calculate three fitness measures (lifetime reproductive success, individual fitness and de-lifed fitness), to measure the strength of selection on helping behaviour, and to assess the environmental and genetic basis of helping behaviour. We combine our findings to improve our understanding of the adaptive basis of reproductive decisions in the cooperatively breeding Seychelles warbler.

6-5 Oral

COOPERATION OVER CARE: DO PARENTS COMPENSATE FOR REDUCED PARTNER EFFORT?

Freya Harrison [1], Zoltán Barta [2], Innes C. Cuthill [3], Tamás Székely [1]

[1]*University of Bath, Department of Biology & Biochemistry, Bath, United Kingdom*
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Biparental care of offspring is a form of cooperation between the sexes. However, this relationship is not free from conflict: by contributing less to care and forcing its partner to work harder, an individual can maintain its energy reserves and increase its chances of remating. So how can selection maintain biparental care given this temptation to defect? The answer lies in how parents react to changes in each other's care effort. Models suggest that cooperation over care is only an evolutionarily stable strategy if each parent partially compensates for any reduction in its partner's care effort. Experimental studies designed to reveal responses to reduced partner effort have focussed on birds; we present the first meta-analysis of these experiments. Across 54 studies, the mean response to partner removal or reduced partner effort was partial compensation, but there was considerable variation in responses. Differences between male and female responses were mediated by the type of manipulation and by life history factors including levels of extra-pair paternity (EPP) and sexual dimorphism. Males may cooperate with the female in an attempt to gain future paternity. Our results may be relevant to understanding biparental care in other animal clades and suggest avenues for future empirical research. We also begin to address whether avian parents negotiate with one another over levels of care provision.

6-6 Oral

THE RESOLUTION OF PARENT-OFFSPRING CONFLICT OVER PARENTAL CARE: DISTINGUISHING BETWEEN ALTERNATIVE MODELS FOR THE EVOLUTION OF OFFSPRING BEGGING

Clare P. Andrews [1], Per T. Smiseth [2]

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Parent-offspring conflict arises as a consequence of the costs that parents incur from providing care for their offspring combined with asymmetries in relatedness between parents and offspring. Three types of models have been put forward to explain how offspring begging can provide an important mechanism underlying the evolutionary resolution of parent-offspring conflict: honest signaling, scramble competition and cost-free models of begging. Distinguishing between these models remains a fundamentally important yet unresolved problem in evolutionary biology because the models share common predictions. However, the models differ in their assumptions concerning who controls resource allocation and whether begging is costly or cost-free. Previous studies on altricial birds provide only limited and ambiguous evidence as to whether resource allocation is under parental or offspring control, and evidence concerning whether begging incurs costs is mixed. Here, we test these critical assumptions in the burying beetle *Nicrophorus vespilloides*. To determine whether resource allocation is under offspring or parental control, we manipulate (i) the offspring's ability to influence resource allocation by establishing asynchronous broods with controlled age-based competitive asymmetries, and (ii) the parent's ability to influence resource allocation by presenting the broods with either a live or a dead parent. We examine whether begging incurs opportunity costs through loss of time spent self-feeding and/or mortality costs through increased risk of filial cannibalism by parents. Our study provides the first comprehensive test of the two critical assumptions in a single study system, allowing us to differentiate between alternative models for the evolution of offspring begging.

6-7 Oral

EVOLUTION OF GENOMIC IMPRINTING WITH BI-PARENTAL CARE: IMPLICATIONS FOR PRADER-WILLI AND ANGELMAN SYNDROMES

Francisco Ubeda [1]

[1]*University of Tennessee at Knoxville, Department of Ecology and Evolutionary Biology, Knoxville, United States*

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Imprinted genes — through an expression conditioned by parental origin — violate Mendelian genetics. This form of genetic memory stirred the imagination of evolutionary biologists. Among the scholarship to unravel genomic imprinting, the Kinship Theory prevails as the most widely accepted explanation due to its capacity to shed many aspects of the imprinted genes' biology. Most assumptions underlying this theory did not escape scrutiny, however. One assumption remains overlooked: mothers are the only source of parental investment in mammals. But, is it reasonable to assume that the fathers' contribution is negligible? In some key mammalian orders, it is not. Besides rodents, the fathers' contribution is hardly negligible among primates, including humans. In this research, I generalize the Kinship Theory of Genomic Imprinting beyond maternal contribution only. As a result, I derive new conditions for the evolution of imprinting and discover that the same gene may show the opposite pattern of imprinting based on different levels of parental investment; the reversion, interestingly, does not require that fathers contribute more resources than mothers. This exciting outcome underscores the intimate connection between the Kinship Theory and the social structure of the organism considered. Finally, the insight gained from my model enabled me to explain the clinical phenotype of Prader-Willi Syndrome. Children suffering from this syndrome exhibit a striking biphasic phenotype characterized by poor sucking and reduced weight before weaning but by voracious appetite and obesity after weaning. Theoretically, the Kinship Theory has been doubted as a reasonable explanation for this clinical phenotype. Practically, the post-weaning phenotype remains the primary concern of pediatricians treating Prader-Willi children. In this research, I reconcile the clinical phenotype of Prader-Willi Syndrome with the Kinship Theory, contending that the relative contribution of paternal resources increases after weaning. I also predict the genetic composition of the PWS/AS cluster, discuss the effects of new types of mutations and contemplate the potential side effects of reactivating silent genes for medical purposes.

6-8 Oral

INCLUSIVE FITNESS: THEORY AND PRACTICE

Andy Gardner [1]

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I review the inclusive fitness approach to social evolution, highlighting the interplay between theoretical modelling and empirical research on this topic.

6-9 Oral

DO QUEEN PHEROMONES FACILITATE COOPERATION OR CREATE CONFLICT?

Luke Holman [1], Stephanie Dreier [1], Charlotte G. Jørgensen [2], John Nielsen [3], Patrizia d'Ettorre [1]

[1]*University of Copenhagen, Section for Ecology and Evolution, Copenhagen, Denmark*
[2]*University of Copenhagen, Department of Medicinal Chemistry, Copenhagen, Denmark*
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Social insect societies have been described both as paradigms of cooperation and as uneasy alliances in which conflict is rife. The simultaneous action of cooperation and conflict is especially apparent in reproductive division of labour, as worker sterility may result from voluntary altruism and/or coercion by other individuals. In many species, queens are thought to produce pheromones that maintain worker sterility, and there has been debate about whether such pheromones are an honest signal to workers or a form of control. Using the ant *Lasius niger*, we show that a number of queen cuticular hydrocarbons reliably predict reproductive maturation and productivity. A synthetic version of the most predictive hydrocarbon inhibited worker ovarian development and aggression in a bioassay, making this the first sterility-inducing pheromone to be identified in any social insect other than the honeybee. Several lines of evidence indicate that the pheromone is mutually beneficial to both the queen and the workers. The pheromone is also apparently used by workers to identify and eliminate the least fertile queens in multi-queen colonies; the honesty of the signal may facilitate punishment of queens that selfishly under-invest in worker production and thereby select for greater cooperation.

6-10 Oral

CONFLICT RESOLUTION IN MUTUALISMS: THE ROLE OF DISPERSAL AND PARTNER DIVERSITY IN THEORETICAL AND EMPIRICAL MODEL SYSTEMS

Aniek. B. F. Ivens [1,2], Ido Pen [1], Jacobus J. Boomsma [2], Franz J. Weissing [1]

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In mutualisms two partner species live closely together and, typically, the partners' interests with respect to energy allocation will not be fully aligned. The stable mutualisms we observe might therefore be the result of ongoing conflict rather than harmonious cooperation.

A potential battleground for conflict between mutualistic partners is dispersal. The role of dispersal is ambiguous: it requires energy to be taken away from the system's productivity, but also has strong stabilizing potential in the form of condition dependent-dispersal by allowing individuals to avoid non-cooperativeness. We present an integrative mechanistic model for the co-evolution between investment into mutualism and condition-dependent dispersal, which enables us to assess the relative importance of dispersal for the evolutionary stability of mutualisms.

Dispersal also directly feeds back on the level of diversity of the dispersing partner, a second potential battlefield, since diversity requires energy allocation towards competition. Here, we investigate conflict resolution on partner diversity by comparing empirical data of two similar mutualisms: leaf-cutting ants and their fungal crops and the ant *Lasius flavus* and its root-aphid cattle. In both systems the mutualist is kept inside the ants' nest and at least fungus-growing ants are known to generally grow their fungus in a genetic monoculture. We now assess the genetic diversity for several species of aphids (displaying various degrees of dispersal) within *L.flavus* nests. This allows us to evaluate whether such reduction in partner diversity is a resolution specific for fungus-growing ants or a more general resolution of the conflict on partner diversity in mutualisms.

6-11 Oral

WHAT IS CHEATING? SELF-PROMOTION AND SOCIAL-REPRESSION IN A SOCIAL AMOEBA

Neil J. Buttery [1], Daniel E. Rozen [1], Jason B. Wolf [1], Christopher R.L. Thompson [1]

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The maintenance of cooperation is an evolutionary conundrum because, when organisms perform costly cooperative acts, they generally set the stage for exploitation by cheaters. Therefore, understanding cooperation also requires an understanding of the nature of cheaters and the strategies used to mitigate their effects. However, there is considerable confusion about how to distinguish social cheating from other possible causes of unequal competitiveness in social situations that can result in winners and losers without the need for cheating. To study this problem, we examined the success of naturally occurring genotypes of *Dictyostelium discoideum* in competitive interactions. Upon starvation, different *D. discoideum* genotypes will form chimeric fruiting bodies, consisting of dead stalk cells and viable spores. Here, we demonstrate that an apparent competitive dominance hierarchy of spore formation in chimera can be explained by dramatic differences among naturally occurring genotypes in their inherent allocation to stalk and spores. However, these data hide complex social interactions, where genotypes change their spore/stalk allocation when developed in chimera, with the magnitude and direction of changes in allocation dependent upon the genotype of their competitor. Using these changes in allocation patterns in chimera, we define and partition cheating into two forms: 1) promotion of individual fitness through selfish behavior ('self-promotion') and 2) coercion of other individuals (or genotypes) to act cooperatively ('social repression'). Our results demonstrate and define social interactions between *D. discoideum* isolates, thus providing a conceptual framework for the study of the genetic mechanisms that underpin social evolution.

6-12 Oral

SPITE AND VIRULENCE IN *PSEUDOMONAS AERUGINOSA*

R. Fredrik Inglis [1], Andy Gardner [2], Pierre Cornelis [3], Angus Buckling [1]

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Social interactions within populations of pathogenic microbes may play an important role in determining disease virulence. One such ubiquitous interaction is the production of anticompetitor toxins; an example of a spiteful behaviour, because it results in direct fitness costs to both the actor and recipient. Following from predictions made by mathematical models, we carried out experiments using the bacterium *Pseudomonas aeruginosa*, to test under what social conditions toxin (bacteriocin) production is favoured and how this in turn affects virulence in the larvae of the wax moth, *Galleria mellonella*. Consistent with theory, we found that the growth of bacteriocin producers relative to sensitive, non-producers is maximised when toxin producers are at intermediate frequencies in the population. Furthermore, growth rate and virulence in caterpillars was minimised when bacteriocin producers have the greatest relative growth advantage. These results suggest that spiteful interactions may play an important role in the population dynamics and virulence of natural bacterial infections.

6-13 Oral

REPRESSION OF COMPETITION AND THE EVOLUTION OF COOPERATION: AN EXPERIMENTAL TEST WITH BACTERIA

Rolf Kuemmerli [1], Piet van den Berg [2], Andy Gardner [1], Stuart A. West [1,3], Ashleigh S. Griffin [1,3]

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The repression of competition has been suggested as a mechanism that unifies the interest of individual entities, and thereby favours cooperation. While the repression of competition is regarded as one of the key forces having driven the major evolutionary transitions – from the chromosome level, to the evolution of multicellularity, to cooperation in human societies – there is a lack of experimental evidence demonstrating its importance. Here, we conduct the first experimental test of this theory using cooperative siderophore production by the bacterium *Pseudomonas aeruginosa* as our model trait. We set up patch-structured populations seeded with an even ratio of siderophore producing bacteria (cooperators) and non-siderophore producing mutants (cheat), and followed the consequences of repression of competition for the cooperator frequency over time. We found that cooperators were favoured when competition between the two strains was repressed. In contrast, cooperators did not increase in frequency when competition between the two strains occurred. These results were confirmed by a simulation model parameterized with the fitness values from our experiment. Altogether, our findings demonstrate the importance of repression of competition as a mechanism that favours cooperation, even in situations where relatedness among interacting individuals is relatively low.

6-14 Oral

COOPERATION COMPETITION AND THE HANDICAP PRINCIPLE

Ammotz Zahavi [1]

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Competition and cooperation are usually discussed as two opposing factors in the evolution of biological systems. Our observation of the cooperative system of the Arabian babblers (a cooperative breeding bird species), as well as our theoretical studies of the pattern of signals within the multicellular organism, suggest that natural selection can use the competition among biological entities as a building block for cooperation in social systems.

The contribution to the common resources of the biological system is usually considered altruism. However, I found that individuals often compete over the privilege to invest in the cooperation. I suggest that in most cases investing in the common good is a signal that advertises the ability or intentions of the investor. That investment is the handicap that proves the honesty of the individual's claim for a share in the common resource. This means that an investment in the cooperation can be achieved by individual selection, making any explanations based on indirect selection redundant.

The selection for reliability in signals (the handicap principle) suggests that signals - including sexual signals - are selected by a distinct selection mechanism, "signal selection", through which evolution can develop adaptive characters which the selection for efficiency alone would not have been able to evolve.

6-1 Poster **A general framework for the evolution of signal reliability**

SARA MITRI[1], DARIO FLOREANO[1], LAURENT KELLER[2]
[1]*Ecole Polytechnique Federale de Lausanne (EPFL), Laboratory of Intelligent Systems, Lausanne, Switzerland*
[2]*University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland*

6-2 Poster **Kin recognition and discrimination based on cuticular chemicals in subsocial spider *Stegodyphus lineatus***

LENA GRINSTED[1], TRINE BILDE[2], PATRIZIA D'ETTORRE[1]
[1]*University of Biology, Centre for Social Evolution, Copenhagen, Denmark*
[2]*University of Aarhus, Department of Biological Sciences, Genetics and Ecology, Aarhus, Denmark*

6-3 Poster **Reproductive conflicts and egg discrimination by workers in a socially polymorphic ant**

JOËL MEUNIER, LUMA DELAPLACE, MICHEL CHAPUISAT
University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

6-4 Poster **Social context predicts recognition systems in cooperative ant queen associations**

STEPHANIE DREIER, PATRIZIA D'ETTORRE
University of Biology, Centre for Social Evolution, Copenhagen, Denmark

6-5 Poster **Resolution of caste fate conflict in a fission-performing ant**

CAMILLE RUEL, XIM CERDÁ, RAPHAËL BOULAY
Estación Biológica de Doñana, C.S.I.C Consejo Superior de Investigaciones Científicas, Seville, Spain

6-6 Poster **Reproductive partitioing across seasons in the black ant *F. fusca***

ANTON CHERNENKO, LISELOTTE SUNDSTRÖM
University of Helsinki, Department of Evolutionary Biology and Ecology, Helsinki, Finland

6-7 Poster **Reduced reproductive polymorphism in an ant with a small distribution range: an evolutionary unstable situation or the result of caste conflicts?**

FERNANDO AMOR, JUAN A. GALARZA, PATROCIÑO ORTEGA, RAPHAËL BOULAY, XIM CERDÁ
Estación Biológica de Doñana, C.S.I.C Consejo Superior de Investigaciones Científicas, Seville, Spain

6-8 Poster **Testing for within-colony kin discrimination in a multiple-queen ant**

LUCY A. FRIEND
University of East Anglia, Department of Biological Sciences, Norwich, United Kingdom

6-9 Poster **Effect of genetic diversity on individual and social disease resistance in an insect society**

ANNA M. SCHMIDT, TIMOTHY A. LINKSVAYER, JACOBUS J. BOOMSMA, JES S. PEDERSEN
University of Copenhagen, Department of Biology, Copenhagen, Denmark

6-10 Poster **The dark side of The Force: genotypic diversity in queenless honeybee colonies reduces fitness**

PETER NEUMANN[1,2], JANUSZ BRATKOWSKI[3], JUREK WILDE[3]
[1]*Swiss Bee Research Centre, Agroscope Liebefeld-Posieux Research Station ALP, Bern, Switzerland*
[2]*Yunnan Agricultural University, Eastern Bee Research Institute, Kunming, China*
[3]*UWM University Apiculture Division, Olsztyn, Poland*

6-11 Poster The genetic causes and consequences of social evolution in an ant

TIMOTHY A. LINKSVAYER, ANNA M. SCHMIDT, JES S. PEDERSEN, JACOBUS J. BOOMSMA

University of Copenhagen, Department of Biology, Copenhagen, Denmark

6-12 Poster Living in kin groups: no safety in numbers but still a safe place

MICHAEL GRIESSER[1,2], SÖNKE EGGERS[1,2], MAGDALENA NYSTRAND[2], JAN EKMAN[2]

[1]Swedish University of Agricultural Sciences, Department of Ecology, Uppsala, Sweden
[2]University of Population Biology and Conservation Biology, Department of Ecology and Evolution, Uppsala, Sweden

6-13 Poster Between-group competition and human cooperation

MIKAEL PUURTINEN, TAPIO O. MAPPES

University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland

6-14 Poster Is “Prisoner’s Dilemma“ the name of the game upon secretion of extracellular enzymes in baker’s yeast?

ANJA SCHROETER[1], EYTAN RUPPIN[2], NAAMA BRENNER[3], GÜNTER THEIßEN[4], JAN-ULRICH KREFT[5], STEFAN SCHUSTER[1]

[1]Friedrich Schiller University, Department of Bioinformatics, Jena, Germany
[2]Tel Aviv University, School of Computer Sciences & School of Medicine, Tel Aviv, Israel
[3]Technion – Israel Institute of Technology, Department of Chemical Engineering, Technion City, Haifa , Israel
[4]Friedrich Schiller University, Department of Genetics, Jena, Germany
[5]University of Birmingham, Centre for Systems Biology, School of Biosciences, Edgbaston, United Kingdom

6-15 Poster Human altruism by lethal group competition

MARTIJN EGAS[1], RALPH KATS[1], XANDER VAN DER SAR[1], ERNESTO REUBEN[2], MAURICE W. SABELIS[1]

[1]Institute for Biodiversity and Ecosystem Dynamics Population Biology, Amsterdam, Netherlands
[2]Kellogg School of Management, Finance Department, Evanston, United States

6-16 Poster Modelling competitions between *Saccharomyces cerevisiae* life-history strategies

THIBAULT NIDELET, AYME SPOR, CHRISTINE DILLMANN, DELPHINE SICARD, DOMINIQUE DE VIENNE, OLIVIER C. MARTIN

University Paris Sud XI UMR 0320/8120, Department of Génétique Végétale, Gif-sur-Yvette, France

6-17 Poster Effects of social environment on lifespan in *Telostylinus angusticollis* depend on sex and condition

MARGO ADLER, RUSSELL BONDURIANSKY

University of New South Wales, Evolution & Ecology Research Centre, Sydney, Australia

6-18 Poster The Effect of Parasites on Cooperation

BENJAMIN J.Z. QUIGLEY

University of Oxford, Department of Zoology, Oxford, United Kingdom

6-19 Poster High symbiont relatedness stabilizes mutualistic cooperation in fungus-growing termites

DUUR K. AANEN

Wageningen University, Laboratory of Genetics Plant Sciences, Wageningen, Netherlands

6-20 Poster **Evolutionary conflicts between a neotropical ant and its host-plant**

PIERRE-JEAN G. MALÉ[1], CÉLINE LEROY[2], JÉRÔME ORIVEL[1], ANGÉLIQUE QUILICHINI[1]
[1]Univsersité Paul Sabatier, Department of Evolution et Diversité Biologique (EDB), Toulouse, France
[2]UMR CIRAD-CNRS-ENGREF-INRA ECOFOG, Kourou, Guyane Française

6-21 Poster **Internally ovipositing non-pollinating fig wasps compete with pollinators: implications for stability in a fig-pollinator mutualism?**

DEREK W. DUNN[1], SARAH AL-BEIDH[2], JAMES M. COOK[1]
[1]University of Reading, School of Biological Sciences, Reading, United Kingdom
[2]Imperial College London, Department of Biological Sciences, Ascot, United Kingdom

6-22 Poster **Invasion of the green body snatchers: how ants may alter the dynamics of the fig pollinator mutualism**

SARAH AL-BEIDH[1], JAMES COOK[2], DEREK W. DUNN[2]
[1]Imperial College London, Department of Biological Sciences, Ascot, United Kingdom
[2]University of Reading, School of Biological Sciences, Reading, United Kingdom

6-23 Poster **Host sanctions and pollinator cheating in the fig tree – fig wasp mutualism**

K. CHARLOTTE JANDÉR[1,2], EDWARD ALLEN HERRE[2]
[1]Cornell University, Department of Neurobiology and Behavior, Ithaca, United States
[2]Smithsonian Tropical Research Institute, Panamá, República de Panamá

6-24 Poster **Free-riding in an infection and the therapeutic potential of antisocial pathogens**

ADIN ROSS-GILLESPIE[1], KENDRA P. RUMBAUGH[2], TIFFANY TAYLOR[1,3], STEPHEN P. DIGGLE[4], STUART A. WEST[1,3], ASHLEIGH S. GRIFFIN[1,3]
[1]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom
[2]Texas Tech University, Health Sciences Centre, Department of Surgery, Lubbock, United States
[3]University of Oxford, Oxford, United Kingdom
[4]University of Nottingham, Institute of Infection, Department of Immunity and Inflammation, Nottingham, United Kingdom

6-25 Poster **Policing in the bumble bee *Bombus terrestris***

LORENZO R.S. ZANETTE[1], SOPHIA MILLER[1], WILLIAM C. JORDAN[2], ANDREW F.G. BOURKE[1]
[1]University of East Anglia, Department of Biology, Norwich, United Kingdom
[2]Zoological Society of London, Institute of Zoology, London, United Kingdom

6-26 Poster **The coevolution of cooperation and sociability**

DÓRA HUSZÁR[1], ZOLTÁN BARTA[1], JOHN M. McNAMARA[2], MICHAEL TABORSKY[3]
[1]University of Debrecen, Department of Evolutionary Zoology and Human Biology, Debrecen, Hungary
[2]University of Bristol, Department of Mathematics, Bristol, United Kingdom
[3]University of Bern, Department of Behavioural Ecology, Bern, Switzerland

6-27 Poster **Cleaner wrasse and their reef-fish clients – a biological market?**

MOSHE KIFLAWI[1,2], VICTOR CHINA[1,2]
[1]Ben-Gurion University, Department of Life Sciences, Beer-Sheva, Israel
[2]The Interuniversity Institute of Eilat, Eilat, Israel

6-28 Poster **Sex-biased dispersal patterns depend on the spatial scale in a social rodent**

BERTRAND GAUFFRE[1,2], ERIC PETIT[3], SALOMON BRODIER[2], VINCENT BERTAGNOLLE[2], JEAN FRANÇOIS COSSON[1]
[1]INRA UMR CBGP (Centre de Biologie et de Gestion des Populations), Montpellier, France
[2]CNRS CEBC (centre d'etudes biologiques de Chizé), Beauvoir sur Niort, France
[3]INRA UMR BIO3P, Rennes, France

6-29 Poster **Siblicide and Cannibalism in Earwig Families**

RALPH DOBLER, MATHIAS KÖLLIKER
University of Basel, Zoological Institute, Department of Evolutionary Biology, Basel, Switzerland

6-30 Poster **Sibling negotiation in the barn owl**

AMELIE N. DREISS, CHARLÈNE RUPPLI, ALEXANDRE ROULIN
University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

6-31 Poster **The inbreeding history of a population influences mating decisions: a game theory model of bark beetles**

AMOS BOUSKILA[1], DAPHNA GOTTLIEB[1], ESTI LEVANT[1], YAEL LUBIN[2], ALLY HARARI[3]
[1]Ben-Gurion University of the Negev, Department of Life Sciences, Beer-Sheva, Israel
[2]Ben-Gurion University of the Negev, Mitrani Department of Desert Ecology, Midreshet Ben-Gurion, Israel
[3]The Volcani Center, Department of Entomology, Bet-Dagan, Israel

6-32 Poster **Mutual mate choice in a cichlid fish: a battleground for sexual conflict over mate quality**

SEBASTIAN A. BALDAUF[1], HARALD KULLMANN[2], THEO C.M. BAKKER[1],TIMO THUENKEN[1]
[1]University of Bonn, Institute of Evolutionary Biology and Ecology, Bonn, Germany
[2]University of Muenster, Muenster, Germany

6-33 Poster **Sexual conflict in penduline tits: hard-working mothers and lazy fathers?**

ÁKOS POGÁNY[1], RENÉ E. VAN DIJK[2], TAMÁS SZÉKELY[2]
[1]Eötvös University, Department of Ethology, Budapest, Hungary
[2]University of Bath, Department of Biology and Biochemistry, Bath, United Kingdom

6-34 Poster **Conflict between females and offspring: consequences for evolution of cannibalism and female's response to oviposition deterring pheromone in ladybirds**

XAVIER MARTINI[1,2], PATSY HACCOU[3], ISABELLE OLIVIERI[4], ALEXANDRA MAGRO[1], JEAN-LOUIS HEMPTINNE[1]
[1]ENFAT UMR CNRS, Department of Evolution & Diversité Biologique, Castanet-Tolosan, France
[2]Université Paul Sabatier, Toulouse, France
[3]Leiden University, Institute of Biology, Leiden, Netherlands
[4]Université Montpellier 2, Institut des Sciences de l'Evolution, Montpellier, France

6-35 Poster **The affect of female preference and competitor density on allopaternal care in the tessellated darter**

KELLY A. STIVER, SUZANNE H. ALONZO
Yale University, Department of Ecology and Evolutionary Biology, New Haven, United States

6-36 Poster **Is sex division of parental care stable? An experimental test in the Kentish plover**

ANDRAS KOSZTOLANYI[1], INNES C. CUTHILL[2], CLEMENS KUEPPER[3], TAMAS SZEKELY[3]

[1] *Eotvos University, Department of Ethology, Budapest, Hungary*
[2] *University of Bristol, School of Biological Sciences, Bristol, United Kingdom*
[3] *University of Bath, Department of Biology and Biochemistry, Bath, United Kingdom*

6-37 Poster **Local sperm competition and its consequences for sex allocation and mating behaviour in a simultaneous hermaphrodite**

TIM JANICKE, LUKAS SCHÄRER

University of Basel, Zoological Institute, Basel, Switzerland

6-38 Poster **Testing a sexual conflict mate guarding model in an androdioecious crustacean**

CHIARA BENVENUTO[1,2], STEPHEN C. WEEKS[1]

[1] *University of Akron, Department of Biology, Akron, United States*
[2] *Kent State University, Kent, United States*

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Program

Wednesday August 26 - **Symposium 7**

Location: Room 2

Evolutionary applications: a symposium sponsored by Wiley-Blackwell Publishing

Organizers:	*Louis Bernatchez, Université Laval, Canada* *Dany Garant, Université de Sherbrooke, Canada*
9.45 - 10.15	**STEPHEN C. STEARNS** (invited) Natural selection acting in contemporary human populations
10.15 - 10.45	**DIETER EBERT** (invited) How well can we predict the evolution of virulence?
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**LUCY WEINERT** The use of phylodynamics to infer transmission patterns of HIV in the UK
11.35 - 11.55	**CAROL EUNMI LEE** Exploring Genomic Signatures of Selection following Invasions into Novel Environments
11.55 - 12.15	**PHILLIP GIENAPP** Could migration time in birds evolve in response to climate change? Phenotypic plasticty and heritability of arrival time in Danish cormorants
12.15 - 12.35	**DYLAN FRASER** Human-induced maladaptation to climate change in salmon
12.35 - 12.55	**ANE T. LAUGEN** Evolutionary impact assessment: Integrating evolutionary consequences of fishing into the ecosystem-approach to fisheries management
12.55 - 13.55	*Lunch*
13.55 - 14.25	**JUHA MERILÄ** (invited) Detecting evolutionary responses in the wild: problems and prospects
14.25 - 14.45	**IAN J. RICKARD** Evolution and the developmental origins of human health
14.45 - 15.05	**GABRIEL G. PERRON** The evolutionary ecology of antibiotic resistance: when the rate of change matters

15.05 - 15.35 *Coffee break*

15.35 - 15.55 **TROY DAY**
The evolution of bleaching resistance in corals

15.55 - 16.15 **ERIC LOMBAERT**
Worldwide routes of invasion of the biocontrol ladybird *Harmonia axyridis*: recurrent invasions from a bridgehead invasive population and admixture

16.15 - 16.35 **RENAUD BAETA**
Agricultural intensification and tree swallows: does landscape characteristics affects primary sex ratio in a natural population?

16.35 - 16.55 **ROBERTO PAPA**
Introgression from modern hybrid varieties into Italian landrace populations of maize

7-1 Oral

NATURAL SELECTION ACTING IN CONTEMPORARY HUMAN POPULATIONS

Stephen C. Stearns [1], Sean G. Byars [1], Douglas Ewbank [2]

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There is a widespread public misconception that because of the effects of culture, in particular of modern medicine, natural selection has stopped acting in human populations. People working on evolutionary medicine, where this misconception is rare, concentrate on the consequences of natural selection acting on pathogens, where the response is rapid, but not on humans, where the response is slow. To expose the general misconception, and to balance the analysis of natural selection within evolutionary medicine, we applied selection gradient analysis to the population of the Framingham Heart Study, which consists of 14,500 people repeatedly measured over 3 generations. We measured significant, but small, selection gradients acting on total cholesterol, body mass index, and other measures. These traits have significant heritabilities and will respond to selection, but the responses will only accumulate and become significant if the selection gradients we measured are maintained consistently for many generations. Because the consistency of selection is not established, and there is some evidence in our study that selection gradients are shifting for some traits at a decadal scale, we cannot predict whether these traits will evolve significantly. We can say that natural selection is operating in contemporary human populations.

7-2 Oral

HOW WELL CAN WE PREDICT THE EVOLUTION OF VIRULENCE?

Dieter Ebert [1]

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Our fight against infectious diseases is largely driven by the need to reduce the damage inflicted by parasites and pathogens on their hosts. Most methods used by us to fight disease agents are by prevention of infection or by the use of curative methods. In recent years, ideas have been developed to influence the evolution of parasites, such that the evolved disease agents become less virulent, i.e. less harmful to their hosts. These suggestions are not based on artificial selection, but rather on approaches comparable to evolutionary experiments. The idea is to alter the environment of a pathogen in such a way that it would be beneficial to express lower levels of virulence. In my presentation I will review to what extent evolutionary experiments resulted in an altered level of virulence and if the observed changes were consistent with the expectations of the researcher. In other words, I will review experimental evidence to answer the question how well can we predict the evolution of virulence?

7-3 Oral

THE USE OF PHYLODYNAMICS TO INFER TRANSMISSION PATTERNS OF HIV IN THE UK

Lucy Weinert [1], Gareth Hughes [1], Esther Fernhill [2], David Dunn [2], Andrew Rambaut [1], Andrew Leigh-Brown [1]

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HIV spreads through a series of sexual contact networks, which include people who have serial monogamous partnerships and people who have concurrent relationships with multiple partners. The shape of these networks and the timing of transmission events determine the incidence and prevalence of HIV today, and help us predict how the epidemic will behave in the future. We inferred discrete transmission clusters from 20,000 HIV partial viral sequences and used time-resolved phylogenies of these clusters to date transmission events. Approximately, 1 in 12 clusters contain more than 10 individuals and many of these clusters date to the late 1990s, a time when the HIV-infected population is known to have doubled in the UK. We also found that a large proportion of transmissions occur within 6 months of infection, when most people do not know they are infected, and when within-host evolution is limited. The sequences were collected throughout the UK and so we were also able to infer the short-term dynamics of geographical spread. These results show how evolutionary inferences can shed light on the epidemiology of HIV.

7-4 Oral

EXPLORING GENOMIC SIGNATURES OF SELECTION FOLLOWING INVASIONS INTO NOVEL ENVIRONMENTS

Carol Eunmi Lee [1], Yuseob Kim [2], Davorka Gulisija [1]

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A fundamental unresolved problem in ecology and evolution regards limits to species distributions. Invasive species provide powerful models for studying limits to species distributions and factors that allow those distributions to shift. Within the past century, the copepod *Eurytemora* affinis has invaded freshwater habitats multiple times independently from saline sources. To dissect evolutionary responses during these independent habitat invasions, we integrated analyses of physiological function with comparative functional genomics. We analyzed evolutionary shifts during invasions for pairs of ancestral saline source and derived freshwater populations across four independent invasions from two genetically distinct clades. We found evolutionary shifts in function (ion efflux, ion uptake), as well as in expression of genes spanning many functional categories, including osmoregulation, energy production, and stress response (based on custom microarrays). In many cases, there were striking parallel evolutionary shifts across independent invasions, particularly with respect to ion uptake activity and expression. Several of the candidate genes appear to show significant signatures of selection based on summary statistics. We are developing a demography + selection model of invasions in order to rigorously test for signatures of selection at our candidate loci. The evolutionary parallelism observed here might have relevance for taxonomically different but ecologically similar species that invade across similar habitat clines.

7-5 Oral

COULD MIGRATION TIME IN BIRDS EVOLVE IN RESPONSE TO CLIMATE CHANGE? PHENOTYPIC PLASTICTY AND HERITABILITY OF ARRIVAL TIME IN DANISH CORMORANTS

Phillip Gienapp [1], Thomas Bregnballe [2]

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Changing migration schedules of birds are among the prominent examples of the impact of climate change. Currently, it is unclear whether earlier migration and earlier arrival at the breeding grounds are a product of phenotypic plastcity or a microevolutionary change. To fully understand how well species will be able to adapt to climate change it is important to disentangle phenotypic and genetic changes. Probing into selection on and genetics of migratory timing has however proven difficult as this requires data on individual migratory timing, reproductive success and relationships among individuals and few such data sets are available. Arrival time of great cormorants, a short-distance migrant, has been closely monitored at the colony on Vorsø (Denmark) since 1984. Because the majority of adult individuals and all chicks have been colour-ringed it was possible to record arrival time, breeding and to construct a multi-generational pedigree for this population. We quantified individual phenotypic plasticity in migration and breeding time and their fitness consequences. Using a so-called 'animal model' to probe into quantitative genetics we estimated genetic variances and heritabilties of these traits. This data enables us to assess whether migration time could evolve in response to climate change and we will discuss our findings in the broader perspective of changing avian migratory timing.

7-6 Oral

HUMAN-INDUCED MALADAPTATION TO CLIMATE CHANGE IN SALMON

Dylan Fraser [1], Coilin Minto [1], Anna Calvert [1], James Eddington [1], Jeffrey A. Hutchings [1]

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Little research has investigated how human activities unrelated to climate change might compound climatic adaptability in migratory species. In the Northwest Atlantic, climate warming is expected at the southern limit of the range of Atlantic salmon. It is anticipated that this may favour wild salmon embryos with faster developmental rates to hatching, to adapt to the earlier onset of spring conditions. However, intensive regional aquaculture of farmed Atlantic salmon leads to the recurrent escape of farmed salmon into rivers harboring depleted populations of wild salmon, where farmed-wild interbreeding can occur. Adopting common-garden experimentation, we showed that embryos of regional farmed salmon and multi-generational farmed-wild hybrids (F_1, F_2, wild backcrosses) had slower developmental rates than those of two regional wild populations with divergent life histories. Hybrid developmental rates were therefore mismatched to environmental conditions and in a direction that, with repeated farmed-wild interbreeding, may impede the adaptability of at-risk wild salmon populations to climate warming. We suggest that greater conservation attention should be paid to understanding how climatically-unrelated human activities may constrain future climatic adaptability in other species.

7-7 Oral

EVOLUTIONARY IMPACT ASSESSMENT: INTEGRATING EVOLUTIONARY CONSEQUENCES OF FISHING INTO THE ECOSYSTEM-APPROACH TO FISHERIES MANAGEMENT

Ane T. Laugen [1,2], Georg H. Engelhard [3], Rebecca Whitlock [4], Robert Arlinghaus [5], Loïc Baulier [6,7], David S. Boukal [8,6,7], Dorothy Dankel [7], Erin S. Dunlop [9,6,7], Anne Maria Eikeset [10], Katja Enberg [6,7], Bruno Ernande [2], Fiona Johnston [4,5], Christian Jørgensen [6,7], Shuichi Matsumura [4,5], Fabian Mollet [11], Sébastien Nusslé [12], Heidi Pardoe [13,14], Nina O. Therkildsen [15], Davnah Urbach [4], Silva Uusi-Heikkila [5], Anssi Vainikka [16,17], Mikko Heino [6,7,4], Adriaan D. Rijnsdorp [11], Ulf Dieckmann [4]

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Although human activity can cause rapid evolution in organisms, quantifying human-induced evolutionary change can be difficult. For example, several commercial fish stocks have undergone remarkable phenotypic changes in recent years, but the extent to which this reflects evolutionary change rather than phenotypic plasticity is the subject of debate. However, increasing evidence supports the argument that modern industrial fisheries exert strong directional selection on life history characters in fish, and that this is at least partly responsible for some of the observed phenotypic changes in certain heavily exploited stocks.

Potential fisheries-induced evolution changes the utility of fish stocks, e.g. by altering utility components such as recovery potential, yield, genetic diversity, trophic interactions and geographical distributions. Therefore, quantifying and characterising the evolutionary effects of fishing is important for both economic and ecological reasons and may assist discussions among stakeholders and facilitate management of affected stocks.

Here we describe the evolutionary impact assessment (EvoIA) and a set of methods for assessing the evolutionary consequences of fishing and for evaluating the merits of alternative management options. EvoIAs may (i) contribute to the ecosystem approach to fisheries management by clarifying how evolution alters stock properties and ecological relations, (ii) support the precautionary approach to fisheries management by addressing a previously overlooked source of uncertainty and risk, and (iii) help realize the Johannesburg summit's commitment to the restoration of sustainable fisheries by assisting fisheries managers account for evolutionary implications of fishing.

7-8 Oral

DETECTING EVOLUTIONARY RESPONSES IN THE WILD: PROBLEMS AND PROSPECTS

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Climate change, human induced habitat changes and harvesting are all factors that impact upon wild populations creating directional selection on heritable phenotypic traits. Since heritable phenotypic traits should respond on directional selection, evolution in response to these human induced selection pressures should be of commonplace occurrence. However, detecting these evolutionary responses is technically challenging because we typically lack means to verify the genetic basis for the observed phenotypic shifts. An additional complication in interpretation of many datasets resides on the realization that evolutionary dynamics of heritable traits under selection are subject to various complexities stemming from inheritance patterns as well as to interactions among genes and environment. In my presentation, I will illustrate and discuss upon the problem of detecting evolutionary changes in response to human induced selection by utilizing examples from long-term genetic studies of natural vertebrate populations.

7-9 Oral

EVOLUTION AND THE DEVELOPMENTAL ORIGINS OF HUMAN HEALTH

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In mammals, including humans, the environmental conditions experienced in early life have profound and long-lasting consequences for phenotype. In humans, this appears to include an effect of poor early nutrition on an increased risk of developing several diseases in adulthood, such as type II diabetes and coronary heart disease. Increasingly, these effects are being seen as not just the product of the environment itself, but due to evolved adaptive responses by the developing individual, which under certain later conditions lead to illness. One hypothesis predicts that when individuals experience challenging environmental conditions during early life, their subsequent development proceeds so as to favour survival in similar conditions as adults. However, the extent to which long-term effects of the early environment on phenotype are the result of developmental constraint, and the extent to which they are evolved adaptive responses are unknown. We use data from pre-industrial Finnish humans to investigate the interactive effects of early and late-life environmental conditions on an individual's survival. We use infant mortality rate in a given year as a general index of environmental quality and track the survival of several thousand men and women born over a 140-year period, between 1750 and 1890. We describe how different environmental regimes experienced during early life and adulthood affect individual mortality risk. We discuss how testing evolutionary hypotheses can help inform our understanding of the environmental induction of human disease and ultimately aid the improvement of population health.

7-10 Oral

THE EVOLUTIONARY ECOLOGY OF ANTIBIOTIC RESISTANCE: WHEN THE RATE OF CHANGE MATTERS

Gabriel G. Perron [1], Andrew Gonzalez [2], Angus Buckling [1]

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Understanding the conditions that favour the evolution and maintenance of antibiotic resistance is a central goal of epidemiology. Adaptation to novel conditions is predicted to be constrained by the selective pressures imposed by the scale and tempo of environmental change. In other words, the rate and the time-scale at which we administer antibiotic treatments will affect the evolution of antibiotic resistance. Here, we present experimental evidences and theoretical predictions on the effect of using different antibiotics treatment strategies on the evolution of bacterial populations. We show that the rate of change of antibiotic concentration can not only affect the rate of evolution of resistance, but also the level of resistance: slow increases in antibiotic result in a more rapid evolution of resistance whilst a steep increase in concentration selected for higher level of resistance. Second, we show that the order in which antibiotics are used in antimicrobial cycling treatment can slow down and even stop the spread of multiply drug-resistant bacterial strains: a result which was previously undermined in the literature. These results demonstrate the predictive power of evolutionary ecology dynamics and the use we can make of experimental evolution to understand and control the emergence and spread of antibiotic resistance.

7-11 Oral

THE EVOLUTION OF BLEACHING RESISTANCE IN CORALS

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Coral bleaching in response to temperature stress is an increasingly important concern as global average temperatures continue to increase. Most of the projections for the future fate of coral reefs ignore the possibility of evolutionary change in thermal tolerance, but researchers are now beginning to incorporate evolutionary biology into their predictions. I will present some results from evolutionary models that explore the evolution of bleaching resistance, and how it is affected by the biological details of the coral-zooxanthellae interaction. I will also discuss some theoretical research that explores the possibility that bleaching is an adaptive phenomenon (the so-called adaptive bleaching hypothesis). This research is joint work with scientists at the Australian Institute of Marine Science.

7-12 Oral

WORLDWIDE ROUTES OF INVASION OF THE BIOCONTROL LADYBIRD *HARMONIA AXYRIDIS*: RECURRENT INVASIONS FROM A BRIDGEHEAD INVASIVE POPULATION AND ADMIXTURE

Eric Lombaert [1], Thomas Guillemaud [1], Jean-Marie Cornuet [2], Thibaut Malausa [1], Benoît Facon [2], Arnaud Estoup [2]

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Initially used as a biocontrol agent against aphids in America and Europe, the Harlequin ladybird *Harmonia axyridis* (HA) has become one of the most famous invasive insect on earth. Native from Asia, invasive HA populations have been recorded in North America since 1988 (South-East USA) and 1991 (North-West USA), Europe since 2001 (Belgium), South America since 2001 (Argentina), and Africa since 2004 (South Africa) and has now widely spread in these areas. Using Approximate Bayesian Computation method, we retraced the routes of invasion of HA in all invaded areas. This work is based on the analysis of the genetic variation of HA populations measured at eighteen microsatellite loci. We showed that the North American outbreaks originate from two independent introduction events from the native area; the South American and African outbreaks both originate from the Eastern USA outbreak; the European outbreak was found to be the result of the admixture of individuals from the Eastern USA outbreak and the European biocontrol population that was used and commercialized in the 90's. The invasive population in Eastern USA is hence the source of all other invasive populations on other continents and is therefore the invasion bridgehead of HA. This result strikingly illustrates the worldwide dissemination of a single successful invasive population in various environments and highlights the importance of precisely deciphering the introduction routes of invasive species to formalize sensible hypotheses to study the instrumental factors of invasion.

7-13 Oral

AGRICULTURAL INTENSIFICATION AND TREE SWALLOWS: DOES LANDSCAPE CHARACTERISTICS AFFECTS PRIMARY SEX RATIO IN A NATURAL POPULATION?

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Over 1500 millions hectares of land are directly devoted to agriculture around the world. Such human activities thus represent major disturbances of the landscape and have direct impacts on every ecosystem components. However, very few studies have assessed the effects of modification in land uses at the individual level that could ultimately influence the overall population dynamics. For birds, one process tightly linked with population dynamics is variation in sex ratio, which is not fully constrained by Mendelian processes and is potentially adaptive. For instance, it is suggested that variation in food availability may influence sex allocation. Yet, very little is known about the way selection acts on sex ratio variation in natural populations and on the potential connections between environmental and individual quality in sex allocation choices. Using molecular techniques, we quantified the primary sex ratio in a tree swallow *Tachycineta bicolor* population nesting in contrasted agricultural environments over a 10 000 ha area in Southern Québec (Canada). We sexed 2500 nestlings over a 3-year period and combined these data with indicators of landscape and individual characteristics to assess their relative role on sex ratio variation. At the population level, we found a constant bias in sex ratio towards females in every year. We found that intensive agriculture and water availability influence sex ratios but that their effects are variable in time. We also found that individual characteristics, such as body mass and hatching date, influence sex ratios with again contrasted effects among years.

7-14 Oral

INTROGRESSION FROM MODERN HYBRID VARIETIES INTO ITALIAN LANDRACE POPULATIONS OF MAIZE

Elena Bitocchi [1], Laura Nanni [1], Monica Rossi [1], Domenico Rau [2], Alessandro Giardini [1],
Elisa Bellucci [1], Anna Buonamici [3], Giovanni G. Vendramin [3], Roberto Papa [1]

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In Italy the cultivation of flint maize landraces is generally linked to the production of 'polenta', for which dent corn is not suitable from a quality point of view. We have studied the evolution of maize landraces from central Italy over 50 years of on-farm cultivation, when dent hybrid varieties were introduced and their use was widespread. We have compared an 'old' collection, conducted during the 1950s before the introduction of hybrids, with a recent collection of maize landraces. A collection of maize landraces from northern Italy, flint and dent hybrids and inbred lines were used as controls. 21 microsatellites and 170 AFLP molecular markers were used. Our results show that the landraces collected in the last 5-10 years have evolved directly from the flint landrace gene pool cultivated in central Italy before the introduction of modern hybrids. The population structure, diversity and linkage disequilibrium analyses show a significant amount of introgression from hybrid varieties into the recent landrace collection. However, the recent landraces did not show genetic erosion, despite the drastic reduction in their cultivation after the introduction of the hybrids. This result suggests that *in-situ* conservation of landraces is an efficient strategy for the preservation of genetic diversity. Finally, the level of introgression detected was very variable among farmer's fields, with most of them (58%) showing a very low level of introgression. This suggests that co-existence between different types of agriculture is possible, adopting more correct practices that are aimed at avoiding introgression from undesired genetic sources.

7-1 Poster **Predation-induced Evolution of Bacterial Virulence**

JI ZHANG[1], VILLE FRIMAN[1], JOUNI LAAKSO[2], JOHANNA MAPPES[1]
[1]*University of Jyvaskyla, Department of Biological and Environmental Science, Jyvaskyla, Finland*
[2]*University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland*

7-2 Poster **Immunogenetic approach in wild natural populations: application to emergent zoonoses**

EMMANUEL GUIVIER, MAXIME GALAN, JEAN-FRANÇOIS COSSON, NATHALIE CHARBONNEL
INRA EFPA, Montpellier, France

7-3 Poster **Invasion of Europe by the western corn rootworm: multiple transatlantic introductions and stratified dispersal with various consequences on genetic diversity**

MARC CIOSI[1], ARNAUD ESTOUP[2], KYUNG SEOK KIM[3], NICHOLAS J. MILLER[3], ROSANNA GIORDANNO[4], STEFAN TOEPFER[5], THOMAS GUILLEMAUD[1]
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[2]*INRA, UMR CBGP (IRD/CIRAD), Montpellier SupAgro, Montferrier-sur-Lez, France*
[3]*Iowa State University USDA-ARS, CICGRU, Genetics Laboratory, Ames, United States*
[4]*Illinois Natural History Survey, Division of Biodiversity and Ecological Entomology, Champaign, United States*
[5]*CABI Europe Team Agricultural Pest Research, Delémont, Switzerland*

7-4 Poster **Impacts of stocking intensity on the genetic integrity of exploited brook charr (*Salvelinus fontinalis*) populations**

MARIE AMANDINE D.[1], LOUIS BERNATCHEZ[2], DANY GARANT[1]
[1]*Université de Sherbrooke, Département de Biologie, Sherbrooke, Canada*
[2]*Université Laval, Institut de Biologie Intégrative et des Systèmes (IBIS), Laval, Canada*

7-5 Poster **Effect of anthropogenic environmental change on the distribution of individual genetic diversity in a wild bird population**

MELODY PORLIER, MARC BÉLISLE, DANY GARANT
Université de Sherbrooke, Département de Biologie, Sherbrooke, Canada

7-6 Poster **Panmixia in the European eel? – population genetics matters**

THOMAS D. ALS[1], MICHAEL M. HANSEN[1], GREGORY E. MAES[2], LOUIS BERNATCHEZ[3]
[1]*Technical University of Denmark, National Institute of Aquatic Resources, Silkeborg, Denmark*
[2]*Katholieke Universiteit, Leuven Laboratory of Animal Diversity and Systematics, Leuven, Belgium*
[3]*Université Laval, Department of Biology, Ville de Québec, Canada*

7-7 Poster **Fisheries-induced evolution of body size and other life-history traits: the impact of gear selectivity**

DAVID S. BOUKAL[1,2], ERIN S. DUNLOP[3], MIKKO HEINO[2,4], ULF DIECKMANN[5]
[1]*Biology Centre of the Academy of Sciences, Department of Theoretical Biology, Ceske Budejovice, Czech Republic*
[2] *Institute of Marine Research, Department of Population Genetics, Bergen, Norway*
[3]*Ontario Ministry of Natural Resources, Aquatic Research and Development Section, Peterborough, Canada*
[4]*University of Bergen, Bergen, Norway*
[5]*International Institute for Applied Systems Analysis Evolution and Ecology Program, Laxenburg, Austria*

7-8 Poster Can Maternal Effects Change the Evolutionary Potential of Biocontrol Agents?

LENA LORENZ
Imperial College London, Department of Biology, London, United Kingdom

7-9 Poster Old genes in a new environment: The role of gene-by-environment interactions in determining lifespan and ageing

BAS J. ZWAAN
Leiden University, Institute of Evolutionary Biology, Leiden, Netherlands

7-10 Poster When are observations of rapid evolution to changes in temperature relevant for potential responses to climate change?

NICOLA J. BARSON[1], THROND O. HAUGEN[2], L. ASBJØRN VØLLESTAD[1]
[1]*University of Oslo, Centre for Ecological and Evolutionary Synthesis, Oslo, Norway*
[2]*Norwegian institute for water research, Unit for Fish and Aquaculture, Oslo, Norway*

7-11 Poster Virulence Evolution Drivers: Marek's Disease Virus and Industrial Agriculture

KATIE E. ATKINS[1], ANDREW F. READ[2], MARK E.J. WOOLHOUSE[1]
[1]*University of Edinburgh, Institute For Immunology And Infection Research, Edinburgh, United Kingdom*
[2]*Pennsylvania State University, Centre For Infectious Disease Dynamics, State College, United States*

7-12 Poster Signatures of past pesticide selection on the genetic variation at the acetylcholinesterase gene in the invasive *Leptinotarsa decemlineata*

SAIJA PIIROINEN[1], LEENA LINDSTROM[1], ANNE LYYTINEN[1], JOHANNA MAPPES[1], ALESSANDRO GRAPPUTO[2]
[1]*University of Jyvaskyla, Department of Biological and Environmental Science, Jyvaskyla, Finland*
[2]*University of Padova, Department of Biology, Padova, Italy*

7-13 Poster Emerfundis, a program to understand the emergence of fungal plant diseases

TATIANA GIRAUD[1], DIDIER ANDRIVON[2], FRANCOIS DELMOTTE[3], HENRIETTE GOYEAU[4], BRUNO LE CAM[5], BENOÎT MARÇAIS[6], CÉCILE ROBIN[3], JEAN CARLIER[7]
[1]*UPSUD CNRS, Department of Ecology Systematic and Evolution, Orsay, France*
[2]*INRA, Rennes, France*
[3]*INRA,Bordeaux, France*
[4]*INRA, Grignon, France*
[5]*INRA, Angers, France*
[6]*INRA, Nancy, France*
[7]*Cirad, Montpellier, France*

7-14 Poster Genetic population structure and Atlanto-Mediterranean oceanographic discontinuities

VÍCTOR H. GARCÍA-MERCHÁN[1], CELIA SCHUNTER1, PERE ABELLÓ[2], ENRIQUE MACPHERSON[3], MARTA PASCUAL BERNIOLA[1]
[1]*Universidad de Barcelona, Departimento de Genética, Barcelona, Spain*
[2]*Institut de Ciències del Mar (CSIC), Barcelona, Spain*
[3]*Centre d'Estudis Avançats de Blanes (CSIC), Blanes, Spain*

7-15 Poster **Evolutionary effects of mortality on the investment into immunity in crayfishes**

ANSSI VAINIKKA, RAINE KORTET

University of Oulu, Department of Biology, Oulu, Finland

7-16 Poster **Environment-dependent use of mate choice cues**

JAN HEUSCHELE, MIIA MANNERLA, PHILLIP GIENAPP, ULRIKA CANDOLIN

University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland

7-17 Poster **Refining the taxonomy of the Rattini tribe: a phylogeny-based delimitation of species boundaries**

MARIE PAGES[1], YANNICK CHAVAL[2], SURACHIT WAENGSOTHORN[3], SERGE MORAND[4], JOHAN MICHAUX[1]

[1]INRA, UMR CBGP, Montferrier sur Lez, France
[2]INRA, UMR CBGP, Forestry, Ecology, Grassland and Wetland, Montferrier sur Lez, France
[3]Thailand Institute of Scientific and Technological Research, Bangkok, Thailand
[4]Institut des Sciences de l'Evolution, CNRS-UM2, Université Montpellier 2, Montpellier, France

7-18 Poster **Genetic diversity of species inhabiting rivers in central-northern Chile correlates with hydrographic flow**

DAVID VELIZ[1,2], MARIA CATALINA SABANDO[3,2], IRMA VILA[1], RAQUEL PEÑALOSA[3], ELIE POULIN[1,2]

[1]Universidad de Chile, Departamento de Ciencias Ecologicas, Santiago, Chile
[2]Instituto de Ecología y Biodiversidad (IEB), Santiago, Chile
[3]Universidad Metropolitana de Ciencias de la Educacion, Departamento de Biologia, Santiago, Chile

7-19 Poster **Phylogeny and phylogeography of the threatened catfish genus *Trichomycterus* in Chile: implications for conservation**

CLAUDIO A. QUEZADA-ROMEGIALLI[1,2], IRMA VILA[1], DAVID VÉLIZ[1,2]

[1]Universidad de Chile, Departamento de Ciencias Ecológicas, Santiago, Chile
[2]Instituto de Ecología y Biodiversidad (IEB), Santiago, Chile

7-20 Poster **Transgenerational Memory Effect of Aging in *Drosophila***

JAMES G. BURNS, FRÉDÉRIC MERY

Centre National de la Recherche Scientifique, Laboratoire Evolution Génomes et Spéciation, Gif sur Yvette, France

7-21 Poster **Evolution of defense against an insect herbivore in *Barbarea vulgaris* (Brassicaceae)**

THURE P. HAUSER[1], FIORELLO TONEATTO[1], MARIAN ØRGAARD[1], JENS K. NIELSEN[2]

[1]University of Copenhagen, Department of Agriculture and Ecology, Frederiksberg, Denmark
[2]University of Copenhagen, Department of Basic Science and Environment, Frederiksberg, Denmark

7-22 Poster **Temperature influences the micro-evolutionary response of *Daphnia magna* exposed to sublethal cadmium**

MARLIES MESSIAEN, KAREL A.C. DE SCHAMPHELAERE, BRITA T. A. MUYSSEN, COLIN R. JANSSEN

University of Gent, Laboratory of Environmental Toxicology and Aquatic Ecology, Gent, Belgium

7-23 Poster **The potential for adaptation to chemical stress in a natural *Daphnia magna* population and its importance for the ecotoxicological derivation of water quality criteria**

KAREL A.C. DE SCHAMPHELAERE, MARLIES MESSIAEN, COLIN R. JANSSEN
Ghent University, Department of Environmental Toxicology and Aquatic Ecology, Gent, Belgium

7-24 Poster **Host-parasite genetic interactions and virulence evolution in natural populations of monarch butterflies**

JACOBUS DE ROODE[1], SONIA ALTIZER[2]
[1]Emory Universit ,Department of Biology, Emory, United States
[2]University of Georgia, Odum School of Ecology, Athens, United States

7-25 Poster **Preventing microbial resistance evolution - insect immunity as a model**

JENS ROLFF[1], ELLIE HAINE[1], YANNICK MORET[2], MICHAEL T. SIVA-JOTHY[1]
[1]University of Sheffield, Departtment of Animal and Plant Sciences, Sheffield, United Kingdom
[2]University of Burgundy, Dijon, France

7-26 Poster **Identifying distinct lineages among sympatric Australian alpine *Poa* species to predict evolutionary responses to climate change**

PHILIPPA C. GRIFFIN[1], LINDA THOMSON[2], ARY A. HOFFMANN[1]
[1]University of Melbourne, Genetics and Zoology Department, Melbourne, Australia
[2]University of Melbourne, Zoology Department, Melbourne, Australia

7-27 Poster **Deforestation in human–environment relationships: A game theory and evolutionary dynamics approach**

ANTÓNIO RODRIGUES[1,2], HEINZ KOEPPL[2], HISASHI OHTSUKI[3,4], AKIKO SATAKE[5]
[1]Gulbenkian Institute of Science, Department of Biology, Oeiras, Portugal
[2]École Polytechnique Fédérale de Lausanne, School of Computer and Communication Sciences, Lausanne, Switzerland
[3]Tokyo Institute of Technology, Department of Value and Decision Science, Tokyo, Japan
[4]PRESTO, Japan Science and Technology Agency, Saitama, Japan
[5]Hokkaido University, Department of Creative Research Initiative "Sousei", Sapporo, Japan

7-28 Poster **Understanding human decision-making process: Contribution of Behavioral Ecology and Evolutionary concepts**

PHILIPPE LOUÂPRE
University of Rennes 1, UMR CNRS 6553, Department of EcoBio, Rennes, France

7-29 Poster **Gene exchange from (transgenic) crops to wild relatives: hybrid barriers, linkage drag and gene hitchhiking**

PETER H. VAN TIENDEREN, DANNY A.P. HOOFTMAN
University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, Amsterdam, Netherlands

7-30 Poster **Genetic diversity of the *Tubercle bacillus*: on the way to deciphering evolutionary dynamics of a devastating disease**

GUISLAINE REFRÉGIER, EDGAR ABADIA, JIAN ZHANG, SOLA CHRISTOPHE
Université Paris-Sud, IGM, Orsay, France

7-31 Poster **Linkage disequilibrium and population structure in wild and domesticated populations of *Phaseolus vulgaris* L.**

MONICA ROSSI[1], ELENA BITOCCHI[1], ELISA BELLUCCI[1], LAURA NANNI[1], DOMENICO RAU[2], GIOVANNA ATTENE[2], ROBERTO PAPA[1]
[1]Università Politecnica delle Marche, SAPROV, Ancona, Italy
[2]Università degli Studi di Sassari, Dipartimento di Scienze agronomiche e genetica vegetale agraria, Sassari, Italy

7-32 Poster **Genetic characterization of European populations of mosquitofish**

ORIOL VIDAL, JUDITH OLLE, JOSE LUIS GARCIA-MARIN
Universitat de Girona, Laboratori d'Ictiologia Genetica, Girona, Spain

7-33 Poster **Considering metapopulation dynamics in the estimation of effective population size for sustainable fisheries management**

SONIA CONSUEGRA[1], CARLOS GARCIA DE LEANIZ[2]
[1]Aberystwyth University, Institute of Biological Environmental and Rural Sciences (IBERS), Aberystwyth, United Kingdom
[2]Swansea University, Department of Biological Sciences, Swansea, United Kingdom

7-34 Poster **Virus-induced control of invasive species as a double-edged sword: Insight from mathematical modeling**

NUNO M. OLIVEIRA[1], FRANK M. HILKER[2]
[1]Instituto Gulbenkian de Ciencia, Oeiras, Portugal
[2]Universidade de Lisboa, Centro de Matemática e Aplicações Fundamentais (CMAF), Complexo Interdisciplinar, Lisboa, Portugal

7-35 Poster **The impact of stocking on the hierarchical genetic structure of Atlantic salmon populations over a 40 years period**

CHARLES PERRIER[1], JEAN-LUC BAGLINIÈRE[1], RENÉ GUYOMARD[2], GUILLAUME EVANNO[1]
[1]INRA UMR ESE, Rennes, France
[2]INRA UMR GABI, Jouy-en-Josas, France

7-36 Poster **Measuring the strength of phenotypic selection in males from the Framingham Heart Study Population**

SEAN G. BYARS[1], STEPHEN C. STEARNS[1], DOUGLAS C. EWBANK[2], DIDDAHALLY R. GOVINDARAJU[3]
[1]Yale University, Department of Ecology & Evolutionary Biology, New Haven, United States
[2]University of Pennsylvania, Sociology Department, Philadelphia, United States
[3]Boston University, Department of Neurology, Boston, United States

7-37 Poster **Short-term evolutionary consequences of population exposure to a toxicant affecting demography: an experimental study in the freshwater snail *Lymnaea stagnalis***

MARIE-AGNÈS COUTELLEC[1,2], LAURENT LAGADIC[1,2], THIERRY CAQUET[1,2]
[1]INRA UMR 985 ESE, Equipe Ecotoxicologie et Qualité des Milieux Aquatiques, Rennes, France
[2]Agrocampus-Ouest, Rennes, France

7-38 Poster **Adapting to an invasive species – are tadpoles responding to an exotic crayfish predator?**

ANA NUNES[1,2], ERIKA ALMEIDA[1], SUSANA ALVES[1], PEDRO ANDRADE[1], CÁTIA GUERREIRO[1], RUI REBELO[1], ANSSI LAURILA[2]
[1]University of Lisbon CBA, Departamento de Biologia Animal, Lisbon, Portugal
[2]Uppsala University EBC, Department of Population and Conservation Biology, Uppsala, Sweden

7-39 Poster **Can we harvest sustainably? An experimental approach with humans as the exploiting agents**

BEATRIZ DIAZ PAULI[1], DOROTHY J. DANKEL[2], MIKKO HEINO[1]
[1]University of Berge, Department of Biology, Bergen, Norway
[2]Institute of Marine Research, Bergen, Norway

7-40 Poster **Are islands the end of the colonization road?**

EVA P. BELLEMAIN[1], ROBERT E. RICKLEFS[2]
[1]Natural History Museum, Oslo, Norway
[2]University of Missouri, Department of Biology, St Louis, United States

7-41 Poster **Antimalarial drugs: are we shifting the balance?**

PETRA SCHNEIDER
University of Edinburgh, School of biological Sciences, Centre for Immunity, Infection and Evolution, United Kingdom

7-42 Poster **Genetic basis of life history evolution in Trinidadian guppies – a model for fisheries-induced evolution**

SERINDE J. VAN WIJK[1], MARTIN I. TAYLOR[1], SIMON CREER[1], COCK VAN OOSTERHOUT[2], GARY R. CARVALHO[1]
[1]Bangor University, Department of Molecular Ecology and Fisheries Genetics, Bangor, United Kingdom
[2]University of Hull, Department of Molecular Ecology and Fisheries Genetics, Hull, United Kingdom

7-43 Poster **Adaptive evolution in Atlantic cod: global and local geographical scales**

JAKOB HEMMER-HANSEN[1], EINAR EG NIELSEN[1], NINA AAGAARD POULSEN[1,2]
[1]Technical University of Denmark, National Institute of Aquatic Resources, Section for Population Genetics, Silkeborg, Denmark
[2]Aarhus University, Aarhus, Denmark

7-44 Poster **Are old ages useless with respect to selection? A reconsideration of the common variants/common diseases hypothesis**

SAMUEL PAVARD[1], JESSICA METCALF[2], BRUNO TOUPANCE[1], EVELYNE HEYER[1]
[1]Muséum National d'Histoire Naturelle Hommes, Natures et Sociétés, Paris, France
[2]Center for infectious disease dynamics, Pennstate, United States

7-45 Poster **Lethal mutagenesis and the evolutionary epidemiology of RNA viruses**

MARTIN GUILLAUME[1], SYLVAIN GANDON[2]
[1]CNRS, ISEM, UMR 5554, Montpellier, France
[2]CNRS CEFE, UMR 5175, Montpellier, France

7-46 Poster Integrating patterns across different markers and landscape variables: A multidisciplinary approach for disentangling forces shaping population structure and distribution

MORTEN T. LIMBORG[1], BEKKEVOLD DORTE[1], REINHOLD HANEL[2], ANDRE CARL[3], ANNA-KARIN RING[3], COSTAS TSIGENOPOULOS[4]

[1]*Technical University of Denmark, National Institute of Aquatic Resources, Section for Population genetics, Silkeborg, Denmark*
[2]*Johann Heinrich von Thünen-Institut (vTI), Federal Research Institute for Rural Areas, Forestry and Fisheries Institute of Fisheries Ecology, Hamburg, Germany*
[3]*University of Gothenburg, Department of Marine Ecology, Tjärnö Marine Biological Laboratory, Tjärnö, Sweden*
[4]*Institute of Marine Biology of Crete, Department of Genetics Molecular Biotechnology, Heraklion, Crete, Greece*

7-47 Poster Invasions as drivers of evolutionary change

RUTH A. HUFBAUER[1,2], AMY C. BLAIR[2], RENÉ SFORZA[3], ROBIN A. MARRS[4]

[1]*Colorado State University, Bioagricultural Sciences and Pest Management, Fort Collins, United States*
[2]*Centre de Biologie et de Gestion des Populations, Campus international de Baillarguet, Montferrier-sur-Lez, France*
[3]*Cornell University, Department of Natural Resources, Ithaca, United States*
[4]*USDA ARS European Biological Control Laboratory, Montferrier-sur-Lez, France*
[5]*Heber, United States*

7-48 Poster Phylogeography reveals the route of introduction in the invasive pathogen of Sunflower Downy Mildew *Plasmopara halstedii*

SOPHIA AHMED, FRANÇOIS DELMOTTE

INRA Bordeaux-Acquitaine, UMR Santé Végétale, Villenave D'ornon, France

7-49 Poster How to preserve a marine harvested forest? The case of two European competing kelp species

MYRIAM VALERO, THOMAS LAMY, CLAIRE DAGUIN, CÉCILE RIBOUT, VALERIA OPPLIGER, CHRISTOPHE DESTOMBE

UMR CNRS/UPMC 7144, Station Biologiqe de Roscoff, Roscoff, France

Male-female coevolution - from molecules to species

eseb •
12th Congress
Turin 2009

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Program

Wednesday August 26 - **Symposium 8**

Location: Room 3

Male-female coevolution - from molecules to species

Organizers: *Claudia Fricke, University of East Anglia, Norwich, United Kingdom*
Tracey Chapman, University of East Anglia, Norwich, United Kingdom

9.45 - 10.15	**MARIANA F. WOLFNER** (invited) Biochemical dissection of a rapidly-evolving *Drosophila* seminal protein
10.15 - 10.45	**KERRY L. SHAW** (invited) Male-female coevolution and the origins of rapid speciation
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**CAROLINE NIEBERDING** Has sexual selection on olfactive communication driven diversification in the African butterfly genus *Bicyclus*?
11.35 - 11.55	**ALEXEI A. MAKLAKOV** Natural and sexual selection in life-history evolution: a case of ageing
11.55 - 12.15	**RHONDA R. SNOOK** Consequences of experimental sexual selection on the evolution of courtship behaviour
12.15 - 12.35	**KRISTINA KARLSSON** Direct fitness cost from mate guarding and parallelism in sexual conflict between two ecotypes of the freshwater isopod *Asellus aquaticus*
12.35 - 12.55	**PETER KORSTEN** Sexual conflict in twins: effects of a male co-twin on birth weight and lifetime breeding success in female Soay sheep
12.55 - 13.55	*Lunch*
13.55 - 14.25	**MOHAMED A.F. NOOR** (invited) The genomics of speciation: Studying diversity, divergence and introgression on a genome-wide scale
14.25 - 14.45	**RICHARD HARRISON** Rapid adaptive evolution of seminal fluid proteins in crickets and butterflies
14.45 - 15.05	**EDWARD H. MORROW** Immunogenic males: a genome-wide analysis of reproduction and the cost of mating in *Drosophila melanogaster* females

15.05 - 15.35	*Coffee break*
15.35 - 15.55	**TOM PRICE** Sex ratio distorter causing sexual conflict promotes male-female co-evolution
15.55 - 16.15	**ERICA H. LEDER** Sex-biased expression and the evolution of sexual dimorphism in three-spine stickleback
16.15 - 16.35	**DENNIS SPRENGER** Mating rates in simultaneous hermaphrodites: male or female driven?
16.35 - 16.55	**LUKAS SCHÄRER** Mating behaviour, sexual conflict and the evolution of sperm design

8-1 Oral

BIOCHEMICAL DISSECTION OF A RAPIDLY-EVOLVING *DROSOPHILA* SEMINAL PROTEIN

Mariana F. Wolfner [1], Alex Wong [1], Adam B. Christopher [1], Norene A. Buehner [1]

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Despite (or perhaps because of) playing important roles in reproduction, a surprising number of seminal fluid proteins show signs of rapid sequence evolution, or other unusual evolutionary dynamics. For example, the *Drosophila melanogaster* seminal protein ovulin, a prohormone that induces ovulation in females after mating, is one of the most rapidly evolving proteins encoded by the *Drosophila* genome. Yet ovulin's sequence also contains short conserved motifs. Our biochemical tests show that these motifs are necessary for the formation of ovulin dimers. Furthermore, we show that ovulin's dimeric structure is conserved in the ovulin orthologs of other *Drosophila* species, even though these proteins diverge from *melanogaster* ovulin by up to 80%. Moreover, dimers can be formed between ovulin proteins of closely related species, suggesting at least some conservation of ovulin tertiary structure. These results will be discussed in the context of conflicting selection pressures on seminal proteins such as ovulin. On the one hand, sexual selection may be driving their rapid sequence evolution. On the other hand, seminal proteins are part of biochemical and physiological pathways involving other male and female molecules, and these interactions likely impose sequence constraints.

8-2 Oral

MALE-FEMALE COEVOLUTION AND THE ORIGINS OF RAPID SPECIATION

Kerry L. Shaw [1], Sky C. Lesnick [2], Chris Wiley [1], Christopher K. Ellison [1]

[1]*Cornell University, Department of Neurobiology and Behavior, Ithaca, United States*
[2]*University of Maryland, Department of Biology, College Park, United States*

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The evolution of sexual communication is most likely caused by sexual selection, possibly the most powerful cause of explosive divergence of form and behavior. However, the diversity of sexual communication systems across species presents a poorly understood paradox, because theory suggests that evolution of such behavior should be impaired by the functional need to maintain coordination between male signals and female preferences. Genetic coupling (tight linkage or pleiotropy) of signal-preference evolution, whereby the same, or nearby, genes control variation in male signal and female preference, can facilitate coordination of male and female communication behaviors. We examined genetic coupling between male signal and female preference in two closely related Hawaiian crickets (genus *Laupala*) with greatly differentiated male songs and female acoustic preferences. We compared the genomic locations of signal and preference quantitative trait loci (QTL) underlying song and preference variation. We document a QTL of moderate effect contributing to female preference that co-localizes with a song QTL. We then assess segregation of songs and preferences among second generation backcrosses, finding unprecedented genetic correlation between loci underlying sexual communication behavior. Contributions of both song and preference QTL are small to moderate between species, conditions that favor a behaviorally coupled mode of signal-preference evolution. Genomic linkage may facilitate rapid speciation by contributing to genetic correlations between sexual signaling behaviors that eventually cause sexual isolation between diverging populations. The genetic architecture of sexual communication may prove to be a powerful determinant of the propensity of certain evolutionary lineages to speciate.

8-3 Oral

HAS SEXUAL SELECTION ON OLFACTIVE COMMUNICATION DRIVEN DIVERSIFICATION IN THE AFRICAN BUTTERFLY GENUS *BICYCLUS*?

Paul Bacquet [1], Oskar Brattström [2], Klaus Fischer [3], Jimmy Andersson [4], Joaquin Bång [5],
Erik Hedenström [5], J-M. Lassance [5], Christer Löfstedt [4], Paul M. Brakerfield [2], Caroline Nieberding [1,2]

[1]*University of Louvain, Biodiversity Research Centre, Louvain-la-Neuve, Belgium*
[2]*University of Leiden, Institute of Biology, Leiden, The Netherlands*
[3]*Greifswald University, Zoological Institute and Museum, Greifswald, Germany*
[4]*HID Sweden University, Department of Natural Sciences, Engineering and Mathematic, Sundsvall, Sweden*
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The role of olfactive communication in reproductive success and isolation by sexual selection remains largely unknown. Based on the African species-rich butterfly genus *Bicyclus* Kirby 1871 (80 spp), we aim at assessing here experimentally: (1) the importance of male sex pheromones in sexual selection by females; (2) the role of sexual selection in driving reproductive isolation in the past. *Bicyclus* is relevant to address these questions because differences in the position and number of androconia, the male wing structures producing the pheromones, are the morphological character used to discriminate among species.

Here we identified the composition of the male sex pheromone in *Bicyclus anynana* by GC-EAD, GC-MS and behavioural experiments. We then quantified the level of pheromone variability and estimated the heritability level of the pheromone blend and of the androconial size using a parent-offspring regression. Variation of pheromone titres and ratios was correlated to age, a fitness-related trait for long-living *Bicyclus* butterflies, and it was shown that *B. anynana* pheromone is used by the female as an indicator of its age. Results together suggest that olfactive communication between sexes in *B. anynana* is under sexual selection. Using GC-MS, the composition of the pheromone bouquet was then screened in various additional *Bicyclus* species caught in the field, and the level of similarity between the bouquets of sympatric versus allopatric species was estimated. This analysis aims at assessing the role of sexual selection on male sex pheromones in driving past and present reproductive isolation of related *Bicyclus* species.

8-4 Oral

NATURAL AND SEXUAL SELECTION IN LIFE-HISTORY EVOLUTION: A CASE OF AGEING

Alexei A. Maklakov [1,2], Russell Bonduriansky [2], Robert C. Brooks [2]

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[2]*University of New South Wales, Evolution & Ecology Research Centre, Sydney, Australia*

Alexei.Maklakov@ebc.uu.se

Life-history theory predicts that selection will optimize the trade-off between reproduction and somatic maintenance. Reproductive ageing and finite lifespan are direct consequences of such optimization. Sexual selection and conflict profoundly affect the reproductive strategies of the sexes and thus can play an important role in the evolution of lifespan and ageing. In theory, sexual selection can favour the evolution of either faster or slower ageing, but the evidence is equivocal. We used a novel selection experiment to investigate the potential of sexual selection to influence the adaptive evolution of age-specific life-history traits. We selected replicate populations of the seed beetle *Callosobruchus maculatus* for age at reproduction ('Young' and 'Old') either with or without sexual selection. We found that life-history selection affected nearly all of the traits we measured, whereas sexual selection failed to affect most traits related to age-specific performance. Intriguingly, even the evolution of mating behavior was primarily affected by life-history selection rather than mating system. There was evidence that sexual selection depressed mean fitness, and failed to promote adaptation. Nonetheless, the evolution of several traits differed between males and females, suggesting that sex differences in reproductive strategy play an important role in trait responses to novel selection pressures. These data challenge the importance of extant sexual selection in rapid adaptation to environmental change but support the hypothesis that sex differences in life-history – a historical signature of sexual selection - are key in shaping an organism's response to selection.

8-5 Oral

CONSEQUENCES OF EXPERIMENTAL SEXUAL SELECTION ON THE EVOLUTION OF COURTSHIP BEHAVIOUR

Nelly Gidaszewski [1], Allen J. Moore [2], Rhonda R. Snook [1]

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Courtship is likely one of the best examples of male-female coevolution driven by both natural and sexual selection. Given that successful interaction between the sexes involves a myriad of signals, including chemical, visual and/or auditory, ample targets are provided for such selection. Indeed, several well-studied examples indicate that sexual conflict may be a driver of courtship behaviour. Here we explore the impact of sexual selection on courtship interactions between males and females in experimentally evolved populations of *Drosophila pseudoobscura* subjected to different intensities of sexual selection. Using a video-computing approach, we recorded courtship behaviours in both females and males from two sexual selection treatments, an enforced monogamy (M) treatment which eliminates sexual selection and an elevated promiscuity (E) treatment with high sexual selection intensity. We had four combinations of males and females; within treatments (MM, EE) and between treatments (ME, EM). We investigated whether there was any divergence in either male or female courtship behaviours among the different pairs. Such an approach allowed us to identify the targeted behaviours and to elucidate the role of sexual selection, including sexual conflict, on the coevolution of male-female courtship behaviour.

8-6 Oral

DIRECT FITNESS COST FROM MATE GUARDING AND PARALLELISM IN SEXUAL CONFLICT BETWEEN TWO ECOTYPES OF THE FRESHWATER ISOPOD *ASELLUS AQUATICUS*

Kristina Karlsson [1], Fabrice Eroukhmanoff [1], Roger Härdling [1], Erik I. Svensson [1]

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Pre-copulatory mate guarding is a male time investment strategy when female receptivity is limited. Pre-copulatory mate guarding could also be subject for a sexual conflict if the male and the female optimal guarding duration differs and if the female suffer a fitness cost from being guarded. In crustaceans, pre-copulatory mate guarding is common since females are receptive to a short time after they moult into maturity and in several a sexual conflict over mate guarding has been proposed. We investigated the fitness costs of mate guarding in the freshwater isopod *Asellus aquaticus* and found a direct negative fitness effect on females from the length of mate guarding. Thus, there is a strong indication of a sexual conflict in this species. Moreover, *A. aquaticus* has, in several south Swedish lakes, recently diverged into two ecotypes that co-exist within lakes but use different habitats. The ecotypes have in earlier studies been found to diverge in parallel in morphological characters, such as size and colouration, presumably as a response to different predatory pressures. Our result suggests that the ecotypes also have diverged in mate guarding duration in a parallel fashion. Isopods in both lakes from the ancestral ("reed") ecotype exhibit a significantly longer mate guarding than the novel ("stonewort") ecotype. In this study, we discuss the implications that colonisation of new environments can bear on the dynamics behind sexual conflict.

8-7 Oral

SEXUAL CONFLICT IN TWINS: EFFECTS OF A MALE CO-TWIN ON BIRTH WEIGHT AND LIFETIME BREEDING SUCCESS IN FEMALE SOAY SHEEP

Peter Korsten [1], Tim Clutton-Brock [2], Jill G. Pilkington [1], Josephine M. Pemberton [1], Loeske E.B. Kruuk [1]

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Males and females often show large differences in morphology, physiology and behaviour. This may lead to different requirements during their early development and give rise to sex-specific interactions between developing offspring. For example, the competition for limited resources *in utero* may be asymmetrical between the sexes, and androgens produced by male foetuses could negatively affect the development of females, with potentially long-lasting consequences. We show here in an unmanaged population of Soay sheep on St Kilda, Scotland, that female twin lambs with a male co-twin have reduced birth weight relative to those with a female co-twin, while there was no such difference in male twins. Lifetime breeding success in females with a male co-twin was also lower, even when controlling for their lower birth weight. This effect appeared to be mainly driven by differences in first-year survival. These results show that sex-specific interactions between offspring during early development can have long-term consequences for survival and reproduction, with potentially important implications for optimal sex allocation.

8-8 Oral

THE GENOMICS OF SPECIATION: STUDYING DIVERSITY, DIVERGENCE AND INTROGRESSION ON A GENOME-WIDE SCALE

Mohamed A.F. Noor [1]

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Many species naturally hybridize without losing their distinction, and regions that experience reduced recombination in hybrids, such as chromosomal inversions, are hypothesized to contribute to their persistence. Examining patterns of genetic variation within and among closely related species at a genome-wide scale can be used to rigorously test this hypothesis. Here, we compare genome sequences of multiple closely related fruit fly taxa from the *Drosophila pseudoobscura* subgroup to understand how these species have evolved through time. We find evidence for a complex evolutionary history, where multiple species separated around the same time, but two of these species appear to have subsequently undergone gene exchange limited to collinear regions of their genome. Nucleotide diversity within species was also correlated with fine-scale recombination rate, suggesting natural selection acted on patterns of variation. We conclude that chromosomal inversion differences between species have been vital to their ongoing persistence despite hybridization, and our research demonstrates how genomic data can reveal processes involved in speciation and divergence.

8-9 Oral

RAPID ADAPTIVE EVOLUTION OF SEMINAL FLUID PROTEINS IN CRICKETS AND BUTTERFLIES

Richard Harrison [1]

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Seminal fluid proteins (SFPs) are proteins transferred along with sperm from males to females during copulation. These proteins have been shown to play an important role in reproductive interactions in *Drosophila*, influencing both female physiology and female behavior. Using genomic and proteomic approaches, we have now identified SFPs in crickets (*Gryllus*) and butterflies (*Heliconius*). In both groups of insects, genes encoding SFPs exhibit rapid evolution (compared to a set of “control” genes), and some of these proteins show a clear signature of positive selection. Patterns of evolution of SFPs appear to be similar in groups of insects that are characterized by different levels of polyandry and by different costs to females of multiple mating. In a pair of hybridizing cricket species, gene genealogies based on genes encoding SFPs show the two species to be strongly differentiated, in contrast to genealogies based on housekeeping genes. Furthermore, using a variety of analytic approaches, we show that patterns of introgression vary strikingly across the genome, and that two loci that show a pattern consistent with absence of introgression encode seminal proteins that are under positive selection. These results raise the possibility that a subset of SFP genes may contribute to reproductive isolation between the two cricket species.

8-10 Oral

IMMUNOGENIC MALES: A GENOME-WIDE ANALYSIS OF REPRODUCTION AND THE COST OF MATING IN *DROSOPHILA MELANOGASTER* FEMALES

Edward H. Morrow [1], Paolo Innocenti [1]

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While the concept of sexual conflict is firmly established within the field of evolutionary biology, our knowledge of the processes and genes evolving under sexually antagonistic selection is largely male-biased. We conducted a genome-wide scan of the post-mating response of female *Drosophila melanogaster* in order to identify processes likely to be involved in the antagonistic interactions with males. Previously, microarrays have been used to examine gene expression of females differing in their reproductive status with the aim of identifying genes influenced by mating. However, since only virgin and single mated females were compared, transcriptional changes associated with reproduction (under natural selection) and male-induced effects (possibly under sexually antagonistic selection) cannot be disentangled. We partitioned these fundamentally different effects by instead examining the expression profiles of virgin, single mated and double mated females. We found substantial effects relating to reproduction and further effects that are only attributable to mating itself. Immune response genes dominate this male-induced effect indicating that the cost of mating may be due partly to this system's activation. We propose that both sexually antagonistic and natural selection have been important in the evolution of the innate immunity genes, thereby contributing to the sexual dimorphism and rapid evolution at these loci.

8-11 Oral

SEX RATIO DISTORTER CAUSING SEXUAL CONFLICT PROMOTES MALE-FEMALE CO-EVOLUTION

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Selfish genetic elements occur in all living organisms and are often associated with poor fertility and sperm competitive ability in male carriers. In the fruit fly *Drosophila pseudoobscura*, recent research shows that the presence of an X-chromosome meiotic driving gene causes females to evolve high levels of polyandry. Increased female remating rates are favoured because it decreases the chances of producing sex ratio biased broods and of offspring inheriting the selfish gene. Here we show that in populations where females evolved increased remating rates, males also evolved an increased ability to prevent females from remating, indicating male-female coevolution. Previous work has shown that *Drosophila* males can evolve ejaculates that are effective at reducing female remating in highly polyandrous populations. Here we provide evidence that a selfish gene that promotes polyandry, creates and evolutionary conflict between male carriers and females, favouring females that remate more frequently, which in turn causes males to evolve to be better at manipulating female receptivity. Although the conflict was initiated by the small proportion of males that carried the selfish gene, the evolutionary consequences affected the entire population. This effect is remarkably powerful as indicated by a direct link between the rate of female remating and males' ability to suppress female receptivity across populations. The results suggest that even rare selfish genetic elements may create evolutionary conflicts that have impacts throughout entire populations.

8-12 Oral

SEX-BIASED EXPRESSION AND THE EVOLUTION OF SEXUAL DIMORPHISM IN THREE-SPINE STICKLEBACK

Erica H. Leder [1], J.M. Cano [2], Tuomas Leinonen [3], Robert B. O'Hara [3], Craig R. Primmer [1], Juha Merilä [2]

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Given that the genome of males and females are almost identical with the exception of genes on the Y (or W-) chromosome or the sex-determining alleles (in organisms without sex chromosomes), it is likely that many downstream processes resulting in sexual dimorphism are produced by changes in gene regulation. In the early stages of sex chromosome evolution, as the Y chromosome degenerates, gene expression should be significantly impacted for genes residing on the sex chromosome pair as regulatory mutations accumulate. However, this has never been examined since most model organisms have clearly diverged sex chromosomes. Fish provide a unique opportunity to examine the evolution of sex chromosomes and their impact on sexual dimorphism since genetic sex determination may have evolved quite recently in some groups of fish. We compared female and male transcription patterns in three-spine stickleback (*Gasterosteus aculeatus*) liver tissue using a long-oligo DNA microarray. Of the 1,282 genes that were differentially expressed between the sexes, 25% were concentrated on chromosome group XIX which corresponds to the nascent sex chromosome group which is also a group where QTL for sexual dimorphism in body shape reside. Additionally, when several genes were examined in detail, coding sequences of the genes were the same in both sexes, but the upstream regions of group XIX genes showed various degrees of dissimilarity. We hypothesize that this degeneration of the Y chromosome results in regulatory mutations that create a sex-specific expression pattern and could be of significant impact in the evolution of sexual dimorphism.

8-13 Oral

MATING RATES IN SIMULTANEOUS HERMAPHRODITES: MALE OR FEMALE DRIVEN?

Dennis Sprenger [1], Rolanda Lange [2], Nils Anthes [3], Nico Michiels [4]

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Conflicts over mating rates appear ubiquitous across animal systems with internal fertilization, potentially leading to a co-evolutionary chase between the sexes. However, expectations about the strength and direction of conflict might depend on the realized gender expression. In separate sex species male fitness tends to be maximized at higher mating rates than female fitness, but females largely control remating. In contrast, in simultaneous hermaphrodites mating rates are predicted to be largely male driven because all individuals inherently express male motivation. This view implies that an individual's male function 'drags' its female counterpart into higher than optimal mating rates. We put the latter theory to test by experimentally investigating the relationship between mating rate and female fitness in the marine gastropod *Chelidonura sandrana*. We further explored how mate encounter rate affects mating rate in a design that disentangles group size and density effects. Our results indicate a female fitness optimum at an intermediate mating rate, conforming to theoretical predictions for separate sex species. Moreover, this intermediate mating rate remained constant irrespective of group size or density. Taken together, our findings challenge the notion of male driven mating rates in simultaneous hermaphrodites and indicate a much stronger component of female control than previously thought.

8-14 Oral

MATING BEHAVIOUR, SEXUAL CONFLICT AND THE EVOLUTION OF SPERM DESIGN

Lukas Schärer [1], D. Timothy J. Littlewood [2], Andrea Waeschenbach [2], Wataru Yoshida [3], Dita B. Vizoso [1]

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Sperm are the most diverse of all animal cell types. Much of this diversity may reflect adaptations to the highly variable conditions under which sperm compete for fertilizations; conditions which may themselves evolve rapidly as a result of sperm competition, cryptic female choice, and resulting sexual conflicts. However, little of the diversity in sperm design is currently understood at the functional level. Here we use a comparative approach in the hermaphroditic flatworm genus *Macrostomum* to show that a complex sperm design is associated with reciprocal mating, and secondarily lost in response to the evolution of coercive mating. Specifically, the complex sperm design – which includes stiff lateral bristles – is likely a male persistence trait associated with sexual conflicts over the fate of received ejaculates, and linked to female resistance traits, namely an intriguing postcopulatory *suck* behaviour, and a thickened epithelium of the sperm-receiving organ. Our results strongly suggest that the nature of the sexual conflicts is drastically altered as a result of the evolution of hypodermic impregnation, favouring simpler and smaller sperm, a simpler sperm-receiving organ, and the loss of the postcopulatory behaviour. We conclude that mating behaviour and sexual conflicts can strongly influence the evolution of sperm design. Moreover, we interpret hypodermic impregnation as a male strategy to by-pass female control, thereby fundamentally changing the requirements for sperm design.

8-1 Poster

Eggshell colouration in a polygynous species: Does blue-green chroma reflect female mating status and quality?

PETR PROCHÁZKA[1], MARCEL HONZA[1], MILICA POŽGAYOVÁ[1,2], MICHAEL I. CHERRY[3]

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[3]University of Stellenbosch, Department of Botany and Zoology, Matieland, South Africa

8-2 Poster

A mechanism for cryptic female choice in a promiscuous bird

ODDMUND KLEVEN[1], ARILD JOHNSEN[1], GEIR RUDOLFSEN[2], JAN T. LIFJELD[1], TERJE LASKEMOEN[1], TROND ØIGARDEN[1]

[1]University of Oslo, Natural History Museum, National Centre for Biosystematics, Oslo, Norway
[2]University of Tromsø, Institute for Biology , Tromsø, Norway

8-3 Poster

The Genetic Architecture of Male and Female Sexual Ornaments in the Fowl, *Gallus gallus*

DOMINIC WRIGHT[1], LEIF ANDERSSON[2], PER JENSEN[1], OLLE KÄMPE[3], CARL-JOHAN RUBIN[3], ANDREAS KINDMARK[3]

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[2]Uppsala University IMBIM, Uppsala, Sweden
[3]Uppsala University, Department of Medical Sciences, Uppsala, Sweden

8-4 Poster

Sex differences in ornamentation are associated with mating systems in Kentish plovers

ARACELI ARGÜELLES-TICÓ[1], JORDI FIGUEROLA[2], ANDRAS KOSZTOLANYI[3], CLEMENS KUEPPER[1], LYDIA LOZANO[4], RENE VAN DIJK[1], TAMAS SZEKELY[1]

[1]University of Bath, Department of Biology and Biochemistry, Bath, United Kingdom
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[3]Eotvos University, Department of Ethology, Budapest, Hungary
[4]Universidad Autonoma de Sinaloa, Escuela de Biologia, Culiacan, Mexico

8-5 Poster

Reproductive success in the river blenny: are the better males always chosen by females?

NOËLLE FABRE, ADOLF DE SOSTOA, EDUARDO GARCIA, IRENE CAPELLI, DOLORS VINYOLES

Universitat de Barcelona, Departamento de Biologia Animal (Vertebrats), Barcelona, Spain

8-6 Poster

The role of indirect and direct sexual selection on diversity of Lake Malawi bower-building cichlid fish

ISABEL S. MAGALHAES, DOMINO JOYCE

Hull University, Department of Biological Sciences, Hull, United Kingdom

8-7 Poster

Sexual selection in mushrooms: male-male competition or female choice?

BART NIEUWENHUIS, ALFONS J.M. DEBETS, DUUR K. AANEN

Wageningen University, Department of Genetics, Wageningen, Netherlands

8-8 Poster Sexual conflict coevolution – population size, divergence and the emergence of new variation

LAURENE GAY[1], DAVID HOSKEN[1], PAUL EADY[2], RAM VASUDEV[2], TOM TREGENZA[1]

[1]University of Exeter Cornwall, Centre for Ecology and Conservation, Penryn, United Kingdom
[2]University of Lincoln, Department of Biological Sciences, Lincoln, United Kingdom

8-9 Poster Sexual selection promotes asymmetric reproductive barriers and underlying changes in the regulatory regions of reproductive genes

MONTSERRAT GOMENDIO[1], JUAN MARTIN-COELLO[1], HERNAN DOPAZO[2], LEONARDO ARBIZA[2], EDUARDO R.S. ROLDAN[1]

[1]Museo Nacional Ciencias Naturales (CSIC), Evolutionary Ecology, Madrid, Spain
[2]Centro de Investigacion Principe Felipe, Department of Bioinformatics and Genomics, Valencia, Spain

8-10 Poster Sexually antagonistic selection: from the laboratory to the field

MIKAEL MOKKONEN[1], ESA KOSKELA[2], TAPIO O. MAPPES[1], SUZANNE MILLS[3]

[1]University of Jyväskylä, Centre of Excellence in Evolutionary Research, Jyväskylä, Finland
[2]University of Jyväskylä, Department of Biological and Environmental Sciences, Jyväskylä, Finland
[3]Université de Perpignan, Department of Biologie et Ecologie Tropicale et Mediterranéenne, Perpignan, France

8-11 Poster The interplay between males and females at mating: economic and gene expression studies

TRACEY CHAPMAN

University of East Anglia, School of Biological Sciences, Norwich, United Kingdom

8-12 Poster The evolution of gender-biased immunocompetence

OLIVIER RESTIF

University of Cambridge, Faculty of Veterinary Medicine, Cambridge, United Kingdom

8-13 Poster Female-driven mechanisms against selfish genetic element

CAROLINE ANGELARD[1,2,3], CATHERINE MONTCHAMP-MOREAU[1,2], DOMINIQUE JOLY[1,2]

[1]CNRS, Laboratoire Evolution, Génomes & Spéciation, Gif-sur-Yvette, Cedex, France
[2]Université Paris-Sud, Orsay, Cedex, France
[3]University of Lausanne, Department of Ecology & Evolution, Biophone Building, Lausanne, Switzerland

8-14 Poster The genetic basis of traits regulating sperm competition and female mating frequency in guppies

JONATHAN P. EVANS

University of Western Australia, Centre for Evolutionary Biology, Nedlands, Australia

8-15 Poster Sperm competition and the effect of queens on ejaculate interactions in social insects

SUSANNE DEN BOER[1], BORIS BAER[2], JACOBUS J. BOOMSMA[1]

[1]University of Copenhagen, Department of Biology, Copenhagen, Denmark
[2]University of Western Australia, Centre for Evolutionary Biology, Crawley, Australia

8-16 Poster Female reproductive success affected by selective male harassment in the damselfly *Ischnura senegalensis*

YUMA TAKAHASHI, MAMORU WATANABE

University of Tsukuba, Graduate School of Life and Environmental Sciences, Tsukuba, Japan

8-17 Poster **Female Genitalia Concealment Promotes Intimate Male Courtship in a Water Strider**

CHANG S. HAN[1], PIOTR G. JABLONSKI[1,2]

[1]Seoul National University, Laboratory of Behavioral Ecology and Evolution, School of Biological Sciences, Seoul, South Korea

[2]Polish Accademy of Sciences, Center for Ecological Research, Lomianki, Poland

8-18 Poster **Trade-off between investments in male and female reproductive functions in the simultaneously hermaphroditic earthworm *Eisenia andrei***

PABLO GONZÁLEZ PORTO, ALBERTO VELANDO, JORGE DOMÍNGUEZ

University of Vigo, Department of Ecology and Animal Biology, Vigo, Spain

8-19 Poster **Sexual conflict and sexual selection in *Caenorhabditis remanei***

NADINE TIMMERMEYER, KAROLINE FRITZSCHE, NICO K. MICHIELS

Eberhard Karls University Tuebingen, Department of Animal Evolutionary Ecology, Tuebingen, Germany

8-20 Poster **Studying the opportunity for sexual selection in a simultaneously hermaphroditic animal: covariation between male and female reproductive success**

BENJAMIN PELISSIE, PATRICE DAVID, PHILIPPE JARNE

CEFE - CNRS, Biologie des Populations, Montpellier, France

8-21 Poster **Variation in female mating costs across populations of the seed bug *Lygaeus equestris***

GETHIN M.V. EVANS[1], DAVID M. SHUKER[1,2]

[1]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom

[2]University of St. Andrews, St. Andrews, United Kingdom

8-22 Poster ***Lutzomyia youngi* (Diptera: Phlebotomiane) a cryptic species within *Verrucarum* group: Female-Male genetic integration without sexual dimorphism**

GABRIEL A. GOLCZER, JAZZMIN C. ARRIVILLAGA

Universidad Simón Bolívar, Enviromental Studies, Caracas, Venezuela

8-23 Poster **The 'inside-story': Evolution of the female internal reproductive system in *Sepsidae* (Diptera)**

NALINI PUNIAMOORTHY[1,2], MARION KOTRBA[3], RUDOLF MEIER[2]

[1]University of Zurich, Zoological Museum, Zurich, Switzerland

[2]National University of Singapore, Department of Biological Sciences, Singapore

[3]Zoologische Staatssammlung München, Munich, Germany

8-24 Poster **The influence of population density on spermathecal structural complexity and consequences for female reproductive fitness**

ANNA L. MILLARD

University of East Anglia, Department of Biological Sciences, Norwich, United Kingdom

8-25 Poster **Ejaculate protection against sexually transmitted microbes**

OLIVER OTTI, RICHARD A. NAYLOR, KLAUS REINHARDT, MICHAEL T. SIVA-JOTHY

University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom

8-26 Poster **Evolution of Seminal Fluid Proteins Mediated by Sexual Conflict**

JAMES BOONE, TRACEY CHAPMAN
University of East Anglia, School of Biological Sciences, Norwich, United Kingdom

8-27 Poster **The making of a successful male: An integrated study of male reproductive success in a pest insect**

PHILIP T. LEFTWICH[1,2]
[1]*University of East Anglia, Department of Biological Sciences, Norwich, United Kingdom*
[2]*Oxitec, Didcot, United Kingdom*

8-28 Poster **Height and attractiveness in Humans**

ALEXANDRE COURTIOL, JEAN BAPTISTE FERDY, BERNARD GODELLE, MICHEL RAYMOND
ISEM, Montpellier, France

8-29 Poster **Size assortative pairing and struggling behaviour amerliorate the costs of male guarding for juvenile females in the Zeus bug, *Phoreticovelia disparata***

THERESA M. JONES[1], MARK A. ELGAR[1], GORAN ARNQVIST[2]
[1]*University of Melbourne, Department of Zoology, Melbourne, Australia*
[2]*Uppsala University, Department of Animal Ecology, Uppsala, Sweden*

On the origins of novelty in development and evolution: from cryptic genetic variation to genetic accommodation

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12th Congress
Turin 2009

9

Program

Wednesday August 26 - **Symposium 9**

Location: Room 4

On the origins of novelty in development and evolution: from cryptic genetic variation to genetic accommodation

Organizers: *Armin P. Moczek, Indiana University, Bloomington, United States*
Emilie Snell-Rood, Indiana University, Bloomington, United States

9.45 - 10.15	**ANDREAS WAGNER** (invited) The relationship between evolutionary innovation and robustness
10.15 - 10.45	**IAN DWORKIN** (invited) Cryptic genetic variation, genetic background effects and the architecture of complex phenotypes
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**EVANDRO FERRADA** Evolutionary Constraints on the Protein Functional Space
11.35 - 11.55	**PIERRE-ALEXIS GROS** Selection for Chaperone Like Mediated Genetic Robustness at Low Mutation Rate: Impact of Drift, Epistasis and Complexity
11.55 - 12.15	**JOANNA MASEL** Complex adaptations drive the evolution of the capacitor [PSI+], even with realistic rates of yeast sex
12.15 - 12.35	**PAUL C. NICHOLS** Hybridizing *Astatotilapia calliptera* populations fuelled Mbuna species radiation by transgressive segregation
12.35 - 12.55	**JULIEN ROUX** Constraints and innovations on vertebrate genome evolution
12.55 - 13.55	*Lunch*
13.55 - 14.25	**SUSAN FOSTER** (invited) Ancestral Plasticity and Evolutionary Diversification: The Stickleback Adaptive Radiation
14.25 - 14.45	**CRISTINA LEDON-RETTIG** Environmental Stress and the Evolution of Novel Feeding Strategies

14.45 - 15.05	**MATHIAS KOELLIKER** Evolutionary novelty in the family by antagonistic parent-offspring co-adaptation
15.05 - 15.35	*Coffee break*
15.35 - 15.55	**A. RICHARD PALMER** Learning, developmental plasticity and the evolution of morphological asymmetry
15.55 - 16.15	**SUZANNE V. SAENKO** Co-option of conserved developmental genes in the evolution of novel wing patterns in Lepidoptera
16.15 - 16.35	**JULIA BOWSHER** Getting a leg up: the evolution of novel abdominal appendages in sepsid flies
16.35 - 16.55	**ARMIN P. MOCZEK** Developmental plasticity and the origins of novelty and diversity in horned beetles

9-1 Oral

THE RELATIONSHIP BETWEEN EVOLUTIONARY INNOVATION AND ROBUSTNESS

Andreas Wagner [1]

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Mutational robustness and a system's ability to produce heritable phenotypic variation harbour a paradoxical tension. On one hand, high robustness implies low production of heritable phenotypic variation. On the other hand, both experimental and computational analyses of neutral networks indicate that robustness enhances evolvability. I here resolve this tension using a molecular study system. To resolve the tension, one must distinguish between robustness of a genotype and a phenotype. I confirm that genotype (sequence) robustness and evolvability share an antagonistic relationship. In stark contrast, phenotype (structure) robustness promotes structure evolvability. A consequence is that finite populations of sequences with a robust phenotype can access large amounts of phenotypic variation while spreading through a neutral network. Population-level processes and phenotypes rather than individual sequences are key to understand the relationship between robustness and evolvability. My observations may apply to other genetic systems where many connected genotypes produce the same phenotypes.

9-2 Oral

CRYPTIC GENETIC VARIATION, GENETIC BACKGROUND EFFECTS AND THE ARCHITECTURE OF COMPLEX PHENOTYPES

Ian Dworkin [1]

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Despite the accumulation of evidence that allelic effects that contribute to variation for traits are often condition dependent, quantitative genetic theory still largely focuses on the contribution of additive effects. While recent theoretical work has done a lot to incorporate Genotype-by-Genotype and Genotype-by-Environment interactions into models of phenotypic evolution, the lack of sufficient empirical work on the mechanistic basis of these conditional genetic effects increase the difficulty in generating assumptions and interpreting such models. As such it is still unclear what role such non-additive effects may have during the evolutionary process, and it is clear that empirical work is required to address these issues.

In my talk I will discuss some of the past and current empirical work on conditional genetic effects, and what these results may tell us about the role of cryptic genetic variation in natural populations. I will also introduce a functional genetic model system that we use in my lab to study genetic background effects. I will use this system to demonstrate that not only are the mean effects of a mutation conditionally dependent, but the interaction between alleles as well. I will also discuss some initial results that contradict the model of conditionally phenotypically silent alleles, in favour of subtle pleiotropic effects.

9-3 Oral

EVOLUTIONARY CONSTRAINTS ON THE PROTEIN FUNCTIONAL SPACE

Evandro Ferrada [1,2], Andreas Wagner [1,2,3,4]

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Experimental and theoretical observations show that protein domains are confined to discrete regions in sequence space. This phenomenon has profound implications on a protein's ability to evolve new functions. In spite of the availability of protein functional annotation, almost nothing is known about the distribution and shape of protein functional space. Similar functions are usually performed by similar structures. However, it has also been observed that extremely different folds can perform the same function. Here, we use structural and functional annotation of single domain proteins to explore the distribution of functions in protein structural space. Additionally, we use principal component analysis to examine the neighborhood of selected representative proteins domains in the protein structural space and discuss the implications of its topology on the evolution of new functions.

9-4 Oral

SELECTION FOR CHAPERONE LIKE MEDIATED GENETIC ROBUSTNESS AT LOW MUTATION RATE: IMPACT OF DRIFT, EPISTASIS AND COMPLEXITY

Pierre-Alexis Gros [1], Olivier Tenaillon [1]

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Genetic robustness is defined as the constancy of a phenotype in the face of deleterious mutations. Over-expression of chaperones, to assist the folding of proteins carrying deleterious mutations, is so far one of the most accepted molecular mechanisms enhancing genetic robustness. Most theories on the evolution of robustness have focused on the implications of high mutation rate. Here we show that genetic drift, which is modulated by population size, organism complexity and epistasis, can be a sufficient force to select for chaperone-mediated genetic robustness. Using an exact analytical solution, we also show that selection for costly genetic robustness leads to a paradox: the decrease of population fitness on long time scales and the long-term dependency on robustness mechanisms. We suggest that selection for genetic robustness could be universal and not restricted to high mutation rate organisms such as RNA viruses. The evolution of the endosymbiont *Buchnera* illustrates this selection mechanism and its paradox: the increase dependency to chaperones mediating genetic robustness. Our model explains why most chaperones might have become essential even in optimal growth conditions.

9-5 Oral

COMPLEX ADAPTATIONS DRIVE THE EVOLUTION OF THE CAPACITOR [PSI+], EVEN WITH REALISTIC RATES OF YEAST SEX

Joanna Masel [1], Cortland K. Griswold [2]

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The [PSI+] prion in yeast is a powerful model system for the origins of novelty. The epigenetically inherited [PSI+] state taps into previously cryptic genetic variation by continuing translation, at a low rate, beyond stop codons and into 3'UTRs. If some combination of readthrough variants is adaptive, [PSI+] acts as a stopgap to buy the lineage time to acquire multiple stop codon mutations at these sites. These mutations both increase expression of adaptive readthrough products and eliminate their dependence on the [PSI+] prion. The lineage can then revert back to the wild-type [psi-] state, completing genetic assimilation. All [PSI+]-mediated variation other than that selected for will then also revert to the cryptic state.

It has previously been unclear whether such an evolvability mechanism could be favored by natural selection. Sex inhibits the evolution of other putative evolvability mechanisms, such as mutator alleles. We explore whether sex also prevents natural selection from favoring modifier alleles that facilitate [PSI+] formation. Sex may permit the spread of “cheater” alleles that acquire the benefits of [PSI+] through mating without incurring the cost of producing [PSI+] at times when it is not adaptive. Using recent quantitative estimates of the frequency of sex in Saccharomyces paradoxus, we calculate that natural selection for evolvability will drive the evolution of the [PSI+] system via modifier alleles, so long as yeast populations occasionally require complex adaptations involving synergistic epistasis between two loci. If adaptations are always simple and require substitution at only a single locus, then the [PSI+] system is not favored by natural selection.

9-6 Oral

HYBRIDIZING *ASTATOTILAPIA CALLIPTERA* POPULATIONS FUELLED MBUNA SPECIES RADIATION BY TRANSGRESSIVE SEGREGATION

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We aim to assess the contribution of transgressive segregation in the rapid radiation of the Lake Malawi cichlid flock, modeling different hybridization scenarios. We quantified the phenotypic variation in extant mbuna cichlids, measuring homologous landmarks in diverged species. We compare this to the standing phenotypic variation within *Astatotilapia calliptera* populations, known to have cryptic genetic variation and which we hypothesis is the putative ancestor, and then calculate the rate of phenotypic change over time expressed in darwins. Previously artificial selection experiments attained a geometric mean rate of 58,000 darwins, translocation experiments with guppies attained a rate of 3700 to 45,000 darwins, while the rate in the fossil record is considerably lower, ranging from 0.7 to 3.7 darwins. Using recently published data on the correlation between genetic divergence with the extent of phenotypic variation released through transgressive segregation in Eudicot plants we estimated the rate of evolutionary change if the mbuna cichlid flock was founded by hybrids rather than by parental *A. calliptera*. This comparison shows that without hybridization, the rate of evolutionary change exceeds that observed in the fossil record by several orders of magnitude. However, with repeated hybridization, this rate is still high, but it falls within the range of that of translocated wild guppy populations. We conclude that hybridization may have released (nonadditive) genetic variation present in the *A. calliptera* riverine populations. This variation has been converted in additive genetic variation, serving as the substrate of subsequent positive Darwinian selection after the ancestral cichlids arrived in a novel habitat of primordial Lake Malawi.

9-7 Oral

CONSTRAINTS AND INNOVATIONS ON VERTEBRATE GENOME EVOLUTION

Julien Roux [1,2], Marc Robinson-Rechavi [1,2]

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It is widely thought that organismal evolution is limited by constraints on embryonic development that prevent certain innovations from being tolerated. We focused on vertebrate genome evolution and we analyzed gene expression data, gene phylogenies and mutant phenotypes from two vertebrates: zebrafish, using a microarray experiment spanning 14 stages of development, and mouse, using EST counts for 26 stages of development.
We show that, in both species, genes expressed early in development (i) have a more dramatic effect of knock-out, and (ii) are less retained in duplicate after whole genome duplication, relative to genes expressed late. This supports high constraints on early stages of vertebrate development, making them less open to innovations (gene doubling or gene loss). The trend across development is clear: following this early peak, constraints decline steadily throughout the rest of development. Genes under weaker constraints are good candidates for studying evolutionary innovation. Mapping of gene expression to developmental ontologies shows that these genes are involved in development of the nervous system in both mouse and zebrafish. Detailed analysis of this pattern is ongoing.

9-8 Oral

ANCESTRAL PLASTICITY AND EVOLUTIONARY DIVERSIFICATION: THE STICKLEBACK ADAPTIVE RADIATION

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Phenotypes are the products of a complex interplay between genetic architecture, epigenetic factors and the timing and pattern of environmental influences. Patterns of phenotypic expression can be modeled as phenotypic norms of reaction that can evolve in response to changing environments, and can be modified over the lifetime of an organism in response to a variety of environmental influences. The adaptive radiation of the threespine stickleback fish, *Gasterosteus aculeatus,* offers a unique opportunity to examine the evolution of phenotypic norms of reaction, and to infer the factors that modify plastic responses to environmental challenges. This is because oceanic populations, thought to closely resemble the ancestor that gave rise to an extremely diverse post-glacial freshwater adaptive radiation, are extant and can be compared to derivative freshwater populations. The derivative populations exhibit high levels of parallelism: similar phenotypes have arisen repeatedly, and independently, in similar, disjunct environments. In divergent environments, predictable differentiation of morphological and behavioral characteristics of populations has been attributed to predictably different patterns of selection. However, the outcome of selection is also contingent upon the nature of expressed phenotypic variation. Here we illustrate the probable influence of ancestral plasticity on the subsequent patterns of adaptive differentiation of both morphological and behavioral traits in the post-glacial freshwater radiation of the threespine stickleback.

9-9 Oral

ENVIRONMENTAL STRESS AND THE EVOLUTION OF NOVEL FEEDING STRATEGIES

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Feeding strategies are diverse, even among closely related taxa, yet little is known about how organisms transition to novel diets. One possibility is that cryptic genetic variation is exposed and amplified when populations experience environmental stressors. Once exposed, this environmentally dependent variation may become modified by natural selection through a process known as "genetic accommodation". Here, we investigate a possible mechanism for releasing cryptic variation, and evaluate whether this mechanism could have operated in natural populations of spadefoot toads. Larvae of the genus *Spea* have evolved the ability to consume shrimp, whereas larvae of their closest sister genus, *Scaphiopus*, consume the ancestral diet of detritus. Previous work has shown that *Scaphiopus* larvae express greater phenotypic variation and produce higher levels of the stress hormone corticosterone (CORT) when consuming shrimp. In the current study, we used hormonal manipulation to test whether shrimp-induced CORT in *Scaphiopus* larvae is responsible for mediating the expression of cryptic variation in traits that are adaptive for consuming shrimp. Further, we used a full-sibship analysis to determine whether this variation has a heritable basis. If *Scaphiopus* is a suitable proxy for ancestral *Spea*, and diet-dependent adaptive variation is heritable, then cryptic genetic variation may have played a significant role in *Spea*'s transition to a novel diet. Moreover, if CORT- and shrimp-induced phenotypic variation are similar, CORT may have mediated the expression of cryptic genetic variation in ancestral *Spea*. In general, results from this work will contribute to our understanding of how genetic accommodation operates in natural populations.

9-10 Oral

EVOLUTIONARY NOVELTY IN THE FAMILY BY ANTAGONISTIC PARENT-OFFSPRING CO-ADAPTATION

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Across the animal and plant kingdoms, offspring have means to influence the amount of parental investment (PI) they receive. In some species they emit subtle cues, while in others they vigorously solicit parental attention. Current theory explains the evolution of offspring influences on PI selection on offspring to solicit more than parents should provide (i.e., parent-offspring conflict). Using dynamic evolutionary models, we present an alternative perspective based on antagonistic selection on the amount of PI individuals *obtain* as offspring and *provide* as parents. We show that fitness payoffs for both offspring and parental strategies are generated once individuals become parents, thereby imposing strong antagonistic selection across life-stages for co-adapted parent and offspring strategies that maximize individual lifetime reproductive success. At evolutionary equilibrium, a neutral space for tightly co-adapted parent-offspring strategy combinations emerges. Using simulation models, we show that, within this space, stochastic processes like mutation and environmental fluctuations can play a major role in their evolution. Offspring solicitation strategies could only invade in association with adequate parental provisioning (co-adaptation), and fast strategy transitions and ongoing co-evolutionary dynamics occurred in populations that appeared stable at the phenotypic level (neutral space). Thus, antagonistic selection across life-stages generates a space for evolutionary innovation, potentially explaining the diversity of forms in family life.

9-11 Oral

LEARNING, DEVELOPMENTAL PLASTICITY AND THE EVOLUTION OF MORPHOLOGICAL ASYMMETRY

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Evolution by natural selection requires three steps. New variants of organisms: must arise, must have an impact on fitness (survival or fecundity), and must (ultimately) be heritable. The first step - how new variants arise - remains controversial. Traditionally, new phenotypes are attributed to novel genotypes (mutants or recombinants). But developmental plasticity may be a more important source of new variants than generally recognized. The absence of heritable variation for direction of asymmetry in species that show a random mixture of asymmetric forms (i.e., equal numbers of right- and left-handed forms), identifies a unique phenotype - 'direction of asymmetry' - for which there is no genotype.A wide-ranging survey of asymmetry variation within and among species of animals and plants offers some of the strongest evidence to date for a 'phenotype-precedes-genotype' mode of evolution. In addition, the tendency of many animals to learn (e.g., handed behavior) may facilitate both the origin and the amplification of right-left morphological differences via developmental plasticity. Such an interplay between learning and developmental plasticity might greatly enhance the rate of morphological evolution.

9-12 Oral

CO-OPTION OF CONSERVED DEVELOPMENTAL GENES IN THE EVOLUTION OF NOVEL WING PATTERNS IN LEPIDOPTERA

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Evolutionary-developmental biology aims to understand how diversification of form has occurred through changes in developmental mechanisms. Exciting issue in evo-devo that has only started to be explored is the origin and modification of novel traits. Co-option, or redeployment of conserved genetic pathways is one of the mechanisms operating in the evolution of lineage-specific traits, and is beautifully illustrated by studies on wing colour patterns in butterflies and moths. Here, we focus on eyespot patterns in the emerging evo-devo model, Nymphalid butterfly *Bicyclus anynana*, and discuss how highly conserved developmental networks, fundamental to embryonic development in most animals, have been re-deployed into performing new functions in painting the patterns of colour on butterfly wings.

In butterflies, wing scales, as well as colour patterns composed by these scales, are lineage-specific, novel traits with known adaptive value (predator avoidance and sexual selection). Eyespots probably evolved from primitive, uniformly-coloured spots through the recruitment and modification of genes belonging to Hedgehog and Wingless pathways, acquisition of signalling activity, and further diversification of colour schemes under the influence of natural selection. Here, we show that one of the Hox genes whose function is highly conserved in all animals, has been recruited and plays a crucial role in eyespot formation in some, but not the other butterfly species.

9-13 Oral

GETTING A LEG UP: THE EVOLUTION OF NOVEL ABDOMINAL APPENDAGES IN SEPSID FLIES

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A major goal of the recent re-synthesis of developmental and evolutionary biology is to understand how evolutionary changes in the molecular processes of development result in changes in morphology. Abdominal appendages in the male sepsid fly *Themira biloba* (Diptera, Sepsidae) are complex novel structures on the fourth abdominal segment that are used during courtship and mating. This family is the only group of insects to have evolved a complex and well-articulated extra-genitalic abdominal appendage. Given the current phylogeny of Sepsidae, abdominal appendages appear to have evolved in a relatively short time period and in more than one instance within the clade. Determining the molecular processes underlying abdominal appendage development will elucidate how complex novel structure can evolve in a relatively short time period. Previous work has established that the abdominal appendages develop during pupation from imaginal histoblast cells on the fourth abdominal segment. We are investigating to what degree the genetic module known to specify thoracic limb development in *Drosophila* has been co-opted into the regulation of the sepsid abdominal appendages and to what degree their development is controlled by novel gene interactions. Although the appendages develop during pupation, the specification of fourth segment as the location for appendage development occurs earlier. We investigated when the abdominal appendages are first specified by examining the expression of the HOX genes in the Bithorax complex that are known to determine the identities of each abdominal segment.

9-14 Oral

DEVELOPMENTAL PLASTICITY AND THE ORIGINS OF NOVELTY AND DIVERSITY IN HORNED BEETLES

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Developmental plasticity is thought to play important roles in organismal diversification and evolutionary innovation. Focusing on the evolutionary developmental biology of horned beetles, we explore several avenues by which developmental plasticity may have mediated the origins of novelty and diversity. Specifically, we argue that phenotypic plasticity generates novel targets for evolutionary processes to act on, as well as brings about unique trade-offs during development and evolution, thereby diversifying evolutionary trajectories available to natural populations. Furthermote, we examine the notion that in those cases in which phenotypic plasticity is underlain by modularity in gene expression, it results in a fundamental trade-off between degree of plasticity and mutation accumulation. On one side, this trade-off limits the extent of plasticity that can be accommodated by modularity of gene expression. On the other, it causes genes whose expression is specific to rare environments to accumulate greater variation within species, providing the opportunity for faster divergence and diversification between species, compared to genes expressed across environments. Phenotypic plasticity therefore contributes to organismal diversification on a variety of levels of biological organization, thereby facilitating the evolution of novel traits and new species.

9-1 Poster **The evolutionary origins of animal light sensitivity**

TODD H. OAKLEY, DAVID C. PLACHETZKI, CAITLIN R. FONG

UC-Santa Barbara, Ecology Evolution Marine Biology, Santa Barbara, United States

9-2 Poster **The atypical mitochondrial genome of terrestrial Crustaceans: dimeric structure, stable transmission of heteroplasmy and evolutionary consequences**

VINCENT DOUBLET, ROLAND RAIMOND, CATHERINE SOUTY-GROSSET, ISABELLE MARCADÉ

Université de Poitiers-CNRS, Laboratory Ecology Evolution Symbiosis, Poitiers, France

9-3 Poster **On the Origin and Evolution of Vertebrate Olfactory Receptor Genes: Comparative Genome Analysis among 23 Chordate Species**

YOSHIHITO NIIMURA

Tokyo Medical and Dental University, Medical Research Institute, Department of Bioinformatics, Tokyo, Japan

9-4 Poster **Expansion of Amino Acid Repeats in Genes: A Gateway for Adaptation**

FERNANDO CRUZ[1,2], MARC ROBINSON-RECHAVI[1,2]

[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland
[2]Swiss Institute of Bioinformatics, Lausanne, Switzerland

9-5 Poster **Lack of evolutionary conservation at positions important for thermal stability in the yeast ODCase**

AGATA JAKUBOWSKA, RYSZARD KORONA

Jagielonian University, Institute of Environmental Sciences, Krakow, Poland

9-6 Poster **Genome size variation and MH diversity in syngnathid fishes**

ANGELA FECHNER, TONY WILSON

University of Zurich, Zoological Museum, Zurich, Switzerland

9-7 Poster **A morphogenetic model delineating a set of possible forms for a morphological pollen character: evolutionary implications**

ALEXIS V. MATAMORO[1], BÉATRICE ALBERT[2], CAROL A. FURNESS[3], PIERRE-HENRI GOUYON[1], SOPHIE NADOT[2], ADRIENNE RESSAYRE[4]

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[3]Royal Botanic Gardens, Micromorphology Sections, Jodrell Laboratory, Kew, United Kingdom
[4]UMR de Génétique Végétale, INRA-Paris XI-CNRS-AgroParisTech , Gif-sur-Yvette, France

9-8 Poster **Evolution of a robust system under heritable perturbations**

K. RYO TAKAHASI

Institute of Genetics, Department of Population Genetics, Misima, Japan

9-9 Poster **Horizontal cross-species transfer of genes in space and time: the case of AtL1, a LINE-1-like retrotransposon of *Arabidopsis thaliana***

NELSON MARMIROLI, GIOVANNA VISIOLI, ELENA MAESTRI

University of Parma, Department of Environmental Sciences, Parma, Italy

9-10 Poster **The use of a non-LTR retrotransposable element to date the formation of a novel gene cluster**

RITA PONCE

Centro de Biologia Ambiental, Faculdade de Ciencias da Universidade de Lisboa, Lisbon, Portugal

Ecological genetics in the genomics era

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12th Congress
Turin 2009

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Program

Thursday August 27 - **Symposium 10**

Location: Room 1

Ecological genetics in the genomics era

Organizers:	*Christopher W. Wheat, University of Helsinki, Finland* *Jay F. Storz, University of Nebraska, Lincoln, United States*

9.45 - 10.15	**JON SLATE** (invited) Ecological genomics, genetic architecture and microevolution in long-term studies of wild vertebrates
10.15 - 10.45	**THOMAS LENORMAND** (invited) The fitness effect of mutations across environments
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**PAR K. INGVARSSON** The genetic basis of adaptations in bud phenology across a latitudinal gradient in European aspen *(Populus tremula)*
11.35 - 11.55	**DIETHARD TAUTZ** Genomic approaches to study the ecological genetics of the house mouse
11.55 - 12.15	**THOMAS L. TURNER** Population resequencing reveals local adaptation of *Arabidopsis lyrata* to serpentine soils
12.15 - 12.35	**ANTI VASEMÄGI** Mapping of fitness related traits in the wild: insights from common garden experiments in Atlantic salmon
12.35 - 12.55	**VERA DOMINGUES** Evolution, Genetics and Development of Adaptive Coloration in Beach Mice
12.55 - 13.55	*Lunch*

10-1 Oral

ECOLOGICAL GENOMICS, GENETIC ARCHITECTURE AND MICROEVOLUTION IN LONG-TERM STUDIES OF WILD VERTEBRATES

Jon Slate [1]

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The arrival of high-throughput sequencing and genotyping platforms has opened up unprecedented opportunities for carrying out ecological genetics research. It is now possible to carry out gene mapping and candidate gene analyses in non-model organisms to identify genomic regions that explain variation in ecologically important traits. If mapping studies are carried out in long-term, individual-based study systems it should be possible to go beyond a description of the genetic architecture of traits, and instead address the more challenging questions of how (and if) genes respond to selection in the natural environment. Using examples from Soay sheep and passerine birds I will show how mapping approaches can be integrated with quantitative genetics to understand the microevolutionary process.

10-2 Oral

THE FITNESS EFFECT OF MUTATIONS ACROSS ENVIRONMENTS

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Understanding fitness in the wild is complicated by the bewildering diversity of environments and conditions. It is also complicated by the bewildering diversity of genetic changes across genomes. These two issues are central to the field of ‘ecological genomics’. I will first illustrate them by describing a case study that has been followed in details for forty years: insecticide resistance in *Culex* mosquitoes. I will then show more generally how the fitness effect of mutations across environments can be modelled using a fitness landscape approach. Finally I will compare these theoretical predictions to the data of mutational effects that have been obtained across species and environments. Overall I will try to show that much of this variation can be captured in a quite simple way. This approach offers an efficient and quantitative way to relate genetic changes and fitness effects across environments.

10-3 Oral

THE GENETIC BASIS OF ADAPTATIONS IN BUD PHENOLOGY ACROSS A LATITUDINAL GRADIENT IN EUROPEAN ASPEN *(POPULUS TREMULA)*

Par K. Ingvarsson [1], David Hall [2], Xiao-fei Ma [2], Stefan Jansson [1]

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The initiation of growth and dormancy represents critical ecological and evolutionary trade-offs in perennial plants and latitudinal clines in important phenological traits are common in many plants. In European aspen (*Populus tremula*) the most important environmental cue regulating dormancy initiation is a shortening of the photoperiod. QTL mapping have implicated genes in the photoperiodic pathway in the control of growth cessation. Here we present data from a study on the genetic basis of variation in phenology in European aspen (*Populus tremula)* across a latitudinal gradient. We show that genetic differentiation at neutral markers is low despite strong differentiation in phenology traits, demonstrating local adaptation to the photoperiodic regime. Sequence data were obtained from about 25 genes from the photoperiodic pathway and patterns of nucleotide polymorphism at several of these genes suggested that the action of natural selection along the environmental gradient. We also identified about 100 SNPs from these genes that were used to test for associations with naturally occurring variation in bud phenology.

10-4 Oral

GENOMIC APPROACHES TO STUDY THE ECOLOGICAL GENETICS OF THE HOUSE MOUSE

Diethard Tautz [1]

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The house mouse (*Mus musculus*) is a particularly suitable model for studying evolutionary processes. It is among the best-established model systems for biomedical research, with all the associated genome technology and options for functional studies, including physiological and behavioural assays. Most importantly, it is part of a species complex that is undergoing an adaptive radiation across the whole world. Having originated on the Indian subcontinent, it has spread across Europe and Asia in postglacial times and more recently into the other continents. It inhabits now all climate zones and is therefore expected to have undergone several - and probably parallel - adaptation cycles. Although its lifestyle is often attached to humans and agricultural storage, it thrives also in areas where no humans live, e.g. on small islands. Hence, environmental adaptations are expected to play a significant role in the success of the spread of the house mouse.

We are using genomic approaches to study natural populations of the house mouse, including outbred colonies from different regions of the world and samples from different continents, including subantarctic islands. We perform systematic screens for selective sweeps in closely related populations, analysis of expression differences based on microarrays and next generation sequencing, as well as dedicated studies on copy number variation. We aim to relate these data to the ecological adaptations that are expected to have occurred in the different populations.

10-5 Oral

POPULATION RESEQUENCING REVEALS LOCAL ADAPTATION OF *ARABIDOPSIS LYRATA* TO SERPENTINE SOILS

Thomas L. Turner [1,2], Eric J. von Wettberg [3], Tina T. Hu [1], Elizabeth C. Bourne [4], Sergey V. Nuzhdin [1]

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Understanding the genetic basis of adaptation is of fundamental interest in biology. This matter is also of great practical interest, as adaptive genetic variation provides a rich source of material which can be used for functional genomic studies and population manipulation. To investigate adaptation from a genomic perspective, we have used high-throughput sequencing to completely resequence four populations of the rock cress *Arabidopsis lyrata* from the mid Atlantic region of the USA. Two of these populations occur on granitic soils, and two occur on serpentinic soils, which are naturally high in heavy metal content and have low calcium-to-magnesium ratios. Of the 8.4 million genomic polymorphisms quantified, those with the most soil-type associated frequencies are enriched near genes involved in heavy metal detoxification, calcium and magnesium transport, and the osmotic stress response. Linked differentiation at these loci is extremely low, providing high resolution to infer putatively functional polymorphisms. Sequencing of candidate loci in the European subspecies of *A. lyrata* indicate parallel differentiation of the same polymorphisms at some loci, confirming ecological adaptation, and different polymorphisms at other loci, possibly indicating convergent evolution. This data set provides strong evidence of local adaptation to serpentine in *A. lyrata*, and an excellent opportunity to investigate the genomic basis of ecological adaptation.

10-6 Oral

MAPPING OF FITNESS RELATED TRAITS IN THE WILD: INSIGHTS FROM COMMON GARDEN EXPERIMENTS IN ATLANTIC SALMON

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Elucidating the genetic basis of phenotypic and fitness differences represents one of the most challenging tasks in evolutionary biology. Here, we describe a series of efforts to further understand the genetic basis of ecologically relevant traits and fitness differences in Atlantic salmon in natural environment. Specifically, we i) report the development of efficient and low cost insertion-deletion genotyping platform (INDEL-PLEX) that enables rapid analysis of intermediate numbers of loci (>75) in hundreds to thousands of individuals with standard laboratory equipment; ii) present the results of QTL mapping of early life-history traits that are expected to have important fitness consequences in the natural environment; iii) describe the results from common garden experiment where the survival and performance of native and non-native (hatchery origin) Atlantic salmon populations were examined under natural conditions; iv) present the analyses aiming to identify genomic regions that directly affect the survival in wild. We discuss the prospects of finding fitness related QTLs with major effect in natural environment and compare the identified QTLs with similar traits in other species. The present study demonstrates the challenges of linking genotype and phenotype in a long-lived outbred species and represents an important step towards identification of functionally important genetic variation in Atlantic salmon.

10-7 Oral

EVOLUTION, GENETICS AND DEVELOPMENT OF ADAPTIVE COLORATION IN BEACH MICE

Vera Domingues [1], Hopi Hoekstra [1]

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Understanding the evolutionary origin of adaptive traits is a central question in evolutionary biology. In particular we would like to know which genes and alleles underlie adaptive phenotypes and how interactions among loci (epistasis) influence adaptive change. The oldfield mouse, *Peromyscus polionotus*, is a unique system to study these questions. This species shows extreme variation in color pattern throughout its range in the southeastern United States. In particular, mice inhabiting the coastal dunes and barrier islands of the Gulf Coast of Florida exhibit an extremely pale coloration, which has been driven by natural selection for crypsis. We have identified three pigmentation genes (*Mc1r*, *Agouti* and *Corin*), which together contribute to color variation in this species. We identified and functionally characterized a derived amino acid change in *Mc1r* that contributes to these color differences. In contrast, there are no differences in the *Agouti* coding region, but *Agouti* mRNA expression was highly correlated with pigmentation. A combination of fine-scale mapping and allele-specific assays suggest that the functional mutation(s) are in *Agouti*'s cis-regulatory region. We are using association studies in natural populations to narrow in on the functional mutation. In addition, we are exploring the interaction between *Mc1r* and *Agouti*. Specifically, introgression experiments demonstrate the effects of these genes individually and in combination, both on adult pigmentation pattern and through development. Using complementary approaches such as classical genetics, association mapping and developmental biology in natural and laboratory populations, we are reconstructing the evolutionary history of allelic variation at these loci, providing a model in which to study the evolution of diversity in nature.

10-1 Poster **Black pigmentation in guppies *(Poecilia reticulata)* is associated with polymorphism of the MC1R gene**

AYUMI TEZUKA[1], HIROAKI YAMAMOTO[2], JUN YOKOYAMA[3], MASAKADO KAWATA[1]

[1]*Tohoku University, Graduate School of Life Sciences, Department of Ecology and Evolutionary Biology, Sendai, Japan*
[2]*Tohoku University, Graduate School of Life Sciences, Department of Developmental Biology and Neurosciences, Sendai, Japan*
[3]*Yamagata University, Faculty of Science, Department of Biology, Yamagata, Japan*

10-2 Poster **Inversion polymorphisms and linkage disequilibrium patterns in Ancestral and Invasive Populations of *Drosophila subobscura***

PEDRO SIMÕES, GEMMA CALABRIA, JOÃO PICÃO-OSÓRIO, ISABELLE NAAS, LLUIS SERRA, JOAN BALANYÀ, MARTA PASCUAL

Universitat de Barcelona, Departamento de Genètica, Barcelona, Spain

10-3 Poster **Genetic variation within a tropical tree species influences the structure of the associated epiphytic plant community**

SHARON E. ZYTYNSKA[1,2], RICHARD F. PREZIOSI[1], MICHAEL F. FAY[2]

[1]*The University of Manchester, Faculty of Life Sciences, Manchester, United Kingdom*
[2]*Royal Botanical Gardens, Kew Conservation Genetics, London, United Kingdom*

10-4 Poster **Birth-and-death processes and selection seem to drive the long term evolution of 5S ribosomal DNA in *Ensis* razor shells (Mollusca)**

JOAQUIN VIERNA, ANA MARIA GONZALEZ-TIZON, ANDRES MARTINEZ-LAGE, VERONICA ROJO

Universidade da Coruña, Departamento de Biologia Celular y Molecular, La Coruña, Spain

10-5 Poster **When the going gets tough: brown trout populations under anthropogenic pressure**

MICHAEL M. HANSEN[1], CINO PERTOLDI[2], KRISTIAN MEIER[1], LASSE F. JENSEN[3], VOLKER LOESCHCKE[2]

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[2]*Aarhus University, Department of Biology, Aarhus, Denmark*
[3]*Fisheries and Maritime Museum , Esbjerg, Denmark*

10-6 Poster **Analysis of intragenomic variation of the nuclear ribosomal DNA spacers in the gooseneck barnacle *Pollicipes pollicipes* (Gmelin, 1790)**

DAVID SEOANE, ALEJANDRA PERINA, ANDRÉS MARTÍNEZ-LAGE, ANA M. GONZÁLEZ-TIZÓN

Universidade da Coruna, Departemento de Biologia Celular y Molecular, La Coruna, Spain

10-7 Poster **The effects of annual and daily rhythms on cold tolerance in *Drosophila montana***

LAURA P. VESALA, ANNELI HOIKKALA, MAARIA KANKARE

University of Jyvaskyla, Department of Biological and Environmental Science, Jyvaskyla, Finland

10-8 Poster **Hybrid Zone dynamics after ecological or genetic divergence: a case study in a salamander ring species**

RICARDO PEREIRA[1,2]

[1]*University of California, Museum of Vertebrate Zoology, Department of Integrative Biology, Berkeley, United States*
[2]*Cibio-Up, Porto, Portugal*

10-9 Poster **Partial sequencing of opine dehydrogenase genes in *Mytilus galloprovincialis***
SANDRA VÁZQUEZ-DORADO, ANGEL S. COMESAÑA, ANDRÉS SANJUÁN, ALEJANDRO DE CARLOS
Universidade de Vigo, Facultade de Bioloxía, Departamento de Bioquímic, Xenética e Inmunoloxía, Vigo, Spain

10-10 Poster **Genetic erosion and consequences on phenotypic plasticity in European tree frog populations *(Hyla arborea)***
EMILIEN LUQUET[1], JEAN-PAUL LENA[1], THIERRY LENGAGNE[1], FREDERIC HERVANT[1], PIERRE JOLY[1], NICOLAS PERRIN[2], SANDRINE PLENET[1]
[1]Universite Lyon1, UMR - CNRS 5023, Laboratoire d'Ecologie des Hydrosystemes Fluviaux, Villeurbanne, France
[2]Universite de Lausanne, Departement d'Ecologie et Evolution , Lausanne, Suisse

10-11 Poster **Colonization dynamics in cyclical parthenogens: the interplay between neutral and selective processes**
JOOST VANOVERBEKE, LUC DE MEESTER
K.U. Leuven, Laboratory of Aquatic Ecology and Evolutionary Biology, Department of Biology, Leuven, Belgium

10-12 Poster **Effects of sequential diets in the comma butterfly: testing predictions from gene expression**
LINA SÖDERLIND, SANDRA ALMEFLO, NIKLAS JANZ, SÖREN NYLIN
Stockholm University, Department of Zoology, Stockholm, Sweden

10-13 Poster **Are transposable elements important agents of microsatellite origin? Three species, two stories**
EMESE MEGLECZ
Université de Provence, IMEP, Marseille, France

10-14 Poster **Gene expression in comma butterfly larvae follows predictions from insect-plant theory**
SÖREN NYLIN[1], HANNA FISCHER[2], DALIAL FREITAK[2], NIKLAS JANZ[1], LINA SÖDERLIND[1], HEIKO VOGEL[2]
[1]Stockholm University, Department of Zoology, Stockholm, Sweden
[2]Max Planck Institute for Chemical Ecology, Department of Entomology, Jena, Germany

10-15 Poster **Molecular differences between cryptic species of the genus *Nassarius* (Mollusca: Gastropoda) based on two mitochondrial genes**
BEATRIZ RODRIGUEZ-IGLESIAS, ALEJANDRO DE CARLOS, ANGEL S. COMESAÑA, ANDRÉS SANJUAN
Universidade de Vigo, Departamento de Bioquimica, Xenetica e Inmunoloxia, Vigo, Spain

10-16 Poster **The genetic consequences of fluctuating population sizes in the large blue butterfly**
LINE V. UGELVIG[1], M. THOMAS P. GILBERT[2], DAVID R. NASH[1]
[1]University of Copenhagen, Centre for Social Evolution and Department of Biology, , Copenhagen, Denmark
[2]University of Copenhagen, Center for Ancient Genetics, Department of Biology, Copenhagen, Denmark

10-17 Poster **Sexually-selected nucleotide variation in a natural *Drosophila* population**
STEVE CHENOWETH
University of Queensland, School of Biological Sciences, St Lucia, Australia

10-18 Poster **Is variability of neutral markers a good predictor of evolutionary potential? A case study in *Drosophila subobscura***

JOSIANE SANTOS[1], PEDRO SIMÕES[2], INÊS FRAGATA[1], MARTA SANTOS[1], ANA MARQUES[1], MARGARIDA LIMA[1], MARTA PASCUAL[2], MARGARIDA MATOS[1]

[1]Universidade de Lisboa, Faculdade de Ciencias, Centro de Biologia Ambiental, Departamento de Biologia Animal, Lisboa, Portugal

[2]Universitat de Barcelona, Facultat de Biologia, Departamento de Genètica, Barcelona, Spain

10-19 Poster **The precision of heritability estimates using different methods to utilize marker information**

ANNA SANTURE[1,2], JINLIANG WANG[1]

[1]Zoological Society of London, Institute of Zoology, London, United Kingdom

[2]University of Sheffield, Department of Animal e Plan Sciences, Sheffield, United Kingdom

10-20 Poster **Evolutionary consequences of an unusual reproduction system: genomic clues to an habitat transition in the Little Fire Ant**

JULIEN FOUCAUD[1,2], BENOÎT FACON[1], ANNE LOISEAU[1], STÉPHANIE ROBERT[1], OLIVIER REY[1], ARNAUD ESTOUP[1]

[1]INRA CBGP, Montpellier, France

[2]CNRS, Gif-Sur-Yvette, France

10-21 Poster **Mapping of sex-specific regions on sex chromosomes of the smut fungus *Microbotryum violaceum***

ANTONINA VOTINTSEVA, DMITRY FILATOV

University of Oxford, Department of Plant Sciences, Oxford, United Kingdom

10-22 Poster **Variable patterns of linkage disequilibrium on zebra finch *(Taeniopygia guttata)* chromosomes**

JESSICA STAPLEY

University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom

10-23 Poster **Genes under Positive Selection in Pathogenic Fungal Species Specialized on Different Host Plants**

GABRIELA AGUILETA[1], JULIETTE LANGELLE[2], SYLVAIN MARTHEY[2], HELENE CHIAPELLO[2], FRANCOIS RODOLPHE[2], ANNIE GENDRAULT[2], ELODIE VERCKEN[1], BENJAMIN DEVIER[1], TATIANA GIRAUD[1]

[1]Universite Paris Sud, Department of Ecologie, Systematique et Evolution, Orsay, France

[2]INRA MIG, Jouy en Josas, France

10-24 Poster **The molecular evolution of the *Pyrococcus* genomes and proteomes**

KONSTANTIN V. GUNBIN, DMITRIJ A. AFONNIKOV, NIKOLAY A. KOLCHANOV

Siberian Branch of the Russian Academy of Sciences, Laboratory of Theoretical Genetics Institute of Cytology and Genetics, Novosibirsk, Russia

10-25 Poster **Ecological genomics: using genome scans to detect the signature of natural selection in wild populations of *Daphnia magna***

LUISA ORSINI, LUC DE MEESTER

Katholieke Universiteit Leuven, Laboratory of Aquatic Ecology and Evolutionary Biology, Leuven, Belgium

10-26 Poster **SCRAPS: Reference-free identification of variation in metagenomic short-read data**

BARTU AHISKA[1], DANIEL FALUSH[2], GILEAN McVEAN[1]
[1]University of Oxford, Department of Statistics, Oxford, United Kingdom
[2] University College Cork, Environmental Research Institute, Cork, Ireland

10-27 Poster **Candidate genes underlying specific pollinator attraction**

PHILIPP M. SCHLUETER[1], SHUQING XU[1,2], VALERIA GAGLIARDINI[1], UELI GROSSNIKLAUS[1], FLORIAN P. SCHIESTL[1]
[1]University of Zurich, Institute of Systematic Botany and Plant Biology, Zurich, Switzerland
[2]Swiss Federal Institute of Technology, Zurich, Switzerland

10-28 Poster **Impact of admixture on adaptive variation in Soay sheep**

PHILINE G.D. FEULNER, JON SLATE
University of Sheffield, Department of Animal & Plant Sciences, Sheffield, United Kingdom

10-29 Poster **Ecogenomics of Sex: gene expression response to fluctuating temperature during development in turtles with polyphenic and genotypic sex determining mechanisms**

NICOLE VALENZUELA, JENNIFER NEUWALD
Iowa State University, Department of Ecology, Evolution, and Organismal Biology, Ames, United States

10-30 Poster **Svere supression of recombination due to chromosomal inversions**

CINTA PEGUEROLES, VICTOR ORDOÑEZ, ALBERT FERRES, PEDRO A. ARAUZ, MARTA PASCUAL, FRANCISCO MESTRES
Universitat de Barcelona, Departamento de Genetica, Barcelona, Spain

10-31 Poster **Genomics of a male killing *Wolbachia***

ANNE DUPLOUY[1], INAKI ITURBE-ORMAETXE[1], SYLVAIN CHARLAT[2], MEG WOOLFIT[1], GREGORY D.D. HURST[3], SCOTT L. O'NEILL[1]
[1]University of Queensland, School of Biological Sciences, Brisbane, Australia
[2]University of Lyon1, CNRS, Lyon, France
[3]University of Liverpool School of Biological Sciences, Liverpool, United Kingdom

10-32 Poster **Evolution of weedy sunflowers: trade-offs between growth rates and stress tolerance in *Helianthus annuus***

NOLAN C. KANE, MAYA MAYROSE, LOREN H. RIESEBERG
University of British Columbia, Department of Botany, Vancouver, Canada

10-33 Poster **An experimental assessment of intraspecific ecological-evolutionary feedback in the wild using aphids**

MARTIN M. TURCOTTE, DAVID N. REZNICK, DANIEL J. HARE
[1]University of California, Department of Entomology, Riverside, United States

10-34 Poster **The genetic basis of natural variation of seed dormancy, vegetative growth and flowering time in *Arabidopsis thaliana***

MARILYNE DEBIEU[1], YU HUANG[2], BENJAMIN STICH[1], MAGNUS NORDBORG[3], MAARTEN KOORNNEEF[1], JULIETTE DE MEAUX[1]
[1]Max Planck Institute for Plant Breeding Research, Department of Plant Breeding and Genetics, Cologne, Germany
[2]University of Southern California, Departmentb of Molecular & Computational Biology, Los Angeles, United States of America
[3]Gregor Mendel Institute of Molecular Plant Biology, Department of Population Genetics, Vienna, Austria

10-35 Poster **Genetic individualization of Brown Bears (*Ursus arctos)* in the Cantabrian Mountains. What can it tell us about the ecology and demography of the species?**

TRINIDAD PEREZ[1], FERNANDO VAZQUEZ[1], JAVIER NAVES[1,2], ALBERTO FERNANDEZ[1,2], ANA CORAO[1], JESUS ALBORNOZ[1], ANA DOMINGUEZ[1]
[1]*Oviedo University, Department of Functional Biology (Genetics), Oviedo, Spain*
[2]*Estación Biológica de Doñana CSIC , Sevilla, Spain*

10-36 Poster **Evolutionary Genomics of Na, K-ATPases and Osmotic Lifestyles**

ALBERTO G. SAEZ[1], ENCARNACION LOZANO[2]
[1]*Museo Nacional de Ciencias Naturales, Department of Biodiversity and Evolutionary Biology CSIC, Madrid, Spain*
[2]*Instituto de Salud Carlos III, Centro Nacional de Microbiologia Majadahonda, Madrid, Spain*

10-37 Poster **Effects of parasite infections on mating success of the Black Grouse**

KAISA ROKKA, HELI SIITARI, RAUNO ALATALO, VINCENT STASZEWSKI
University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland

10-38 Poster **Adaptive genetic diversity in brown trout across altitudinal gradients**

JOLANDA SCHULER[1,2], IRENE KELLER[2], OLE SEEHAUSEN[1,2]
[1]*University of Bern, Institute of Ecology and Evolution (IEE), Bern, Switzerland*
[2]*EAWAG Center of Ecology, Evolution and Biogeochemistry (CEEB) , Dübendorf, Switzerland*

10-39 Poster **SNPs, respirometry and a radar: a mechanistic study on butterfly flight and dispersal**

KRISTJAN NIITEPÕLD, OTSO OVASKAINEN, ILKKA HANSKI
University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland

10-40 Poster **How often does jumping DNA make it across species barriers? An arthropod community approach**

DAPHNE REISS, SYLVAIN CHARLAT
University of Lyon, CNRS (UMR 5558), Laboratoire Biometrie & Biologie Evolutive, Lyon, France

10-41 Poster **A simulation study of the determinants of adaptation and molecular evolution of an invasive species**

ERIC BAZIN, JEAN CARLIER, VIRGINIE RAVIGNÉ
CIRAD, Département BIOS, Montpellier, France

10-42 Poster **Multi-scale genetic structure of *Ceratosolen fusciceps*, the wasp pollinating *Ficus racemosa*: substantial gene flow could constraint on the coevolutionary process**

NOPPOL KOBMOO, FINN KJELLBERG
CEFE - CNRS , Montpellier, France

10-43 Poster **Mapping the geography and genetics of fear – a case study with predators and their prey**

JULIA REGER, ANDREW P. BECKERMAN, JON SLATE
University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom

10-44 Poster **Towards 'admixture mapping' of ecological species differences in European *Populus***

THELMA BARBARÁ[1], CHRISTIAN LEXER[2]

[1]Royal Botanic Gardens Kew, Jodrell Laboratory Genetics Section, Richmond Surrey, United Kingdom
[2]University of Fribourg, Department of Biology Unit of Ecology & Evolution, Fribourg, Switzerland

10-45 Poster **The dark side of evolution: characterizing opsin nonfunctionalisation in subterranean isopods (Crustacea)**

SEBASTIEN CALVIGNAC, CELINE COLSON, ISABELLE NAAS, LARA KONECNY, CHRISTOPHE D. DOUADY

Universite de Lyon, UMR 5023 CNRS LEHF, Lyon, France

10-46 Poster **Impact of domestication on the ADP-glucose pyrophosphorylase (AGPase) nucleotide diversity**

JONATHAN CORBI[1], MAUD I. TENAILLON[1], DOMENICA MANICACCI[2]

[1]CNRS, UMR de Genetique Vegetale, Ferme du Moulon, Gif sur Yvette, France
[2]University Paris sud XI, UMR de Genetique Vegetale, Ferme du Moulon, Gif sur Yvette, France

10-47 Poster **Growing large leaves from a small-leaf gene pool: evolutionary trajectories and morphology in *Populus nigra* L. (black poplar)**

JENNIFER DE WOODY, HARRIET TREWIN, MAUD VIGER, GAIL TAYLOR

University of Southampton, School of Biological Sciences, Southampton, United Kingdom

10-48 Poster **Sex and tissue specific protein polymorphism in a social insect**

KALEVI TRONTTI[1], CHRISTOPHER W. WHEAT[1,2], LISELOTTE SUNDSTRÖM[1]

[1]University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland
[2]Pennsylvania State University, Department of Biology, University Park, United States

10-49 Poster **Insight into the beetle association of *Pristionchus* nematodes: from the wild into the laboratory**

ISABELLA D'ANNA, MATTHIAS HERRMANN, WERNER E. MAYER, RALF J. SOMMER

Max Planck Institute for Developmental Biology, Department of Evolutionary Biology, Tuebingen, Germany

10-50 Poster **Molecular characterization of MHC IIB genes in the herring gull species complex *(Larus argentatus sensu lato)***

ANNA DUBIEC[1], MAGDALENA ZAGALSKA-NEUBAUER[1,2], WIESŁAW BABIK[2], JACEK RADWAN[2]

[1]Polish Academy of Sciences, Museum and Institute of Zoology, Warszawa, Poland
[2]Jagiellonian University, Institute of Environmental Sciences, Kraków, Poland

10-51 Poster **A genome scan reveals rapid evolution of multigenic resistance to the bacterio-insectide bti in mosquitoes**

MARGOT PARIS, AURÉLIE BONIN, GUILLAUME TETREAU, JEAN PHILIPPE DAVID, LAURENCE DESPRÉS

Université Joseph Fourier, Laboratoire d'Ecologie Alpine, CNRS UMR 5553, Grenoble, France

10-52 Poster **Adaptation in response to climate change: exploring evolution during range expansion in the Brown Argus butterfly *Aricia agestis***

JON BRIDLE, JAMES BUCKLEY

University of Bristol, School of Biological Sciences, Bristol, United Kingdom

10-53 Poster **Contrasted multi-scale genetic patterns in populations of the model ectomycorrhizal Basidiomycete *Laccaria amethystina***

LUCIE VINCENOT[1], JESSY LABBÉ[2], SARA HORTAL-BOTIFOL[2], MARC-ANDRÉ SELOSSE[1]
[1]CEFE-CNRS, Biologie des populations, Montpellier, France
[2]INRA Interactions arbres-microorganismes, Champenoux, France

10-54 Poster **Evolution of MHC class I in *Ctenophorus ornatus***

KATARZYNA GAC, JACEK RADWAN
Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland

10-55 Poster **Genetic and Phenotypic differentiation in willow warblers across a migratory divide in central scandinavia**

NILS MÜLLER
Lund University, Department of Animal Ecology, Lund, Sweden

10-56 Poster **Quantitative trait locus analysis in a wild bird population**

MAJA TARKA[1], BENGT HANSSON[1], DARIO BERALDI[2], DENNIS HASSELQUIST[1], JULES HERNÁNDEZ-SÁNCHEZ[2], MIKAEL ÅKESSON[1], STAFFAN BENSCH[1]
[1]Lund University, Department of Animal Ecology, Lund, Sweden
[2]University of Edinburgh, Institute of Evolutionary Biology, King's Buildings, Ashworth Laboratories, Edinburgh, United Kingdom

10-57 Poster **What shape the species composition and population genetic structure in a mining area: human impact or natural variation?**

PERNILLE B. EIDESEN[1], ELISABETH COOPER[2], INGER G. ALSOS[1]
[1]UNIS - The University Centre in Svalbard, Department of Arctic Biology, Longyearbyen, Norway
[2]Tromsø University, Biology Department, Tromsø, Norway

10-58 Poster **Geographic adaptation and experimental evolution in natural populations of the model plant *Arabidopsis thaliana***

JON ÅGREN[1], DOUGLAS W. SCHEMSKE[2]
[1]Uppsala University, Department of Ecology and Evolution Evolutionary Biology Centre, Uppsala, Sweden
[2]Michigan State University, Department of Plant Biology and Kellog Biological Station, East Lansing, United States

10-59 Poster **Upper thermal limit variation in *Drosophila* due to experimental methodology: are our estimates of trait heritability accurate?**

KATHERINE MITCHELL[1,2], ARY HOFFMANN[1,2]
[1]The University of Melbourne, Department of Genetics/Department of Zoology, Melbourne, Australia
[2]Centre for Environmental Stress and Adaption Research, Melbourne, Australia

10-60 Poster **The transcriptional architecture of the trade-off between lifespan and offspring**

L. BASTEN SNOEK, ANA VIÑUELA, EVERT W. GUTTELING, AGNIESZKA DOROSZUC, JOOST A.G. RIKSEN, JAN E. KAMMENGA
Wageningen University, Laboratory of Nematology, Wageningen, Netherlands

The phenotype-fitness map re-visited: agents of selection and the importance of ecology in evolutionary studies

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12th Congress
Turin 2009

11

Program

Wednesday August 26 - **Symposium 11**

Location: Room 5

The phenotype-fitness map re-visited: agents of selection and the importance of ecology in evolutionary studies

Organizers:	*Alexis Chaine, CNRS, Moulis, France* *Erik Svensson, Lund University, Sweden*
9.45 - 10.15	**CRAIG W. BENKMAN** (invited) The ecology of selection
10.15 - 10.35	**ANDRES LOPEZ-SEPULCRE** Experimental decoupling of direct and indirect effects of predation on the rapid evolution of guppy life-histories
10.35 - 11.15	*Coffee break*
11.15 - 11.35	**ROMAIN ROUCHET** Plant – herbivore insect interactions: Reproductive succes of the weevil *Exapion ulicis* in relation to the phenology of its host plant, *Ulex europaeus*
11.35 - 11.55	**HANS VAN DYCK** Range expansion by ecotype evolution in anthropogenic landscapes: the speckled wood case
11.55 - 12.15	**ANNE ATLAN** Temporal fluctuations and the maintenance of genetic diversity: the case of flowering phenology in *Ulex europaeus* L. (Fabaceae)
12.15 - 12.35	**MARTINE E. MAAN** Poison or passion: warning and attraction in a polymorphic poison frog
12.35 - 12.55	**TOM TREGENZA** Natural and sexual selection in a wild insect population
12.55 - 13.55	*Lunch*
13.55 - 14.25	**STEVAN J. ARNOLD** (invited) Evolution along selective lines of least resistance
14.25 - 14.45	**W. SCOTT ARMBRUSTER** Do Floral Integration and Conflicting Selection influence the Macroevolution of Adaptive Accuracy in Flowering Plants?

14.45 - 15.05	**SHAWN KUCHTA** Predator-mediated selection in a natural population of the damselfly *C. splendens*
15.05 - 15.35	*Coffee break*
15.35 - 15.55	**MATTHEW R. WALSH** Experimentally induced life history evolution in natural fish populations in response to the introduction of guppies
15.55 - 16.15	**JULIO M. ALCANTARA** Divergent selection between environments promotes phenotypic differentiation of vegetative traits in Iberian Columbines (Gen. *Aquilegia*)
16.15 - 16.35	**MACHTELD VERZIJDEN** Changing landscapes: the effect of hybridization on female preferences and male fitness landscapes
16.35 - 16.55	**BEN SHELDON** Spatial scaling of temporal synchrony: natural selection on reproductive timing over five decades in a wild bird population

11-1 Oral

THE ECOLOGY OF SELECTION

Craig W. Benkman [1], Eduardo T. Mezquida [2]

[1]*University of Wyoming, Department of Zoology and Physiology, Laramie, United States*
[2]*Polytechnic University of Madrid, Department of Ecology and Edaphology, Madrid, Spain*

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Many recent studies have found that the evolutionary outcome of species interactions varies geographically and temporally. However, why such variation arises is poorly known. In our work on crossbills and conifers, we have found that the presence and absence of a preemptive competitor (tree squirrels) often alters in a predictable manner the strength of selection exerted by crossbills on conifers. Other factors however also alter the interaction and selection exerted, and they too are likely to be general to many interactions. We will discuss our attempts to understand how community context, resource variability, and habitat area and structure affect the form of selection in species interactions. We find that crossbills and tree squirrels and the selection they exert on conifers are differentially affected by variation in the above factors. These differences however are easy to interpret given our knowledge of these species. Because some species interactions are inherently difficult to study, we suspect that additional studies that focus on species that are well understood and easily characterized will be especially important for furthering our understanding of the causes of geographic and temporal variation in species interactions.

11-2 Oral

EXPERIMENTAL DECOUPLING OF DIRECT AND INDIRECT EFFECTS OF PREDATION ON THE RAPID EVOLUTION OF GUPPY LIFE-HISTORIES

Andres Lopez-Sepulcre [1], David N. Reznick [1]

[1]*University of California at Riverside, Department of Biology, Riverside, United States*

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While multiple environmental factors are inherently correlated in nature, the predictive ability of evolutionary biology relies on the logical and experimental decoupling of such potential selective forces. When released from predation, Trinidadian guppies evolve a higher age and size of maturation. Traditionally, this change has been attributed to a decrease in mortality rates and the subsequent relaxation of selection for a fast life-history. An alternative explanation is that guppy life histories respond to increased competition for resources, an indirect result of reduced predation via the consequent increase in population density. To discern between these two hypotheses, we performed two pairs of translocation experiments in the wild, moving guppies from high to low predation environments. We trimmed the canopy above two of the four introduction streams in order to increase the light, and hence the level of basal resources. Since their introduction individuals in all four populations have been uniquely marked, monitored monthly, and genotyped to reconstruct their pedigree. After 12 months since the first pair of introductions, individuals from the control stream, but not the treatment stream, show significantly bigger maturation sizes. This result is consistent with the hypothesis that higher maturation sizes are a result of increased competition for resources (resulting from higher population densities) rather than a direct response to mortality. The consequences of this result for an ecologically consistent understanding of life-history evolution will be discussed.

11-3 Oral

PLANT – HERBIVORE INSECT INTERACTIONS: REPRODUCTIVE SUCCESS OF THE WEEVIL *EXAPION ULICIS* IN RELATION TO THE PHENOLOGY OF ITS HOST PLANT, *ULEX EUROPAEUS*

Romain Rouchet [1,2]

[1]*University of Zürich, Institute of Zoology, Zürich, Switzerland*
[2]*University of Rennes1 / CNRS, UMR Ecobio, Rennes, France*

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An optimal synchrony with their hosts enable fitness optimization of phytophagous insects. The link between the fitness of *Exapion ulicis*, the gorse *Ulex europeaus* weevil, with its plant phenology and with both its competitors and parasitoids has been considered. Pods are produced by the host plant from autumn to spring's end, but only pods produced in spring are infested by *E. ulicis* larvae. Eggs deposited in spring have not enough time to complete their development and die because pods and larvae have different growing speed. The reason is a gap between both growing speeds due to a different response to climatic conditions. Eggs deposited at the end of the spring are subject to a high parasitism pressure by the parasitoid *Pteromalus sequester* and a pressure by the competitor caterpillar *Cydia succedana*. Moreover, a large inter-annual variation in the oviposition period is described, depending on climatic conditions. Thus, there are strong constraints on *E. ulicis* phenology which cause a partial asynchrony with the host plant, preventing apion to benefit from the entire pod production. It is the first time that the interaction between *E. ulicis* and *U. europaeus* phenologies has been described on the insect side.

11-4 Oral

RANGE EXPANSION BY ECOTYPE EVOLUTION IN ANTHROPOGENIC LANDSCAPES: THE SPECKLED WOOD CASE

Hans Van Dyck [1], Melanie Gibbs [1], Sofie Vandewoestijne [1]

[1] *Université catholique de Louvain (UCL), Biodiversity Research Centre, Behavioural Ecology & Conservation Group, Louvain-la-Neuve, Belgium*

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Although several species face difficulties in coping with rapidly changing anthropogenic environments, some appear to be highly successful. As has been suggested for invasive species, successful indigenous species may also undergo rapid evolution, but this issue has yet received little attention. The speckled wood (*Pararge aegeria* L.) is a woodland butterfly that has expanded its habitat-use also to agricultural landscapes which has resulted in a strong increase in distribution and abundance in NW-Europe. Woodland and agricultural landscape represent, however, clearly different thermal environments for a flying heliotherm insect with also differences for other key resources. With a series of common garden breeding, reciprocal transplant and experimental flight experiments, we have tested hypotheses on adaptive differences in functional morphology, life history and behaviour among both ecotypes. In agricultural landscapes, selection for increased flight appears to have driven an evolutionary divergence for improved locomotor performance. However, strong fecundity selection and improved locomotor performance may carry an energetic cost, resulting in a physiological trade-off with somatic maintenance and reducing lifespan. Forced flight reduced longevity by 21% in woodland females, but had no effect on agricultural females. Both environments have differently shaped the life history and morphology of *P. aegeria*. We also present preliminary genetic data on landscape-related differences between populations along a latitudinal gradient from France to The Netherlands. More generally, our speckled wood case shows that we need to consider evolutionary consequences of anthropogenic-induced environmental change on life history traits, functional morphology and behaviour in order to understand particular range modifications.

11-5 Oral

TEMPORAL FLUCTUATIONS AND THE MAINTENANCE OF GENETIC DIVERSITY: THE CASE OF FLOWERING PHENOLOGY IN *ULEX EUROPAEUS* L. (FABACEAE)

Anne Atlan [1], Benjamin Hornoy [1], Michèle Tarayre [1]

[1] *CNRS/Université Rennes1, ECOBIO, Rennes, France*

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Temporal fluctuations in fitness due to environmental variations can allow polymorphism to be maintained within populations, but only under very restrictive conditions. Indeed, the genotype with the largest geometric mean fitness ultimately wins over all others (Gillespie 1991). Haldane and Jayakar (1963) showed that a stable polymorphism could be maintained if (i) the variance in the reproductive success of the phenotypes differs, and (ii) the most variable phenotype is recessive - but this theoretical result has received little experimental evidence.

The flowering phenology of *Ulex europaeus* may provide an example of such a situation. In Brittany (France), two flowering types coexist within all natural populations: a short synchronous one in spring and an extended one from autumn until spring. To understand the maintenance of this unusual polymorphism, we monitored 16 natural populations and raised a collection of 20 maternal families in a common garden.

We demonstrated the genetic basis of this polymorphism, and showed that the two phenotypes reduce seed predation by two different ways: escape in time or predator satiation, with disruptive selection. By flowering in three seasons, the long-flowering plants decrease the variance in their reproductive success between years. In contrast, the plants that only flower in spring have a reproductive success that is related to the environmental conditions of a single season, and have a greater variability between years. We suggest that the pattern and inheritance of flowering phenology in this species allows this polymorphism to be maintained by inter-annual variability of climatic conditions and seed-predation pressure.

11-6 Oral

POISON OR PASSION: WARNING AND ATTRACTION IN A POLYMORPHIC POISON FROG

Martine E. Maan [1,2], Molly E. Cummings [1]

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Because animal signals are subject to both natural and sexual selection, evaluation of both selective forces is necessary to understand their spectacular diversity in nature. Such approaches may also elucidate speciation mechanisms, because animal signals are central to the evolution and maintenance of species boundaries. Here, we focus on the evolution of aposematic colour polymorphism. Because aposematic (warning) signals are thought to evolve in the context of predator avoidance, which favours signal convergence rather than divergence, aposematic diversity is difficult to understand. However, in addition to predator deterrence, aposematic colour signals may function in intraspecific communication as well.

The poison frog *Oophaga [Dendrobates] pumilio* shows striking diversity in colour and pattern between geographically isolated populations in western Panama. We show that this colour diversity mediates population-assortative mating preferences, and that male coloration is also subject to directional sexual selection by female choice. These female preferences for male coloration may interact with natural selection pressures in at least two ways. First, we find that colour pattern divergence through sexual selection may be facilitated by generalised avoidance by predators. Second, we find extreme variation in frog toxicity between populations, probably due to spatial variation in the availability of toxic compounds. This variation may generate natural selection for variable levels of conspicuousness, which in turn may affect female preferences.

11-7 Oral

NATURAL AND SEXUAL SELECTION IN A WILD INSECT POPULATION

Tom Tregenza [1], Rolando Rodríguez-Muñoz [1], Amanda Bretman [1], Jon Slate [2]

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Field crickets have become a model system for studies of mating behaviour and sexual selection. However, in common with all invertebrates, we have only limited information about their behaviour in the wild. This reflects a general divide in evolutionary ecology which is dominated by field systems (large vertebrates) that are hard to use in controlled experiments, and lab systems (invertebrates) that often have a completely unknown natural ecology. We have developed an array of 96 infra-red video cameras and microphones that have continuously monitored a population of individually marked crickets, *Gryllus campestris*, in northern Spain over three entire adult seasons. All adults are tagged with a unique code that can be read on the video and genotyped using microsatellite markers. This allows us to observe key traits such as calling effort by males, who mates with whom, how males and females meet, how long individuals live and so forth. We can combine these data with measures of fitness through direct measures of reproductive success as determined from the number of adults each individual contributes to the following generation. Our approach is designed to allow us to quantify sources of selection on these wild insects with the ultimate aim of combining field observations with manipulative experiments.

11-8 Oral

EVOLUTION ALONG SELECTIVE LINES OF LEAST RESISTANCE

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The selective line of least resistance for a population, ω-max, is the major axis (leading eigenvector) of its adaptive landscape (AL). This major axis can be estimated in contemporary populations from conventional, multivariate measures of directional and stabilizing selection (β and γ). The importance of ω-max rests on two propositions. First, the AL tends to retain a characteristic shape on an evolutionary time scale (conservation of configuration). Second , the optimum of the AL tends to move along the selective line of least resistance (conservation of direction of movement). One reason to expect this second proposition to be true is that the design constraints that shape variation within populations may often extrapolate in a predictable way to mold the pattern of morphological radiation. If both propositions are true, then ω-max may be the predominant direction of evolution during adaptive radiations. The aims of this talk are to review the evidence for both propositions (conservation of AL configuration and direction of movement) and to argue for the importance of ω-max in adaptive radiations. In particular, the principle of evolution along ω-max may explain many persistent patterns of bivariate dispersion in which diversification takes the form of cigar-shaped clusters in morphospace. Examples include interspecific allometry, scaling laws, and interspecific patterns in bilateral symmetry. Finally, the prospects for testing for evolution along ω-max will be illustrated with the case of vertebral evolution in snakes, analyzed with the software package MIPod.

11-9 Oral

DO FLORAL INTEGRATION AND CONFLICTING SELECTION INFLUENCE THE MACROEVOLUTION OF ADAPTIVE ACCURACY IN FLOWERING PLANTS?

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We hypothesise that an adaptive ridge describes the response of fitness to variation in where pollen is placed on, and picked up from, pollinators. This ridge is, in turn, expected to govern the divergence of floral traits of populations and species of many groups of plants. We use measures of adaptive accuracy, precision, and mean optimality to assess how close populations lie to the hypothesised adaptive ridge and compare patterns of adaptive accuracy of pollen placement and receipt across species in three study systems, *Dalechampia* (Euphorbiaceae), *Collinsieae* (Plantaginaceae), and *Stylidium* (Stylidiaceae). We found that departure from the optimum was the most important factor generating inaccuracy in *Dalechampia*, whereas female imprecision and departure from the optimum were about equally important in Collinsieae. Stamen and stigma imprecision were equally important in *Stylidium*, but departure from optimality was not detected. Possible reasons for imprecision and departure from the optimum were assessed using phylogenetically informed methods, and the results indicate important roles of limited floral integration in generating imprecision, especially in *Dalechampia*, and conflicting selective pressure associated with outcrossing in generating departure from the optimum and imprecision in *Collinsia*.

11-10 Oral

PREDATOR-MEDIATED SELECTION IN A NATURAL POPULATION OF THE DAMSELFLY *C. SPLENDENS*

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Individuals must avoid predation if they are to survive long enough to reproduce, and thus predators can impact mean population fitness and select for the evolution of alternative prey phenotypes. The selective consequences of predation are difficult to study, however, because predation removes individuals from the population and thereby prevents their measurement. Here we present a study of the strength and direction of selection on the damselfly *Calopteryx splendens* (Odonata: Zygoptera) imposed by avian predators, wagtails in the genus *Motacilla*. Wagtails catch damselflies and return to “slaughter stations” where they remove the wings and consume the body. To calculate the strength of natural selection on wing traits, we collected wings from slaughter stations and compared them to the variation present in the population. Wing shape was quantified using geometric morphometric techniques. In addition to correlational studies of trait-fitness covariation, we tested the hypothesis that increased wing melanization leads to increased predation pressure by conducting a phenotypic manipulation experiment in a natural population of *C. splendens*. In this experiment, the color patches on wings were extended beyond the range of natural variation, such that they were very similar to the congeneric species *C. virgo*, and longevity in the field monitored. Our results indicate that increased melanization has negative fitness consequences. In summary, we find that predation by wagtails imposes selection on the wings of *C. splendens*, including elements of shape and patterns of melanization. Elements of predator-mediated selection in space and time will be discussed.

11-11 Oral

EXPERIMENTALLY INDUCED LIFE HISTORY EVOLUTION IN NATURAL FISH POPULATIONS IN RESPONSE TO THE INTRODUCTION OF GUPPIES

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Guppies are famous as the victims of predation, but sometimes the tables are turned and they are the predators. In streams in Trinidad where guppies co-occur with the killifish *Rivulus hartii*, they prey on newborn *Rivulus*. Early life history theory predicts that increased rates of predation on juveniles favors the evolution of delayed maturation and reduced reproductive effort. However, such theory ignores the ecology of the target organism; guppies have indirect effects as *Rivulus* densities decline and growth rates increase in sites with guppies compared with sites in which *Rivulus* are alone. Derived theories that incorporate these ecological effects often yield different predictions. Here we report the findings of long-term perturbation experiments that demonstrate extensive life history evolution consistent with derived theories. *Rivulus* from sites with guppies are smaller at maturity, produce many small eggs, and exhibit increased reproductive investment compared with sites with just *Rivulus*. Laboratory experiments on 2nd generation lab-born fish reared on food levels that mimicked natural differences in growth, show that these trait differences are heritable, although the patterns of divergence depend on food availability. These results contrast with demographic theory and argue that differences in resource availability, which are likely an indirect effect of guppies, shape evolution in *Rivulus.* To prove that guppies cause evolution in *Rivulus*, we evaluated the response to selection after guppies were introduced into two streams that contained just *Rivulus*. This perturbation caused a similar trajectory of evolution, including analogous food-dependent patterns of trait variation within 25 years or 70 generations.

11-12 Oral

DIVERGENT SELECTION BETWEEN ENVIRONMENTS PROMOTES PHENOTYPIC DIFFERENTIATION OF VEGETATIVE TRAITS IN IBERIAN COLUMBINES (GEN. *AQUILEGIA*)

Julio M. Alcantara [1], Jesus M. Bastida [1], Pedro J. Rey [1], Rafael Jaime [1]

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Divergent selection caused by differences in the environment is the key mechanism promoting adaptive phenotypic differentiation. Thus, its analysis is fundamental to understand processes of adaptive radiation. The most compelling approaches to study divergent selection use field experimental manipulations of the environment or reciprocal transplants. For logistical reasons, these approaches can deal with few environmental factors, few levels of them, and few populations or taxa. Recent studies use the classical Lande-Arnold approach to estimate the strength divergent selection in wild populations and to compare the patterns of divergent selection and phenotypic differentiation between ecotypes. We propose a similar approach to (a) quantify the strength of divergent selection in wider sets of populations or taxa, (b) to assess the role of multiple environmental factors in determining the patterns of divergent selection, and (c) to test whether the observed phenotypic differentiation within and between taxa could be the result of the current patterns of divergent selection. We use this approach in a set of 15 populations from 4 taxa of Iberian columbines (Gen. *Aquilegia*). Our results, focused only on vegetative traits, show that differences in soil rockiness impose divergent selection on inflorescence height. Occupation of different altitudes imposes divergent selection on the number of leaves per plant and leaf length. Divergent selection on these traits is significantly related to the patterns of phenotypic differentiation. In the case of leaf number and size, divergent selection promotes ecotypic differentiation within taxa. In the case of inflorescence height, divergent selection might have promoted taxonomic differentiation.

11-13 Oral

CHANGING LANDSCAPES: THE EFFECT OF HYBRIDIZATION ON FEMALE PREFERENCES AND MALE FITNESS LANDSCAPES

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The fitness landscape for males is substantially shaped by the landscape of female mating preferences. Interspecific hybridization transforms both multivariate male phenotypes and multivariate female preference landscapes, and natural hybridization therefore provides an insight into how one shapes the other. We study the effects of hybridization on sexual selection in several independent natural hybrid zones in swordtail fish. These hybrids occur in an altitudinal ecotone between habitats of their parental species, and show no evidence of reduced viability. Hybridization can cause dramatic changes in the direction of sexual selection, through a number of mechanisms. First, interactions between two species' genomes change both the phenotypic covariance structure and the range of phenotypes produced; swordtail male sexual phenotypes show transgressive segregation. Hybridization can also change female preference landscapes, either by altering underlying genetic architecture or by changing the nature of socially (learned) determined preferences, through the change in phenotypic variation that an individual may experience. We have determined the shape of wild caught female preference landscapes in 3 male sexual trait dimensions of two independent hybrid populations and two populations of their parental species, showing differences in the interaction between traits on female preferences. We will also show the effect of both short-term adult experience and early ontogenetic experience on female preferences.

11-14 Oral

SPATIAL SCALING OF TEMPORAL SYNCHRONY: NATURAL SELECTION ON REPRODUCTIVE TIMING OVER FIVE DECADES IN A WILD BIRD POPULATION

Ben C. Sheldon [1], Teddy A. Wilkin [1], Amy E. Hinks [1]

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Strong natural selection caused by variation in the degree to which organisms synchronise their reproduction with the timing of other trophic levels is an excellent example of the importance of ecological context in understanding evolutionary dynamics. Over almost five decades, natural selection on reproductive synchronisation of a wild population of great tits *Parus major* with their caterpillar prey, particularly the larvae of the winter moth *Operophtera brumata* has been strong and consistent at the population level, and the maintenance of this synchrony is a key part of adaptation to changing climatic conditions. However, phenological timing of is variable over small spatial scales, and given that these birds are highly constrained central-place foragers, they should be very sensitive to small-scale variation in timing. Hence, the birds face the challenge of optimising timing with respect to both local and global effects. I will show that the importance of local timing depends on the scale at which it is measured, and also on the variance in synchrony between birds and individual oak trees that provide the habitat for the birds key food supply. I will further describe how local experience and dispersal act to translate ecological variation (timing) into natural selection in this system.

11-1 Poster Pelvic anti-predator armor reduction in a threespine stickleback population

KJARTAN ØSTBYE[1], TOM KLEPAKER[2], ASBJØRN VØLLESTAD[1], LOUIS BERNATCHEZ[3]

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[2]*Aquatic behavioural ecology research group, Department of Biology, University of Bergen, Norway*
[3]*Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Canada*

11-2 Poster A multivariate approach to understanding predator-driven phenotypic plasticity

STUART R. DENNIS[1], MAURICIO J. CARTER M.[2], WILLIAM HENTLEY[1], ANDREW P. BECKERMAN[1]

[1]*University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom*
[2]*Universidad de Chile, Departamento de Ciencias Ecológicas, Santiago, Chile*

11-3 Poster Evolution of male reproductive strategies in a marsupial in response to python predation

JANE L. DeGABRIEL[1,2], SARAH E. KERR[3], MICHELLE WAYCOTT[3], BEN D. MOORE[3,4],CHRISTOPHER N. JOHNSON[3]

[1]*Australian National University, School of Botany and Zoology, Canberra, Australia*
[2]*University of Aberdeen, Aberdeen, United Kingdom*
[3]*James Cook University School of Marine and Tropical Biology, Townsville, Australia*
[4]*Macaulay Institute, Aberdeen, United Kingdom*

11-4 Poster Local adaptations of life history traits of a *Drosophila* parasitoid, *Leptopilina boulardi*: climate and host distribution as agents of selection

JOFFREY MOIROUX[1,2], CÉCILE LE LANN[1], MAJEED A. SEYAHOOEI[2], PHILIPPE VERNON[1], JEAN-SÉBASTIEN PIERRE[1], JOAN VAN BAAREN[1], JACQUES J.M. VAN ALPHEN[2,1]

[1]*University of Rennes 1, UMR 6553 ECOBIO, Rennes, France*
[2]*Leiden University Institute of Biology, Leiden, The Netherlands*

11-5 Poster Exploring selection on reproductive traits in a feral sheep population: a demographic approach using the integral projection model

DYLAN Z. CHILDS[1], MARK REES[1], TIM COULSON[2]

[1]*University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom*
[2]*Imperial College London, Department of Biology, London, United Kingdom*

11-6 Poster Density-dependent sexual selection (and some thoughts on the measurement of sexual selection)

HOPE KLUG[1], KAI LINDSTRÖM[2], HANNA KOKKO[1]

[1]*University of Helsinki, Department of Biological and Environmental Science, Helsinki, Finland*
[2]*Åbo Akademi, Department of Environmental and Marine Biology, Åbo, Finland*

11-7 Poster Ecology and evolution in a nonmodel species, wild Eurasian perch *(Perca fluviatilis* L.*)*

JASMINCA BEHRMANN-GODEL

University of Konstanz, Limnological Institute, Department of Biology, Konstanz, Germany

11-8 Poster **Interactions between colour pattern, temperature and life history traits in three coccinellid species (*Harmonia axyridis*, *Adalia bipunctata* and *Adalia decempunctata*)**

LAURA JANE MICHIE
University of Cambridge, Department of Genetics, Cambridge, United Kingdom

11-9 Poster **Selection on flowering time and size in natural populations of *Arabidopsis thaliana***

REIKO AKIYAMA, JON ÅGREN
Uppsala University, Department of Plant Ecology, Evolutionary Biology Centre (EBC), Uppsala, Sweden

11-10 Poster **A diffusion-based approach to stochastic individual growth and energy budget, with consequences to life-history and population dynamics**

IDO FILIN
University of Helsinki, Department of Mathematics and Statistics, Helsinki, Finland

11-11 Poster **Parasite-mediated selection and variation in host immune response and resistance in three-spined sticklebacks, *Gasterosteus aculeatus***

JOB DE ROIJ, ANDREW D.C. MacCOLL
The University of Nottingham, School of Biology, Nottingham, United Kingdom

11-12 Poster **Can chorusing species communicate within a chorus? The case of female mate choice in the European treefrog *Hyla arborea***

CHRISTINA RICHARDSON[1], JEAN-PAUL LENA[1], MARC THERY[2], PIERRE JOLY[1], SANDRINE PLENET[1], THIERRY LENGAGNE[1]
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[2]Muséum National d, UMR 8571 Laboratoire d, Brunoy, France

11-13 Poster **Evolution of dominance and assortative mating under frequency-dependent disruptive selection**

STEPHAN PEISCHL, KRISTAN A. SCHNEIDER
University of Vienna, Faculty of Mathematics, Vienna, Austria

11-14 Poster **Is nestling immune response under selection in the collared flycatcher (*Ficedula albicollis*)?**

NATALIA PITALA[1], LARS GUSTAFSSON[2], JOANNA SENDECKA[2], JON E. BROMMER[3]
[1]University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland
[2]Uppsala University, Department of Animal Ecology, Uppsala, Sweden
[3]University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland

11-15 Poster **The sexual selection landscape: natural genetic variation interacts with population density to shape the social environment**

JULIA SALTZ[1,2], BRAD FOLEY[3]
[1]University of California, Population Biology Graduate Group, Davis, United States
[2]University of Southern California, Los Angeles, United States
[3]University of Southern California, Department of Molecular and Computational Biology, Los Angeles, United States

11-16 Poster **Feature theory and the two-step hypothesis of mimicry evolution**

ALEXANDRA C.V. BALOGH, GABRIELLA GAMBERALE-STILLE, BIRGITTA S. TULLBERG, OLOF LEIMAR
Stockholm University, Department of Zoology, Stockholm, Sweden

11-17 Poster **Population consequences of male behaviour in a sexual-asexual species complex**

KATJA U. HEUBEL, DANIEL J. RANKIN, HANNA KOKKO
University of Helsinki,Laboratory of Ecological and Evolutionary Dynamics, Department of Biological and Environmental Sciences, Helsinki, Finland

11-18 Poster **The intrasexual handicap in the green swordtail fish**

EDUARDO A. GARCÍA-GALEA, NOËLLE FABRE, DOLORS VINYOLES
University of Barcelona, Department of Animal Biology, Barcelona, Spain

11-19 Poster **Evolution of chromosomal polymorphisms during adaptation to a novel environment**

JOSIANE SANTOS[1], INÊS FRAGATA[1], PEDRO SIMÕES[2], ANA MARQUES[2], MARTA SANTOS[2], MARGARIDA MATOS[2], MAURO SANTOS[3], MARTA PASCUAL[2], JOAN BALANYÀ[2]
[1]Universidade de Lisboa, Faculdade de Ciências, Centro de Biologia Ambiental, Departamento de Biologia Animal, Lisboa, Portugal
[2]Universitat de Barcelona, Facultat de Biologia, Departament de Genètica, Barcelona, Spain
[3]Universitat Autònoma de Barcelona Departament de Genètica i de Microbiologia, Bellaterra (Barcelona), Spain

11-20 Poster **Male sexually selected antimicrobial glands enhance hatching success in a blenny fish**

MATTEO PIZZOLON[1], EVA GIACOMELLO[1], LAURA MARRI[2], DANIELA MARCHINI[2], FRANCESCO PASCOLI[1], CARLOTTA MAZOLDI[1], LISA LOCATELLO[1], MARIA B. RASOTTO[1]
[1]University of Padova, Department of Biology, Padova, Italy
[2]University of Siena, Department of Evolutionary Biology, Siena, Italy

11-21 Poster **Testing an assumption of a model for the evolution of placentas**

AMANDA I. BANET, ARTHUR G. AU, DAVID N. REZNICK
University of California, Department of Biology, Riverside, United States

11-22 Poster **How not to be seen; does eutrophication influence stickleback sneaking behaviour?**

LEON VLIEGER, ULRIKA CANDOLIN
University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland

11-23 Poster **Evolution of cuticular hydrocarbons in solitary Hymenoptera**

THOMAS SCHMITT[1], MAREIKE WURDACK[1], HEIKE FELDHAAR[2], CARLO POLIDORI[3]
[1]University of Freiburg, Department of Evolutionary Biology and Animal Ecology, Freiburg, Germany
[2]University of Osnabrück, Department of Behavioural Biology, Osnabrück, Germany
[3]Università degli Studi di Milano, Dipartimento di Biologia, Milano, Italy

11-24 Poster **The adaptive significance of phenotype alteration to short-term larval nutritional limitation in a tropical butterfly *Bicyclus anynana***

MARJO A.K. SAASTAMOINEN
University of Leiden, Institute of Biology, Section of Evolutionary Biology, Leiden, Netherlands

11-25 Poster **Heritability of mate choice in collared flycatchers: overlooked variance components**

GERGELY HEGYI[1], MÁRTON HERÉNYI[1], ALASTAIR J. WILSON[2], LÁSZLÓ Z. GARAMSZEGI[3], BALÁZS ROSIVALL[1], MARCEL EENS[3], JÁNOS TÖRÖK[1]
[1]Eotvos Lorand University, Department of Systematic Zoology and Ecology, Budapest, Hungary
[2]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom
[3]University of Antwerp, Department of Biology, Wilrijk, Belgium

11-26 Poster **Temporal variation in productivity weakens the effect of evolution on ecological dynamics of predator-prey interaction**

VILLE-PETRI FRIMAN[1,2], JOUNI LAAKSO[2]
[1]University of Jyväskylä, Department of Environmental and Biological Sciences, Jyväskylä, Finland
[2]University of Helsinki, Department of Environmental and Biological Sciences, Helsinki, Finland

11-27 Poster **Contemporary Rapid Evolution: Dynamics and Persistence in Complex Ecological Communities**

TEPPO HILTUNEN[1,2], JOUNI LAAKSO[3], FRIMAN VILLE-PETRI[2], LAURA E. JONES[1], NELSON G. HAIRSTON JR.[1], STEPHEN P. ELLNER[1]
[1]Cornell University, Department of Ecology and Evolutionary Biology, Ithaca, United States
[2]University of Jyväskylä, Department of Biology and Environmental Science, Jyväskylä, Finland
[3]University of Helsinki, Department of Biology and Environmental Science, Helsinki, Finland

11-28 Poster **Male salamanders remember individuals based on chemical or visual cues**

NANCY R. KOHN[1,2], ROBERT G. JAEGER[1]
[1]University of Louisiana at Lafayette, Department of Biology, Lafayette, United States
[2]LEGS, CNRS, Gif sur Yvette, France

11-29 Poster **Why are mountain *Melanagia galathea* (Lepidoptera, Nymphalidae) darker than low altitude ones?**

GABRIEL NEVE
Universite de Provence, Institut mediterraneen d'Ecologie et Paleoecologie UMR 6116, Marseille, France

11-30 Poster **Intraspecific Competition Can Promote the Maintenance of Genetic Recombination**

SOL ACKERMAN, DONAL HICKEY
Concordia University, Department of Biology, Montreal, Canada

11-31 Poster **Fire drives the selective landscape: niche partitioning along a space-time continuum**

GRAEME ARMSTRONG
Charles Darwin University, School of Environmental Research, Darwin, Australia

11-32 Poster **Activation of the immune system promotes insect dispersal in the wild**

JUKKA SUHONEN, JOHANNA HONKAVAARA, MARKUS J. RANTALA
University of Turku, Department of Biology, Section of Ecology, Turku, Finland

11-33 Poster **The advantage of being worse: suboptimal intragroup signaling strategies show high robustness to intergroup competition**

STEFFEN WISCHMANN[1,2], DARIO FLOREANO[2], LAURENT KELLER[1]
[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland
[2]EPFL Laboratory of Intelligent Systems, Lausanne, Switzerland

11-34 Poster **Rearing environment and whole plumage reflectance in male and female collared flycatchers**

MIKLÓS LACZI[1], LÁSZLÓ Z. GARAMSZEGI[2], BALÁZS ROSIVALL[1], JÁNOS TÖRÖK[1], GERGELY HEGYI[1]
[1]Eotvos Lorand University, Department of Systematic Zoology and Ecology, Budapest, Hungary
[2]University of Antwerp, Department of Biology, Wilrijk, Belgium

11-35 Poster **How does breeding synchrony affect extra-pair paternity frequency in a colonial bird?**

MICHAEL J.L. MAGRATH[1], GREG J. ADCOCK[1], SIMON C. GRIFFITH[2], NAOMI E. LANGMORE[1]
[1]Australian National University, School of Biology, Canberra, Australia
[2]Macquarie University, Centre for the Integrative Study of Animal Behaviour, Sydney, Australia

11-36 Poster **Multifarious selection by environmental stress: acidity driven adaptive divergence of Swedish moor frogs *(Rana arvalis)***

KATJA RASANEN
ETH-Zurich & Eawag, Department of Aquatic Ecology, Institute of Integrative Biology, Duebendorf, Switzerland

11-37 Poster **Ontogenetic foraging shifts and correlative life history evolution in Satyrine butterflies**

DAVID BERGER[1,2], KARL GOTTHARD[2], CONSTANTÍ STEFANESCU[3]
[1]Univeristy of Zürich-Irchel, Zoological Museum, Zürich, Switzerland
[2]Stockholm University, Department of Zoology, Stockholm, Sweden
[3]Museu de Granollers, Departamento de Ciències Naturals, Granollers, Spain

11-38 Poster **Coping with climate: adaptation and plasticity of life history traits in the tropical butterfly *Bicyclus anynana***

MAAIKE A. DE JONG, FANJA M.H.N. KESBEKE, BAS J. ZWAAN, PAUL M. BRAKEFIELD
Leiden University, Department of Evolutionary Biology, Leiden, Netherlands

11-39 Poster **Assumptions about the size advantage affect the timing of sex change**

EREM KAZANCIOGLU, SUZANNE H. ALONZO
Yale University, Department of Ecology and Evolutionary Biology, New Haven, United States

11-40 Poster **Fitness consequences of experimental manipulation of incubation temperature in blue tits**

ANDREAS NORD, JAN-ÅKE NILSSON
Lund University, Department of Animal Ecology, Lund, Sweden

11-41 Poster **Ecology of sexual dimorphism and clinal variation in coloration in a damselfly**

IDELLE A. COOPER
University of Wisconsin, Department of Zoology, Madison, United States

11-42 Poster **Evolution of energy storage in stochastic environments**

BARBARA FISCHER[1,2], ULF DIECKMANN[1], BARBARA TABORSKY[2,1]
[1]International Institute for Applied Systems Analysis (IIASA), Evolution and Ecology Program, Laxenburg, Austria
[2]University of Bern, Zoological Institute, Division of Behavioural Ecology, Hinterkappelen, Switzerland

11-43 Poster **Consequences of periodically changing resource environment on evolutionary and ecological dynamics of a two species bacterial community**

MINNA H. PEKKONEN, JENNI KORHONEN, JOUNI T. LAAKSO
University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland

11-44 Poster **Division of labor in honeybee colonies and Phosphoglucomutase genotypes**

MERAL KENCE
Middle East Technical University, Department of Biology, Ankara, Turkey

11-45 Poster **Eco-Evolutionary Dynamics of Mutualists and Exploiters**

EMILY I. JONES[1], JUDITH L. BRONSTEIN[1], RÉGIS FERRIÈRE[1,2]
[1]University of Arizona, Department of Ecology and Evolutionary Biology, Tucson, Arizona, United States
[2]École Normale Supérieure, Paris, France

11-46 Poster **Adaptive changes in life history traits following a new guppy introduction**

SWANNE GORDON[1], DAVID N. REZNICK[1], ANDREW HENDRY[2]
[1]University of California Riverside, Department of Biology, Riverside, United States
[2]McGill University, Department of Biology, Montreal, Canada

11-47 Poster **Egg size in threespine stickleback as a system for studying rapid evolution via natural selection**

JOHN A. BAKER, DAVID C. HEINS
Clark University, Department of Biology, Worcester, United States
Tulane University, Department of Ecology & Evolutionary Biology, New Orleans, United States

11-48 Poster **Relationship between melanin-based coloration and parasite resistance: implications for sexual selection and maintenance of coloration variation in feral pigeons**

LISA JACQUIN[1,2], PHILIPPE LENOUVEL[1], CLAUDY HAUSSY[1], ANNE-CAROLINE JULLIARD[3,4], JULIEN GASPARINI[1]
[1]*Université Pierre et Marie Curie, Laboratoire Ecologie et Evolution, Paris, France*
[2]*Université Paris10 - Nanterre, France*
[3]*Université Paris-Sud, Laboratoire Ecologie, Systématique, Evolution, Orsay, France*
[4]*Institut des Sciences de la Communication, Paris, France*

11-49 Poster **Reproductive adjustments in female lizards, *Lacerta vivipara***

JOSEFA BLEU[1], MANUEL MASSSOT[2], JEAN-FRANÇOIS LE GALLIARD[2]
[1]*Université Pierre & Marie Curie, UMR 7625 Ecology and Evolution, Paris, France*
[2]*CNRS UMR 7625 Ecology and Evolution, Paris, France*

11-50 Poster **Male reproductive strategies, pair bond and their genetic consequences in the Common Quail *(Coturnix coturnix)***

INES SANCHEZ-DONOSO[1], JORGE ECHEGARAY[2], MANEL PUIGCERVER[3], CARLES VILÀ[2], J. DOMINGO RODRIGUEZ-TEIJEIRO[1]
[1]*Universitat de Barcelona, Department of Animal Biology, Barcelona, Spain*
[2]*Estación Biológica de Doñana-CSIC, Sevilla, Spain*
[3]*Universitat de Barcelona, Didactica de les Ciencies Experimentals i la Matematica, Barcelona, Spain*

11-51 Poster **Mapping chemical phenotypes and susceptibility to herbivores in forest ecosystems: the importance of scale in plant-herbivore interactions**

BEN D. MOORE[1], GLENN R. IASON[1], WILLIAM J. FOLEY[2], COLIN M. BEALE[1], JACK J. LENNON[1]
[1]*Macaulay Institute, Ecology Group, Aberdeen, United Kingdom*
[2]*Australian National University ANU, College of Medicine, Department of Biology and Environment, Canberra, Australia*

11-52 Poster **Identifying causal mechanisms of fitness differences in the model population, ΦX174 Bacteriophage, under different environmental conditions**

DONALD V. GRIFFIN[1,2]
[1]*Florida State University, Department of Biological Science, Tallahassee, Florida, United States*
[2]*University of Oslo, Centre for Ecological and Evolutionary Synthesis (CEES), Oslo, Norway*

11-53 Poster **Evolution of growth strategy in size-structured plant communities**

DANIEL S. FALSTER[1], ÅKE BRÄNNSTRÖM[2,3], MARK WESTOBY[1], ULF DIECKMANN[3]
[1]*Macquarie University, Department of Biological Sciences, Sydney, Australia*
[2]*Umeå University, Department of Mathematics and Mathematical Statistics, Umeå, Sweden*
[3]*International Institute for Applied Systems Analysis (IIASA), Ecology and Evolution Program, Laxenburg, Austria*

11-54 Poster **Survival selection on melanin-based plumage coloration in Northern tawny owls: the impact of winter severity and cyclic food abundance**

PATRIK KARELL, KARI AHOLA, TEUVO KARSTINEN, JON E. BROMMER
University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland

11-55 Poster Geographic differentiation in compensatory growth in the common frog *(Rana temporaria)*

EMMA DAHL, ANSSI LAURILA
Uppsala University, Faculty of Population biology, Department of Ecology and Evolution, Uppsala, Sweden

11-56 Poster Antler growth phenology and sexual selection

MICHELLE N. CLEMENTS[1], JOSEPHINE M. PEMBERTON[1], STEVE D. ALBON[2], TIM H. CLUTTON-BROCK[3], LOESKE E.B. KRUUK[1]
[1]University of Edinburgh, Institute of Evolutionary Biology, United Kingdom
[2]The Macauly Institute, Aberdeen, United Kingdom
[3]University of Cambridge, Large Animal Research Group, Department of Zoology, Cambridge, United Kingdom

11-57 Poster Maternal effects and offspring immune defence in the speckled wood butterfly, *Pararge aegeria*

MELANIE GIBBS[1], CASPER J. BREUKER[1], HELEN HESKETH[2], ROSIE HAILS[2], HANS VAN DYCK[1]
[1]Université catholique de Louvain (UCL), Behavioural Ecology & Conservation Group, Biodiversity Research Centre, Louvain-la-Neuve, Belgium
[2]Centre for Ecology & Hydrology, Oxford, United Kingdom

11-58 Poster Invasive salmonids as agents of selection

CARLOS GARCIA DE LEANIZ[1], KATHLEEN E. WHITLOCK[2], PAUL N. HOWES[1]
[1]Swansea University, Biological Sciences, Swansea, United Kingdom
[2]Universidad de Valparaíso, Centro de Neurociencia de Valparaíso, Valparaíso, Chile

11-59 Poster Evolution of anti-predatory behaviour in juvenile salmon

LAURA J. ROBERTS, CARLOS GARCIA DE LEANIZ
Swansea University, Schoolof the Environment and Society, Swansea, United Kingdom

11-60 Poster Contrasting selection on allometric relationship in guppy secondary sexual trait

CAMILLA KALVATN EGSET[1,2], CHRISTOPHE PÉLABON[1,2], JOHN A. ENDLER[3], GUNILLA ROSENQVIST[1,2]
[1]NTNU, Department of Biology, Trondheim, Norway
[2]Norwegian University of Science and Technology, Trondheim, Norway
[3]University of Exeter, Centre for Research in Animal Behaviour, Exeter, United Kingdom

11-61 Poster A data-based model of adaptive diversification in fishes along an environmental temperature-depth gradient

JAN OHLBERGER[1,2], ÅKE BRÄNNSTRÖM[3,4], ULF DIECKMANN[4]
[1]Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Department of Biology and Ecology of Fishes, Berlin, Germany
[2]University of Oslo, Centre for Ecological and Evolutionary Synthesis, Oslo, Norway
[3]Umeå University, Department of Mathematics and Mathematical Statistics, Umeå, Sweden
[4]International Institute for Applied Systems, Analysis Evolution and Ecology Program, Laxenburg, Austria

11-62 Poster Adaptive dynamics of phytoplankton stoichiometry: evolutionary convergence towards nonequilibrium communities

PEDRO BRANCO, MARTIJN EGAS, JEF HUISMAN
University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, Amsterdam, Netherlands

11-63 Poster Mismatch in phenology of a host plant and natural enemies results in enemy-free space for *Phyllotreta nemorum*

NIELS A. G. KERSTES[1], PETER W. DE JONG[2]
[1]ETH Zurich, Environmental Sciences, Zurich, Switzerland
[2]Wageningen University, Laboratory of Entomology, Wageningen, Netherlands

11-64 Poster Life span in butterflies: the effects of temperature, dietary restriction and altitudinal origin

STEPHANIE S. BAUERFEIND[1], ISABELL KARL[2], KLAUS FISCHER[3]
[1]University of Zurich, Zoological Museum, Zurich, Switzerland
[2]University of Bayreuth, Department of Animal Ecology I, Bayreuth, Germany
[3]University of Greifswald, Zoological Institute and Museum, Greifswald, Germany

11-65 Poster Personality under frequency-dependent selection. Fitness consequences in a natural population of great tits

EVA FUCIKOVA, PIET J. DRENT, KEES VAN OERS
NIOO-CTE, Department of Animal Population Biology, Heteren, Netherlands

11-66 Poster A demo-genetic approach of the interaction between environmental heterogeneity and gene flow in the adaptive trajectory of a continuous tree population

MARIANE ALLEAUME-BENHARIRA, SYLVIE ODDOU-MURATORIO, FRANCOIS LEFEVRE
INRA, Unité d'Ecologie des Forets Mediterraneennes, Avignon, France

11-67 Poster The operation of sexual selection in a promiscuous species

JULIE M.M. COLLET[1], KIRSTY WORLEY[2], DAVID S. RICHARDSON[2], TOMMASO PIZZARI[1]
[1]Edward Grey Institute, Department of Zoology, Oxford, United Kingdom
[2]University of East Anglia, School of biological Sciences, Norwich, United Kingdom

11-68 Poster Causes of population variation in nest structure

MEGAN L. HEAD, IAIN BARBER
University of Leicester, Department of Biology, Leicester, United Kingdom

The genetic consequences of reproductive modes: insights from asexual species

eseb

12th Congress

Turin 2009

12

Program

Thursday August 27 - **Symposium 12**

Location: Room 2

The genetic consequences of reproductive modes: insights from asexual species

Organizers:	*Karine Van Doninck, University of Namur, Belgium* *Diego Fontaneto, Imperial College London, Ascot Berkshire, United Kingdom*

9.45 - 10.15	**DAVID B. MARK WELCH** (invited) Gene Copy Evolution in Bdelloid Rotifers
10.15 - 10.45	**SHANNON M. HEDTKE** (invited) Rare genetic capture by asexual paternal clones in the clam genus *Corbicula*
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**SOLENN STOECKEL** Taking stock of asexual reproduction on population genetics' parameters
11.35 - 11.55	**MAURINE NEIMAN** A high rate of mutation accumulation in asexual vs sexual *Potamopyrgus antipodarum*, a New Zealand snail
11.55 - 12.15	**KEN KRAAIJEVELD** Rampant proliferation of a transposable element in an asexual parasitoid
12.15 - 12.35	**KATHRIN P. LAMPERT** Clonal erosion in over-wintering *Daphnia* populations
12.35 - 12.55	**TANJA SCHWANDER** Positive feedback loops in the transition from sexual reproduction to parthenogenesis in *Timema* stick insects
12.55 - 13.55	*Lunch*

12-1 Oral

GENE COPY EVOLUTION IN BDELLOID ROTIFERS

David B. Mark Welch [1,2]

[1]Marine Biological Laboratory, Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Woods Hole, United States
[2] Brown University, Department of Ecology and Evolutionary Biology, Providence, United States

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The evolutionary success of bdelloid rotifers may be due to a combination of their adaptation to desiccation-prone environments and the dynamics of genome evolution in the absence of meiosis and syngamy. One genetic consequence of their amictic reproductive mode is the accumulation over time of sequence divergence between gene copies that no longer segregate. These gene copies should follow the evolutionary pattern of duplicated genes, with either the functional differentiation of the two copies or the loss of one copy. Limited genomic and transcriptomic sequencing of multiple bdelloid species has revealed no cases where a gene is not present in at least two copies, a phenomenon that may be driven by the need to maintain templates for the repair of DNA double-strand breaks during recovery from desiccation. Analysis of synonymous and nonsynonymous changes between gene pairs suggests that many pairs have been under positive selection and may be functionally differentiated. The large fraction of functionally differentiated gene pairs is consistent with the absence of segregation and may contribute to the success of bdelloids by providing a general purpose geneotype well adapted to a wide environmental spectrum.

12-2 Oral

RARE GENETIC CAPTURE BY ASEXUAL PATERNAL CLONES IN THE CLAM GENUS *CORBICULA*

Shannon M. Hedtke [1]

[1]*University of Texas at Austin, Section of Integrative Biology, Austin, United States*

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Androgenesis is a form of asexuality in which offspring are clones of the father. In sympatric North American populations of two invasive, androgenetic species in the clam genus *Corbicula*, restriction digest mapping of rDNA failed to detect recent nuclear exchange. However, mitochondrial markers not shared in allopatric populations were shared between species in sympatric populations. Androgenetic clams appear able to parasitize eggs of closely related species. While mitochondria are retained in the fertilized egg, maternal nuclear chromosomes are expelled, and the mother incubates male clones of another species. We additionally performed phylogenetic analyses of two nuclear introns and one mitochondrial marker from multiple sexual and androgenetic species from across the global distribution. Our results suggest that androgenesis evolved relatively recently in *Corbicula*, and that genetic capture of maternal nuclear DNA from other species may rarely occur. While over evolutionary time scales asexual lineages are expected to go extinct, the rare capture of genetic material from other species may permit the long-term persistence of androgenesis.

12-3 Oral

TAKING STOCK OF ASEXUAL REPRODUCTION ON POPULATION GENETICS' PARAMETERS

Solenn Stoeckel [1], Jean-Christophe Simon [1]

[1]*INRA, UMR BiO3P, Rennes, France*

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Mating systems hold key parameters to understand the evolutionary processes shaping both the genetic diversity and differentiation. Despite the number of species concerned, the consequences of partial asexual reproduction on population genetics' parameters remain poorly understood. Most of our knowledge comes from works published since the last decade. We proposed to take stock of the current knowledge and to synthesize advances we obtained by simulations confronted with plant and insects' datasets.

First, we will give an overview of theoretical expectations that predict how asexual reproduction via limited recombination rates and clonal dynamics may affect classical population genetic parameters. Field and experimental data from Insects (aphids'species) and a tree species (*Prunus avium* L.) will illustrate each effect of partial and pure asexual reproduction on genetic parameters. Then, we will present simulations results obtained under varying asexual rates and values of life cycle key components to emphasize the general tendencies of genetic diversity and population differentiation' responses. Finally, we will discuss about the unexplored questions raised when switching from classical (panmictic sex) population genetics' models and give some perspectives to get deeper insights from asexual consequences on evolution.

12-4 Oral

A HIGH RATE OF MUTATION ACCUMULATION IN ASEXUAL VS SEXUAL *POTAMOPYRGUS ANTIPODARUM*, A NEW ZEALAND SNAIL

Maurine Neiman [1], Gery Hehman [1], Joe Miller [2], John Logsdon Jr. [1], Douglas Taylor [3]

[1]*University of Iowa, Biology/Roy J. Carver Center for Comparative Genomics, Iowa City, United States*
[2]*The Australian National Herbarium, Centre for Plant Biodiversity Research, Canberra, Australia*
[3]*University of Virginia, Department of Biology, Charlottesville, United States*

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Theory suggests that effective clearance of harmful mutations is one of the major benefits of sexual reproduction, but the extent to which mutation accumulation contributes to the maintenance of sex in natural populations is both unclear and hotly debated. We used whole-mitochondrial genome sequencing in *Potamopyrgus antipodarum*, a snail system that has become the best-characterized system for empirical investigation of the maintenance of sex, to ask 1) whether increased mutation accumulation is associated with asexuality, and 2) whether it occurs rapidly enough to be detectable in recently-derived asexual lineages. Obligately sexual female *P. antipodarum* occasionally produce obligately asexual daughters, resulting in the frequent occurrence of mixed sexual/asexual populations. This means that, unlike any other study of mutation accumulation in natural populations to date, mutation accumulation can be directly compared in sexuals vs. asexuals. Asexual lineage age in *P. antipodarum* has also been characterized, meaning that the system can be used to address a key prediction of mutational models for sex: that older asexual lineages will have higher mutation loads. We show that asexual *P. antipodarum* lineages experience heightened mutation accumulation, and at a relatively young age. Older asexual lineages were also characterized by higher mutational loads. These results point to a direct link between asexuality and mutation accumulation. In particular, our findings suggest that increased mutation accumulation in asexual lineages can occur on an ecologically relevant time scale; that is, before asexual lineages coexisting with sexual counterparts become extinct.

12-5 Oral

RAMPANT PROLIFERATION OF A TRANSPOSABLE ELEMENT IN AN ASEXUAL PARASITOID

Ken Kraaijeveld [1], Brechtje Zwanenburg [1], Jacques van Alphen [1]

[1]Institute of Biology, Department of Animal Ecology, Leiden, Netherlands

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Recent theory suggests that asexual taxa face early extinction because they lack an effective means of purging transposable elements. Transposable elements are capable of autonomous self-replication and can thus increase in copy number much faster than other types of mutations. Hence, Muller's ratchet should operate much faster for transposable elements than for other mutations. The evidence for this idea rests mostly on the observation that bdelloid rotifers, an ancient asexual group, lack all of the major types of transposable elements. If accumulation of transposable elements is what caused the extinction of asexual taxa other than bdelloids, we should see higher copy numbers in recent asexuals than in their sexual relatives. Here, we test this idea in a species of parasitoid wasp in which some, but not all, populations reproduce asexually. We compare the copy number of a newly identified *gypsy*-like retrotransposon between twelve genetically distinct asexual lines and eight sexual strains using quantitative PCR. The results show that without exception, the asexual strains harbour more copies of the retrotransposon than the sexual strains. While we currently find no evidence for fitness differences between the sexual and asexual strains, our results suggest that the asexuals are in the process of accumulating copies of this retrotransposon, which may eventually create a significant genetic load.

12-6 Oral

CLONAL EROSION IN OVER-WINTERING *DAPHNIA* POPULATIONS

Kathrin P. Lampert [1]

[1]*University of Bochum, Department of Animal Evolutionary Ecology and Biodiversity, Bochum, Germany*

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Daphnia have a dual reproduction mode including parthenogenetic reproduction during favourable environmental conditions as well as sexual reproduction when environmental conditions deteriorate, e.g. in the fall. I use microsatellites to investigate the seasonal fluctuations of the clonal composition in a Norwegian *Daphnia pulex* field population. These *Daphnia* use both over-wintering strategies, as parthenogenetic females or (sexual) ephippial resting eggs. I am interested in whether there is clonal erosion due to selection or random drift in the pelagic population during the winter months, and if the genotypic variability is restored during spring by hatchlings from the resting egg bank. I am also investigating whether different clones of *Daphnia* invest differently in clonal and sexual reproduction and may be selected for either strategy. From combining the population genetic results with ecophysiological data I expect synergisms and a deeper insight into the evolution of alternative survival- and reproductive strategies.

12-7 Oral

POSITIVE FEEDBACK LOOPS IN THE TRANSITION FROM SEXUAL REPRODUCTION TO PARTHENOGENESIS IN *TIMEMA* STICK INSECTS

Tanja Schwander [1]

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Understanding the evolution of new phenotypes is often complex because the intermediate stages in the transition from the ancestral to the derived phenotype typically remain elusive. Here we suggest and provide evidence for a mechanism that may result in the transition from sexual reproduction to parthenogenesis. In many sexually reproducing invertebrates, a small proportion of unfertilized eggs hatch spontaneously, because errors during meiosis can result in the production of diploid eggs. We hypothesized that in marginal populations, where some proportion of females might be unable to find mates, an initially low rate of spontaneous parthenogenesis may result in the loss of males through a positive feedback loop. Because unmated females will only produce a small number of daughters, the sex ratio in the next generation will become more females biased and the population density will decrease, resulting in a yet larger proportion of females not finding mates. Thus, the strength of selection for spontaneous parthenogenesis increases as the prevalence of spontaneous parthenogenesis increases in the sexual population. We tested this prediction across populations of sexually reproducing stick insects of the genus *Timema*. As predicted, the capacity for parthenogenesis (i.e., the proportion of unfertilized eggs that hatched) increased as the density of individuals decreased. In addition, sex ratios became more female biased as the density of individuals decreased. Our results suggest a simple mechanism through which parthenogenesis can evolve in a sexually reproducing population.

12-1 Poster **Can synergistic epistasis explain the evolution of sex?**
LUKASZ JASNOS, KATARZYNA TOMALA, DOROTA PACZESNIAK, RYSZARD KORONA
Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland

12-2 Poster **Adaptive Evolution in Asexual Populations**
PAULO R. CAMPOS, CAIO SATIRO, JOSEILME GOUVEIA, VIVIANE OLIVEIRA
Universidade Federal Rural de Pernambuco, Departamento de Fisica, Recife, Brazil

12-3 Poster **Evolutionary feedbacks in the genomes of meiotic parthenogens**
MICHAEL E. HOOD
Amherst College, Biology Department, Amherst, United States

12-4 Poster **Mutation accumulation in *Tetrahymena***
ISABEL GORDO, ELSA GUILHERME, INÊS CONCEIÇÃO, PATRÍCIA H. BRITO , HELENA SOARES
Instituto Gulbenkian de Ciência, Evolutionary Biology, Oeiras, Portugal

12-5 Poster **Unusual H2A variants and degenerate tetraploidy in bdelloid rotifers**
KARINE VAN DONINCK, MORGAN L. MANDIGO, JAE H. HUR, MATTHEW MESELSON
University of Namur, Research Unit in Organism Biology, Namur, Belgium

12-6 Poster **Asexuality in the fungus-growing ant *Mycocepurus smithii*: no sex in fungus-farmers or their crops**
ANNA HIMLER
University of Arizona, Ecology and Evolutionary Biology, University of Arizona, United States

12-7 Poster **Domestication in red algae: how farming practices favor asexual reproduction and heterozygosity**
MARIE LAURE GUILLEMIN[1], CHRISTOPHE DESTOMBE[2], SYLVAIN FAUGERON[3], FRÉDÉRIQUE VIARD[4], JUAN CORREA[3], MYRIAM VALERO[2]
[1]*Universidad Austral de Chile, Instituto de Ecologia y Evolucion, Campus Isla Teja, Valdivia, Chile*
[2]*Université Pierre et Marie Curie, UMR 7144 CNRS/UPMC, Station Biologique, Roscoff, France*
[3]*Pontificia Universidad Católica de Chile, Departamento de Ecología and Center for Advanced Studies in Ecology and Biodiversity, Santiago, Chile*
[4]*Université Pierre et Marie Curie, UMR 7144, Département de Adaptation et diversité en Milieu Marin, Roscoff, France*

12-8 Poster **Effects of rice domestication on the evolution of recombination of its main fungal pathogen *Magnaporthe oryzae***
DOUNIA SALEH
Université de Montpellier, UMR BGPI, Département de Biologie et Génétique des interactions plante-parasite, Montpellier, France

12-9 Poster **The advantage of honest signalling in yeast spores**
SAMUEL J. TAZZYMAN
University College of London, Complex, London, United Kingdom

12-10 Poster **High genetic diversity in a parthenogenetic earthworm: comparing populations from natural and metal contaminated soils**
EMILY K. KNOTT, JARI HAIMI
University of Jyvaskyla, Biological & Environmental Sciences, Jyvaskyla, Finland

12-11 Poster High genetic variability in the parthenogenetic earthworm *Aporrectodea trapezoides* (Oligochaeta, Lumbricidae)

ROSA M. FERNANDEZ, MARTA NOVO, JUAN B. JESUS, ANA ALMODOVAR, DARIO J. DIAZ COSIN

Complutense University, Department of Zoology and Physical Anthropology, Madrid, Spain

12-12 Poster Maintenance of genetic variation in parthenogenetic bagworm moths

ALESSANDRO GRAPPUTO[1], JOHANNA MAPPES[2]

[1]*University of Padova, Department of Biology, Padova, Italy*

[2]*University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland*

12-13 Poster New insights in the phylogeny of invasive Asiatic clams (*Corbicula* spp.)

LISE-MARIE PIGNEUR[1], ANGE-MARIE RISTERUCCI[2], JEAN-PIERRE DESCY[1], KARINE VAN DONINCK[1]

[1]*University of Namur (FUNDP), Laboratory of freshwater ecology (URBO), Namur, Belgium*

[2]*Université de Montpellier, CIRAD UMR DAP, Unité Mixte de Recherche-Développement et Amélioration des Plante, Montpellier, France*

12-14 Poster Genetic structure of the grapevine downy mildew *Plasmopara viticola* in Europe and the impact of asexual reproduction on genetic clustering algorithm

MICHAEL C. FONTAINE[1], TATIANA GIRAUD[1], FREDERIC AUSTERLITZ[1], RICHARD S. CERVERA[2], FRANÇOIS DELMOTTE[2]

[1]*Université Paris-Sud XI, CNRS UMR 8079, Laboratoire de Ecologie Systématique et Evolution, Orsay, France*

[2]*INRA Institut des Sciences de la Vigne et du Vin, UMR 1065 Santé Végétale (INRA-ENITAB), Centre de Recherche Bordeaux-Aquitaine, Bordeaux, France*

12-15 Poster Geographic variation in the mating system of an alga with a haploid diploid life cycle

STACY A. KRUEGER, DENIS ROZE, MYRIAM VALERO

Université Pierre et Marie Curie, Station Biologqiue, Roscoff, France

12-16 Poster Population genetic structure of sea anemone *Aulactinia stella* in the White and the Barents seas as a result of two reproductive modes

EKATERINA S. BOCHAROVA

Moscow State University, Department of Invertebrate Zoology, Moscow, Russia

12-17 Poster Gynogenesis as a dispersal strategy – parasite communities vs. genetic structure of clonal stocks of invasive Prussian carp *(Carassius gibelio)* in Finland and Germany

MANUEL DEINHARDT[1], DUNJA K. LAMATSCH[2], JUKKA JOKELA[3], JOUNI TASKINEN[1]

[1]*University of Jyväskylä, Aquatic Sciences, Jyväskylä, Finland*

[2]*Austrian Academy of Sciences Institute for Limnology, Mondsee, Austria*

[3]*Swiss Federal Institute of Aquatic Science and Technology, Duebendorf, Switzerland*

12-18 Poster **Phylogeograhy & population genetics of sexual spotted seal *(Phoca largha)* and finless porpoise *(Neophocaena Phocaenoides)* in China**

XIANG LI[1], ATHANASIA C. TZIKA[2], YING Y. LIU[3], KARINE V. DONINCK[1], QIAN ZHU[4], MICHEL C. MILINKOVITCH[2]

[1] *University of Namur (FUNDP), Unité de Recherche en Biologie des Organismes (URBO), Namur, Belgium*
[2] *University of Geneva Department of Zoology and Animal Biology, Geneva , Switzerland*
[3] *Shandong University, Weihai Ocean College, Weihai, China*
[4] *Third Institute of Oceanography, State Oceanic Administration, Xiamen, China*

12-19 Poster **Characterization of a MuSashI-like transcript in a colonial chordate, phylogenetic analysis of the protein group and differential expression patterns in sexual versus asexual development**

FABIO GASPARINI, VALENTINA DEGASPERI, ELENA RUFFONI, PAOLO BURIGHEL, LUCIA MANNI

Università degli Studi di Padova, Dipartimento di Biologia, Padova, Italy

12-20 Poster **Novel developmental mechanisms among embryogenesis, asexual fission, and regeneration in *Nematostella vectensis***

PATRICK M. BURTON[1], MIKE VICK[1], JOHN F. FINNERTY[2]

[1] *Wabash College, Department of Biology, Crawfordsville, United States*
[2] *Boston University, Department of Biology, Boston, United States*

Evolution of time-keeping mechanisms

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Program

Thursday August 27 - **Symposium 13**

Location: Room 3

Evolution of time-keeping mechanisms

Organizers: *Rinaldo C. Bertossa, University of Groningen, The Netherlands*
Gabriella Mazzotta, University of Padova, Italy

9.45 - 10.15	**URS ALBRECHT** (invited) The circadian clock mechanism in various organisms
10.15 - 10.45	**RODOLFO COSTA** (invited) Adaptive features of circadian clocks
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**VOLODYMYR DVORNYK** Building-up the Cyanobacterial Circadian Clock: An Evolutionary Perspective
11.35 - 11.55	**TOBIAS S. KAISER** Lunar emergence time is locally adapted, heritable and correlated to circadian emergence time in the marine midge *Clunio marinus*
11.55 - 12.15	**GUY BLOCH** The social clock of bees: division of labor and plasticity in the circadian system of honey bees and bumble bees
12.15 - 12.35	**SONJA V. SCHAPER** Reproductive timing in Great Tits is influenced by early spring temperatures
12.35 - 12.55	**MALCOLM VON SCHANTZ** Diurnal preference alleles and evolution in the human clock genes PER3 and CLOCK
12.55 - 13.55	*Lunch*

13-1 Oral

THE CIRCADIAN CLOCK MECHANISM IN VARIOUS ORGANISMS

Urs Albrecht [1]

[1]*University of Fribourg, Department of Medicine/Biochemistry, Fribourg, Switzerland*

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Life on earth is characterized by recurring changes in environmental conditions caused by the earth's rotation around its own axis. These fluctuation follow a rthythm of 24 hours, the time it takes for the earth to complete one rotation. The periodic succession of light and darkness provided the base for relative timing of biological processes over the 24 hours of a day. Because energy supply is the limiting parameter for survival, a system for optimal timing of energy expenditure and uptake developed. The mechanism of this system took the shape of a cycle reflecting the recurrence of sunrise and sunset, and is termed a "circadian clock" - a clock with a period of about one day (latin: *circa diem*). The internalization of environmental time within the organism not only allows organization of biological processes along the 24-hour time scale but also prediction of recurring events, such as availability of food and emergence of predators. Having an internal clock therefore is beneficial in a competitive environment. This is probably the reason why most orgnanims from cyanobacteria to humans have a circadian clock. Although the priciple of the molecular clock mechanism is conserved among species, the genes involved are completely different. I will describe the main principle behind the circadian clock mechanism and highlight the differences in clock gene composition in distinct species. We will see that the circadian clock evolved probably several times for the puropose of optimally anticipating and adjusting the organism to the environment under competitive conditions.

13-2 Oral

ADAPTIVE FEATURES OF CIRCADIAN CLOCKS

Rodolfo Costa [1]

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It has been 25 years since the first circadian clock genes was cloned, and the extraordinary molecular insights into endogenous oscillators that have followed have revealed that circadian clocks probably originated more than once during evolution, and that the 'clock-gears' of bacteria, fungi, plants and animals do not share any detectable homology. Nevertheless, they are all regarded as convergent adaptations to the endless circadian light/dark and temperature cycles produced by the rotation of the earth about its axis. There are many experiments in the laboratory and some in the field that illustrate how disrupting circadian rhythms, either genetically, or by environmental manipulations, may have implications for fitness. For example, behavioural and functional analyses of mutants that are arrhythmic, or have changes in period, suggest that in a rhythmic environment, the clock allows the organism to 'prepare' itself by anticipating regular geophysical transitions, and that 'resonance' with the external cycle is beneficial. While the results of many of these studies are impressive, in themselves, they do not reveal the presence of natural selection. A different approach involves studying natural variation on clock genes with the methods of population genetics, and in *Drosophila*, this has revealed a more complete understanding of how selection may influence clock genes and the phenotypes they control. I shall discuss a few circadian systems that have been scrutinized from these adaptive perspectives, both under laboratory conditions and in the wild.

13-3 Oral

BUILDING-UP THE CYANOBACTERIAL CIRCADIAN CLOCK: AN EVOLUTIONARY PERSPECTIVE

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Circadian rhythmicity in cyanobacteria was discovered less than two decades ago and has received an increased attention of researchers since then. Evolutionary studies not only reconstruct a history and chronology of the circadian system's assembly, but also help to determine possible adaptive significance of the observed evolutionary changes. According to the molecular data, the origin of the circadian system may be estimated about 2.8-3.3 billion years ago. During its evolution, the circadian system and its elements underwent several significant structural transformations, which might be associated with global environmental changes, such as day length and the level of UV radiation. The evolutionary modifications of the circadian system were probably of adaptive significance and lead to its diversification. Currently, at least three main types of the circadian system in cyanobacteria are recognized. They have different sets of elements in the input and the central oscillator of the system, but functional significance of these differences remains unknown. Reconstruction of the circadian clock macroevolution in cyanobacteria provides a framework for further functional studies of the identified structural differences and mutations, and their probable adaptive value under various natural conditions. The presented evolutionary scenario for the circadian system is based on the currently available data and will certainly be corrected by future studies as updated sequencing and genomic data become available.

13-4 Oral

LUNAR EMERGENCE TIME IS LOCALLY ADAPTED, HERITABLE AND CORRELATED TO CIRCADIAN EMERGENCE TIME IN THE MARINE MIDGE *CLUNIO MARINUS*

Tobias S. Kaiser [1], Dietrich Neumann [2], David G. Heckel [1]

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Lunar rhythms have been described for a number of marine organisms. They are generally assumed to synchronise reproduction within populations to suitable tides. For a handful of species it has been shown that the lunar rhythm is endogenously controlled by a circalunar clock, the molecular and genetic basis of which is still poorly understood.

In a crossing experiment with stocks of the marine midge *Clunio marinus* (Chironomidae, Diptera) that differ in both circadian and lunar emergence times, we found genetic control of the lunar emergence time. The pattern suggests genetic adaptation to the tidal regime of the place of origin.

Genetic control and local adaptation of circadian emergence times has been shown previously (Neumann 1967) and was also observed in our crosses. Our experiment revealed that while both lunar and circadian emergence times are polygenic traits, they are not inherited independently. This suggests either that a set of genetic factors influences both traits or that evolution has shaped the genetic architecture to stabilize adaptive combinations of lunar and circadian emergence times through genetic linkage. In either case, these two life history traits are not entirely free to evolve independently. We put forward the hypothesis that this constraint can be considered adaptive in the intertidal zone, an environment defined by the tides.

13-5 Oral

THE SOCIAL CLOCK OF BEES: DIVISION OF LABOR AND PLASTICITY IN THE CIRCADIAN SYSTEM OF HONEY BEES AND BUMBLE BEES

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In both honey bees and bumble bees “nurses” typically care for brood around-the-clock whereas foragers have strong circadian rhythms and a sleep-like behavior during the night. It is thought that this chronobiological plasticity is functionally significant because it improves the division of labor and overall colony efficiency. We found that in a bumble bee (*Bombus terrestris*), in which the division of labor is based on body size, foragers have more cells expressing the clock neuropeptide Pigment Dispersing Factor (PDF). On the other hand, in the honey bee *Apis mellifera* in which the division of labor relates to age, there is a similar number of PDF immunoreactive cells in nurses and foragers. Nurses that are typically young, care for brood around-the-clock with attenuated or no oscillation in the abundance of the putative clock genes *Period* and *Cryptochrom-m*, irrespective of the illumination regime. However, nurses showed circadian rhythms in locomotor activity and forager-like molecular oscillations in brain clock gene expression shortly after transfer from the hive to constant laboratory conditions. These results suggest that the social environment of the hive modulates the molecular clockwork. Together these studies suggest that even in closely-related taxa, task-related chronobiological plasticity can be achieved by multiple mechanisms: in honey bee workers plasticity in the circadian clock occurs during the adult stage and is socially modulated, in bumble bees there is variation in the pre-adult development of neural circuits related to the brain circadian clock.

13-6 Oral

REPRODUCTIVE TIMING IN GREAT TITS IS INFLUENCED BY EARLY SPRING TEMPERATURES

Sonja V. Schaper [1], Alistair Dawson [2], Peter J. Sharp [3], Samuel P. Caro [1], Marcel E. Visser [1]

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Seasonal timing of reproduction is crucial in Great Tits (*Parus major*), which rely on a narrow caterpillar food peak to rear their nestlings. Year-to-year variation in the arrival of spring has to be anticipated already weeks before egglaying, as gonadal development starts in winter. Therefore the time of decision-making and the time of selection (nestling survival) are decoupled and birds need to integrate environmental cues to make predictions. Increasing spring temperatures are good indicators for the timing of egglaying in the field, but is there a direct causation or is temperature perceived via spring phenology or invertebrate abundance?

We performed experiments in climatized aviaries to see how different temperature regimes affected reproductive development of both male and female birds, the timing of egg laying and onset of moult. We lowered ambient temperatures for specific times between February and April to identify when Great Tits are most sensitive to temperature changes. As plasticity in laying is heritable, we used siblings from early or late laying families of known genetic background.

Our results show that low temperatures early in spring are perceived as cues and influence the onset and duration of laying, interacting with the genetic background of the female. Furthermore, a continuous warm spring leads to earlier gonadal regression in males and earlier onset of moult in females after breeding. These implications are relevant under a climate change scenario that predicts an increase in late spring temperatures in the Netherlands, inducing an advanced caterpillar peak. In contrast, comparably less warming in early spring may be causal for the observed mistiming of Great Tit reproduction.

13-7 Oral

DIURNAL PREFERENCE ALLELES AND EVOLUTION IN THE HUMAN CLOCK GENES PER3 AND CLOCK

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Circadian period length is a normally distributed polygenic trait associated with variability in circadian clock genes. Determining period length in humans is intrusive and expensive. An alternative is to study self-reported diurnal preference, which has been shown to correlate with period length. We obtained diurnal preference scores and DNA samples from UK-based individuals, and selected extreme morning and evening types for genetic analysis. The *PER3* gene has a primate-specific coding-region VNTR polymorphism, in which an 18-amino-acid motif is repeated four or five times). The longer allele was significantly more frequent in morning types. However, no significant evidence was found for differential or balancing selection in *PER3*. A previous report has suggested that the 3111C allele in *CLOCK* associates with evening preference. This association was not present in our population, but we found a haplotype in the *CLOCK* gene, independent of this polymorphism, which associated with extreme eveningness. Analysis of HapMap data revealed strong linkage disequilibrium across the entire gene and three well-defined haplogroups present in all ethnic groups studied, indicating that these lineages diverged prior to the first movements of humans out of Africa. Derived allele patterns of these haplogroups were remarkably consistent and unlikely to occur under neutrality, with positive Tajima's D values failing in the >95 percentile of an empirically-derived genome-wide distribution in Europeans and East Asians. This persuasive evidence for selection on *CLOCK* is the first report of balancing selection acting on a human clock gene.

13-1 Poster Bar-coded ants reveal their societies' rhythm

DANIELLE MERSCH[1], ALESSANDRO CRESPI[2], LAURENT KELLER[1], MEHDI TAFTI[3]

[1]University of Lausanne ,Department of Ecology and Evolution, Lausanne , Switzerland
[2]Ecole Polytechnique Fédérale de Lausanne, Biologically Inspired Robotics Group, Lausanne, Switzerland
[3]University of Lausanne, Center for Integrative Genomics , Lausanne, Switzerland

13-2 Poster Months of asynchrony in offspring production but synchrony in adult emergence - how does an ectoparasite make it?

LAURA HARKONEN, ARJA KAITALA

University of Oulu, Department of Biology, Oulu, Finland

13-3 Poster The genetic background of reproductive diapause and locomotor activity of two northern *Drosophila virilis* group species

TIINA SALMINEN, HANNELE KAURANEN, MAARIA KANKARE, ANNELI HOIKKALA

University of Jyvaskyla, Department of Biological and environmental science, Jyvaskyla, Finland

13-4 Poster The molecular and genetic basis of diapause and diapause variation in *Nasonia* wasps

RINALDO C. BERTOSSA[1], SILVIA PAOLUCCI[1], LOUIS VAN DE ZANDE[1], LEO W. BEUKEBOOM[1], DOMIEN G. M. BEERSMA[2]

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13-5 Poster Evolutionary Genetics of Timing in a Wild Mammal Population

JEFFREY E. LANE[1], F. STEPHEN DOBSON[2], LOESKE E. B. KRUUK[1]

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Selection in subdivided populations

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12th Congress
Turin 2009

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Program

Tuesday August 25 - **Symposium 14**

Location: Room 5

Selection in subdivided populations

Organizers:	*Juliette de Meaux, Max Planck Institute for Evolutionary Biology, Cologne, Germany* *Par K. Ingvarsson, Umeå University, Sweden*

9.45 - 10.15	**JOHANNA SCHMITT** (invited) Natural selection on life history traits in *Arabidopsis thaliana* across the European climate range
10.15 - 10.45	**JEROME GOUDET** (invited) Factors influencing the FST/QST contrast under neutrality and selection
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**SAM YEAMAN** Multi-locus adaptation under migration-selection balance and the accuracy of the Gaussian approximation
11.35 - 11.55	**CHRISTOPHER W. WHEAT** From molecules to metapopulations: finding the variation affecting butterfly dispersal in a fragmented and dynamic landscape
11.55 - 12.15	**ARMANDO CABALLERO** Ast, a new measure of allelic differentiation in subdivided populations
12.15 - 12.35	**XAVIER VEKEMANS** Patterns of genetic structure within and among populations and species in genomic regions subject to strong frequency-dependent selection
12.35 - 13.35	*Lunch*
13.35 - 13.55	**OPHELIE RONCE** Local adaptation versus inbreeding: the ambiguous consequences of increased isolation for genetic load in complex genomes
13.55 - 14.15	**ILKKA KRONHOLM** Local adaptation in *Arabidopsis thaliana* - Seed dormancy as a case study
14.15 - 14.35	**ANEIL AGRAWAL** Ecology of selection on deleterious mutations in subdivided populations: theory and data
14.35 - 14.55	**CHRISTIAN LEXER** Intraspecific admixture and the study of selection in subdivided populations of the European aspen *(Populus tremula)*
14.55 - 15.25	*Coffee break*

14-1 Oral

NATURAL SELECTION ON LIFE HISTORY TRAITS IN *ARABIDOPSIS THALIANA* ACROSS THE EUROPEAN CLIMATE RANGE

Johanna Schmitt [1], Martha Cooper [1], Amity Wilczek [1]

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The genetic model species *Arabidopsis thaliana* exhibits substantial population structure, as well as substantial geographic differentiation in life history traits. To test whether this differentiation is adaptive, and whether it is associated with known allelic variation in candidate flowering time genes, we grew 320 ecotypes originating across the native European climate range in common garden experiments in 5 field sites spanning that climate range. Phenotypic data on flowering time, survival, and fecundity from these experiments were used to test for natural selection on flowering time in different climates and seasons, as well associations of flowering time and fitness with natural allelic variation at candidate flowering time loci. Genotypic selection analysis reveals differences in the strength and mode of selection on flowering time across sites and seasons. Natural variation at candidate loci is significantly associated with flowering time and fitness in mixed model analyses controlling for population structure, but the effects and significance of these associations depend upon the climatic and seasonal environment.

14-2 Oral

FACTORS INFLUENCING THE FST/QST CONTRAST UNDER NEUTRALITY AND SELECTION

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The contrast between population differentiation estimated from quantitative traits (QST) and molecular markers (FST) is commonly used to detect whether selection is acting on the traits under scrutiny. Under neutrality and additivity, theory predicts that FST=QST for any type of population structure, whereas QST>FST indicates diversifying selection and QST<FST is a sign of homogenising selection. However, several factors other than selection can affect the relation between QST and FST. Under neutrality, it has been shown that dominance and epistasis tend to deflate QST compared to the additive situation. The effects of different mutation rate for molecular markers and loci underlying quantitative traits have not been investigated. Moreover, little is known concerning the relation between QST and FST in populations that are not at equilibrium between drift, selection and migration. In particular, scenarios of invasion of new habitats or of fragmentation of existing habitats have not been investigated. Here I will review the empirical and theoretical recent litteraturewe, and I will present results on these issues using a new individual based computer model, Quantinemo (Neuenschwander *et.al.*, 2007).

14-3 Oral

MULTI-LOCUS ADAPTATION UNDER MIGRATION-SELECTION BALANCE AND THE ACCURACY OF THE GAUSSIAN APPROXIMATION

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Studies of adaptation under migration-selection balance commonly rely upon simplifying assumptions about the genetic architecture underlying the phenotype. Simulation studies often use diallelic mutations with equal effect sizes, while quantitative genetic models typically assume infinitely many small mutations of equal effect. The natural world, however, has yielded many examples of adaptation due to QTL's of large effect and very heterogeneous distributions of effect size across differentiated loci. Here we explore the evolution of multi-locus adaptation for traits with flexible genetic architecture using a combination of analytical theory and individual-based simulations. We use analytical models to explore the consequences of migration-selection-drift balance on the divergence of large vs. small effect mutations, and show that local adaptation under migration load will tend to favour divergence at the fewest possible loci. We then use individual-based simulations to compare the evolutionary dynamics for traits with this genetic architecture to analytical predictions based on the Gaussian approximation for genetic variation and response to selection. In many cases, the interaction of migration and diversifying selection generates considerable skew in the distribution of genetic values, which greatly limits the accuracy of the Gaussian approximation for predicting response to selection and divergence at equilibrium. In conjunction with the common observation of QTL's of large effect, these results suggest that the Gaussian approximation is often unsuitable for modeling migration-selection processes.

14-4 Oral

FROM MOLECULES TO METAPOPULATIONS: FINDING THE VARIATION AFFECTING BUTTERFLY DISPERSAL IN A FRAGMENTED AND DYNAMIC LANDSCAPE

Christopher W. Wheat [1,2], Howard W. Fescemyer [2], Jouni Kvist [1], J. Cris Vera [2],
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Most species are comprised of metapopulations, or networks of local populations, which exist in a dynamic balance between local colonization and extinction. Long-term ecological study and modeling of the Glanville fritillary butterfly *(Melitaea cinxia)* has identified dispersal to be critical for metapopulation persistence (i.e. population fitness). Dispersal variation is heritable and much of this variation is predictable from the age and spatial connectivity of local populations. Flight metabolic rate and population age are associated with coding variation in the metabolic enzyme phosphoglucose isomerase, quantitative variation in alternative splicing of the muscle gene troponin-t, and extensive variation in global gene expression, most notably in hypoxia responsive genes and egg development pathways. We have validated these findings using gene product manipulation and detailed study of independent biological samples. Genetic polymorphisms in coding, expression, and alternative splicing that affect flight performance appear to be sorted and maintained by metapopulation dynamics in a fragmented landscape. The implications of these findings for population and conservation genomics are discussed.

14-5 Oral

AST, A NEW MEASURE OF ALLELIC DIFFERENTIATION IN SUBDIVIDED POPULATIONS

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Most developments regarding the analysis of genetic variation are based on measures of heterozygosity and gene frequency differentiation (F_{ST}) among subpopulations. However, allelic diversity (number of alleles segregating in the population) is an alternative criterion with key importance in long-term selection response and population history. A method is proposed for the analysis of allelic diversity in the context of subdivided populations. The partition of total diversity into within- and between-subpopulation components allows for the definition of a measure of allelic differentiation between subpopulations (A_{ST}) analogous to the classical F_{ST}. The defined parameter is contrasted with a previous proposal of allelic richness differentiation and with F_{ST} values for a range of situations. The partition of allelic diversity makes it possible to establish the relative contribution of each subpopulation to within and between-subpopulation components of diversity with implications in evolutionary biology and priorisation for conservation. The applications of the method are illustrated with simulated and empirical data.

14-6 Oral

PATTERNS OF GENETIC STRUCTURE WITHIN AND AMONG POPULATIONS AND SPECIES IN GENOMIC REGIONS SUBJECT TO STRONG FREQUENCY-DEPENDENT SELECTION

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Understanding the causes of the wide variation occurring in patterns of genetic structure across genomes is one of the great challenges of the population genomics era. High peaks of among population differentiation suggest the occurrence of strong diversifying selection. In contrast, genomic regions of low genetic structure may reveal the action of some form of balancing selection. We studied the effect of strong negative frequency-dependent selection, a form of balancing selection occurring at plant self-incompatibility loci, on expected patterns of genetic structure at three different levels: (1) within a continuous population with restricted pollen and seed dispersal; (2) among populations; (3) among closely related species. At each level, we identify statistical tools that enable to discriminate regions under balancing selection from the genomic background, and use numerical simulations to validate the approaches. We then analyze allelic and nucleotide data from the self-incompatibility locus in *Arabidopsis halleri*, as well as from its genomic neighborhood, to assess the magnitude of reduction in genetic structure at all three levels and its genomic extent. We use a sample of 29 unlinked genes to assess genetic structure in the genomic background. The results indicate a strong signature of selection on patterns of genetic structure, but which is strikingly narrowly distributed around the self-incompatibility region.

14-7 Oral

LOCAL ADAPTATION VERSUS INBREEDING: THE AMBIGUOUS CONSEQUENCES OF INCREASED ISOLATION FOR GENETIC LOAD IN COMPLEX GENOMES

Ophelie Ronce [1,2], Francois Rousset [1,2], Frank H. Shaw [3], Ruth G. Shaw [4], Sebastien Lopez [1,2]

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Disruption of gene flow among demes accompanying landscape fragmentation can facilitate local adaptation but increases the effect of drift and inbreeding. We lack predictions about the joint effects of these conflicting forces on mean fitness. We have explored through simulations the effect of increased isolation on the evolution of genetic load when fitness depends in part on local adaptation. In particular, we modeled complex genomes, where a subset of the loci is under divergent selection in different localities. Ignoring genetic effects on demography, we explored the consequences of isolation both in the short and long term. The consequences of increased isolation differed strikingly depending on the size of local demes. In general, increased isolation had negative consequences for fitness in smaller demes and provided very little improvement in local adaptation. In contrast, increased isolation could have beneficial effects in larger demes when a fraction of loci were under heterogeneous selection. The optimal number of migrants per generation lay between one and ten. Migration of individuals of non-local origin into very small demes may therefore be less destructive than in larger demes.

14-8 Oral

LOCAL ADAPTATION IN *ARABIDOPSIS THALIANA* - SEED DORMANCY AS A CASE STUDY

Ilkka Kronholm [1], Carlos Alonso-Blanco [2], Maarten Koornneef [1], Juliette de Meaux [1]

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Local adaptation occurs when natural selection favours different phenotypes in different populations. There are many studies of local adaptation, but only in a limited number of cases has the genetic basis of local adaptation been elucidated. We are studying seed dormancy in *Arabidopsis thaliana*, the plant model organism. Germinating at the right season is important for plant fitness and germination is influenced by a number of environmental and genetic factors. Seed dormancy is a mechanism that controls the timing of germination in plants. One QTL, *DOG1*, controlling variation in seed dormancy has been cloned. We conducted a population genetics study combining quantitative genetic and molecular marker based approaches using F_{ST} vs. Q_{ST} comparisons. Our sampling is hierarchical consisting of three regions (Spain, France and Norway) and several populations within each region. In this framework, we ask the following questions: I) Is dormancy (and other traits) variation adaptive in *A. thaliana*? II) If there is local adaptation, at what geographical scale it exists? III) Is *DOG1* involved in local adaptation? Preliminary results indicate that genetic differentiation in *DOG1* is higher than expected from neutral markers, especially between different regions. This may indicate the action of natural selection.

14-9 Oral

ECOLOGY OF SELECTION ON DELETERIOUS MUTATIONS IN SUBDIVIDED POPULATIONS: THEORY AND DATA

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Population subdivision can influence selection on deleterious mutations in two ways, one genetic and the other ecological. While the genetic consequences (increased homozygosity) are well known, the ecological consequences have received less attention even though they may be more important. In subdivided populations, fitness can depend on an individual's performance relative to the global average (hard selection) or its fitness relative to the local average (soft selection). These ideas of hard and soft selection are historically associated with the relative strengths of global vs. local density regulation but this connection has not been examined empirically. Here I will present some simple theoretical results of how the "softness" of selection affects mutation load and discuss what types of assumptions have been made in the literature with respect to the "hardness" of selection. Finally, I will present novel data from fly experiments assessing these assumptions for the first time.

14-10 Oral

INTRASPECIFIC ADMIXTURE AND THE STUDY OF SELECTION IN SUBDIVIDED POPULATIONS OF THE EUROPEAN ASPEN *(POPULUS TREMULA)*

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Population geneticists interested in mapping fitness-related variation in the wild have long been aware of the potentially confounding effects of population structure. In contrast, little consideration has been given to the explicit use of intraspecific admixture for mapping fitness-related genes. Current methods of admixture mapping used in human medical genetics utilize the known axis of variation between two divergent gene pools of a subdivided population. This approach holds great potential for studying how natural selection shapes phenotypic and molecular variation in wild animals and plants, but its true potential in evolutionary biology has not yet been assessed. A Europe-wide survey of population structure in *Populus tremula* (European aspen) based on 70 nuclear microsatellites reveals genetic admixture between a Western and an Eastern European lineage of this widespread forest tree in Central Sweden. FST- and diversity-based tests clearly indicate a role for adaptive population divergence operating at this spatial scale. We will discuss the impact of admixture in European aspen in terms of the shapes, variances, and covariances of geographic clines for candidate adaptive traits. We will use these data to highlight the potential of intraspecific admixture for studies of how drift, gene flow, and natural selection shape the phenotypes and genomes of wild species.

14-1 Poster

Multilocus polymorphism in subdivided populations

BÜRGER REINHARD
Universitiy of Vienna, Department of Mathematics, Vienna, Austria

14-2 Poster

Inter- and intrapopulation variation in thermal reaction norms for growth rate: evolution of latitudinal compensation in ectotherms with a genetic constraint

KAZUNORI YAMAHIRA
Niigata University, Department of Environmental Science, Niigata, Japan

14-3 Poster

Phylogeography and diversity of *Ranunculus parnassifolius* (Ranunculaceae)

EDUARDO CIRES, CANDELA CUESTA, ELENA L. PEREDO, MARÍA ÁNGELES REVILLA, JOSÉ ANTONIO FERNÁNDEZ PRIETO
University of Oviedo, Departamento de Biología de Organismos y Sistemas, Oviedo, Spain

14-4 Poster

Ecological genetics of altitudinal adaptation in *Arabidopsis thaliana*

YONGHAI LUO, NICOLAS QUEBRE, ALEX WIDMER, SOPHIE KARRENBERG
ETH Zurich, Department of Integrative Biology, Zurich, Switzerland

14-5 Poster

Patterns of population structure at genetic loci surrounding a gene controlling wing colour pattern in the regionally polymorphic, mimetic butterfly, *Heliconius melpomene*

NICOLA J. NADEAU, CHRIS D. JIGGINS
University of Cambridge, Zoology, Cambridge, United Kingdom

14-6 Poster

How heterogeneity in predation risk has selected for size-dependent social behaviours in subpopulations of a freshwater fish

GWENDOLEN M. RODGERS
University of Leeds, Institute of Integrative and Comparative Biology, Leeds, United Kingdom

14-7 Poster

Adaptation and gene flow in *Philaenus spumarius*, a highly colour-polymorphic species

SOFIA G. SEABRA, JOSE A. QUARTAU, OCTAVIO S. PAULO
Faculdade de Ciencias da Universidade de Lisboa, Centro de Biologia Ambiental / Departamento de Biologia Animal, Lisboa, Portugal

14-8 Poster

Gene flow in *Arabidopsis lyrata* – integrating the effect of seed banks in population substructuring

MOHSEN FALAHATI-ANBARAN[1], SVERRE LUNDEMO[1], JON ÅGREN[2], HANS K. STENØIEN[3]
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[3]*Norwegian University of Science and Technology Museum of Natural History and Archaeology, Section of Natural History Systematics and Evolution Group, Trondheim, Norway*

14-9 Poster

Species range: adaptation in space and time

JITKA POLECHOVA[1], GLENN MARION[2], NICK BARTON[3]
[1]*Institute for Science and Technology, Klosterneuburg, Austria*
[2]*BioSS, Edinburgh, United Kingdom*
[3]*IST Austria , Klosterneuburg, Austria*

14-10 Poster **Temporal rather than spatial fragmentation of breeding activity in Mediterranean Parsley frog**

HELENE JOURDAN-PINEAU, PATRICE DAVID, PIERRE-ANDRE CROCHET

Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier, France

14-11 Poster **Evolution of several adaptive traits under abrupt environmental change: a simulation study**

MARTA BENITO-GARZON[1], PAULINE GARNIER-GERE[2], FREDERIC AUSTERLITZ[1]

[1]Universite Paris-Sud XI, Ecologie Systématique et Evolution, Paris, France
[2]INRA BioGeCo, Bordeaux, France

14-12 Poster **Genetic variation and structure of house sparrow populations: is there an island effect?**

HENRIK JENSEN[1], RUNE MOE[1], ANNA MARIE HOLAND[1], JARLE TUFTO[2], BERNT-ERIK SÆTHER[1]

[1]Norwegian University of Science and Technology, Centre for Conservation Biology Department of Biology, Trondheim, Norway,
[2]Norwegian University of Science and Technology, Centre for Conservation Biology Department of Mathematical Sciences, Trondheim, Norway

14-13 Poster **Natural selection contributes evolution of flowering time genes in *Arabidopsis lyrata***

ESA A. AALTO, ANNE NIITTYVUOPIO, TANJA PYHÄJÄRVI, OUTI SAVOLAINEN

University of Oulu, Department of Biology, Oulu, Finland

14-14 Poster **Adaptive Genetic Diversity of Coniferous Forest Trees of the Italian Alps**

ELENA MOSCA[1], NICOLA LA PORTA[2], GIOVANNI G. VENDRAMIN[3], DAVID B. NEALE[1]

[1]University of California at Davis, Department of Plant Sciences, Davis, United States
[2]Fondazione Edmund Mach Natural Resources, S. Michele, Italy
[3]Consiglio Nazionale delle Ricerche Plant Genetics Institute, Florence division, Sesto Fiorentino, Italy

14-15 Poster **A model for geographic parthenogenesis**

YIXIAN SONG[1], BARBARA DROSSEL[1], IRENE AMENT[2], STEFAN SCHEU[3]

[1]Darmstadt University of Technology, Department of Physics, Darmstadt, Germany
[2]University of Mainz , Department of Physical Chemistry, Mainz, Germany
[3]University of Goettingen, Department of Biology, Goettingen, Germany

14-16 Poster **Allele fixation and genetic diversity in a dynamic landscape**

ROBIN AGUILÉE[1], DAVID CLAESSEN[2], AMAURY LAMBERT[3]

[1]UPMC Universitè Paris 06, Ecology & Evolution Laboratory, Paris, France
[2]Ecole Normale Supérieure CERES-ERTI, Paris, France
[3]UPMC Universitè Paris 06, Laboratoire de Probabilités et Modèles Aléatoires, Paris, France

14-17 Poster **Introduction history of *Plasmodium falciparum* in South America and its adaptation to new host environments**

ERHAN YALCINDAG

Genetique et Evolution des Maladies Infectieuses (GEMI) - IRD Montpellier, France

14-18 Poster **Variation of genetic and phenotypic traits in *Rana arvalis* over habitat mosaic at a fine-grained scale**

ALEX RICHTER-BOIX, MARIA QUINTELA, ANSSI LAURILA
Evolutionary Biology Centre Uppsala University, Department of Population and Conservation Biology, Uppsala, Sweden

14-19 Poster ***Plantago lanceolata* L. as a key species to detect genetic diversity in the context of land use**

STEPHANIE SOCHER, DANI PRATI, MARKUS FISCHER
University of Bern, Institut of Plant Sciences, Department of Plant Ecology, Bern, Switzerland

14-20 Poster **Molecular population genetics of inducible herbivore resistance genes in *Populus tremula***

CAROLINA TEGSTRÖM, PÄR K. INGVARSSON
Umeå University, Department of Ecology and Environmental Science, Umeå, Sweden

14-21 Poster **Effects of migration models on the fixation probability of beneficial alleles in structured populations**

SEVERINE VUILLEUMIER, JÉRÔME GOUDET, NICOLAS PERRIN
University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

14-22 Poster **Population differentiation in the perch. Environmental effects on gene flow?**

SARA BERGEK
Uppsala University, Evolutionary Biology Centre (EBC), Department of Animal Ecology, Uppsala, Sweden

14-23 Poster **Ocellated lizard *Lacerta lepida* variation across Iberian Peninsula: patterns of neutral and adaptive divergence and morphology in structured populations**

VERA L. NUNES[1], MARK A. BEAUMONT[2], ROGER K. BUTLIN[3], OCTÁVIO S. PAULO[1]
[1]Faculty of Sciences of the University of Lisbon, Centre for Environmental Biology / Department of Animal Biology, Lisbon, Portugal
[2]University of Reading, School of Animal and Microbial Sciences, Reading, United Kingdom
[3]University of Sheffield, Department of Animal and Plant Sciences, Sheffield , United Kingdom

14-24 Poster **Population fragmentation and MHC variation in the spotted suslik *Spermophilus suslicus***

JACEK RADWAN[1], ALEKSANDRA BIEDRZYCKA[2]
[1]Jagiellonian Univeristy, Institute of Enviromnetnal Sciences, Krakow, Poland
[2]Polish Academy of Sciences Institute of Nature Preservation, Poland

14-25 Poster **Phenotypic and genetic responses to environmental change in an Alpine caddisfly metapopulation**

LISA N.S. SHAMA, CHRISTOPHER T. ROBINSON
EAWAG, Aquatic Ecology, Duebendorf, Switzerland

14-26 Poster **Can genetic drift explain geographic differentiation of morphological characters in house sparrows?**

ANNA M. HOLAND[1], HENRIK JENSEN[1], JARLE TUFTO[1], RUNE MOE[2], BERNT-ERIK SÆTHER[1]

[1] *Norwegian University of Science and Technology, Centre for Conservation Biology, Department of Biology, Trondheim, Norway*
[2] *University of Oslo, Department of Medical Genetics, Oslo, Norway*

14-27 Poster **Emergence of biological diversity through dispersal evolution in stable patchy habitats**

FRANCOIS MASSOL[1], ANNE DUPUTIE[2], PATRICE DAVID[2], PHILIPPE JARNE[2]
[1] *CEMAGREF, UR HYAX, Aix-en-Provence, France*
[2] *CNRS CEFE, Montpellier, France*

14-28 Poster **Genetic signatures of patch-level dynamics in plant populations with contrasting sexual systems**

GRAZYNA KORBECKA, JOHN R. PANNELL
University of Oxford, Department of Plant Sciences, Oxford, United Kingdom

14-29 Poster **The Genetics of Cold Adaptation in *Drosophila melanogaster*: a gene hunt approach on the X-chromosome**

RICARDO WILCHES, NICOLAS SVETEC, WOLFGANG STEPHAN
University of Munich, Department of Evolutionary Biology, Planegg-Martinsried, Germany

14-30 Poster **A systematic search for signatures of selective sweeps**

ANNA BUENTGE, MEIKE TESCHKE, DIETHARD TAUTZ
Max-Planck-Institute for Evolutionary Biology, Department of Evolutionary Genetics, Ploen, Germany

14-31 Poster **Deep mithocondrial divergence without apparent reproductive isolation in the common redstart *Phoenicurus phoenicurus***

SILJE HOGNER, ARILD JOHNSEN, JAN T. LIFJELD
Natural History Museum, University of Oslo, National Centre for Biosystematics, Oslo, Norway

14-32 Poster **What can Fst make you learn about adaptation and speciation?**

PAULINE GARNIER-GÉRÉ, TIANGE LANG, THIBAUT DECOURCELLE, VALÉRIE LÉGER, FRANÇOIS HUBERT, PIERRE ABADIE, CATHERINE BODÉNÈS, ANTOINE KREMER
INRA - UMR BioGeCo, Bordeaux, France

14-33 Poster **The spread of incompatibility-inducing parasites in sub-divided host populations**

MAX REUTER[1], LAURENT LEHMANN[2], FRÉDÉRIC GUILLAUME[3]
[1] *University College London, Department of Genetics, Evolution and Environment, London, United Kingdom*
[2] *Stanford University, Department of Biological Science, Stnford, United States*
[3] *University of British Columbia, Department of Zoology, Vancouver, Canada*

14-34 Poster High levels of genetic variation in small Atlantic salmon populations

WILLIAM C. JORDAN[1], KATE CIBOROWSKI[1], SONIA CONSUEGRA[2], CARLOS GARCIA DE LEANIZ[3], MARK BEAUMONT[4], JINLIANG WANG[1]

[1]Zoological Society of London, Institute of Zoology, London, United Kingdom
[2]University of Aberystwyth, Institute of Biological, Environmental and Rural Sciences, Aberystwyth, United Kingdom
[3]University of Wales Swansea, Department of Biological Sciences, Swansea, United Kingdom
[4]University of Reading, School of Animal and Microbial Sciences, Reading, United Kingdom

14-35 Poster Migration, selection and levels of genetic diversity in the Little Shearwater, *Puffinus assimilis,* in the NE Atlantic: a multi-locus approach

MONICA C. SILVA[1], PEDRO SILVA[1], NUNO FERRAND[2], MANUELA COELHO[1]

[1]Universidade de Lisboa, Centro de Biologia Ambiental, Lisboa, Portugal,
[2]Universidade do Porto Centro de Investigacao em Biodiversidade e Recursos Geneticos, Porto, Portugal

14-36 Poster Unravelling the evolutionary forces maintaining the patterns of plumage colour variation in pied flycatcher *(Ficedula hypoleuca)* males

PAULA K. LEHTONEN[1], TONI LAAKSONEN[1], ALEXANDR V. ARTEMYEV[2], EUGEN BELSKII[3], CHRISTIAAN BOTH[4], STANISLAV BURES[5], ANDREY V. BUSHUEV[6] INDRIKIS KRAMS[7], MARKO MÄGI[8], JUAN MORENO[9], ANDREAS NORD[10], JAIME POTTI[11], GLENN-PETER SÆTRE[12], PÄIVI M. SIRKIÄ[1], CRAIG R. PRIMMER[1]

[1]University of Turku, Department of Biology, Turku, Finland,
[2]Karelian Research Centre, Russian Academy of Science, Department of Biology, Petrozavodsk, Russia
[3]Russian Academy of Science, Institute of Plant and Animal Ecology, Ekaterinburg, Russia
[4]University of Groningen, Centre for Ecological and Evolutionary Studies, Haren, Netherlands
[5]Palacky University Laboratory of Ornithology, Olomouc, Czech Republic
[6]Moscow State University Department of Vertebrate Zoology, Moscow, Russia
[7]University of Daugavpils, Institute of Systematic Biology, Latvia
[8]University of Tartu, Department of Zoology, Institute of Ecology and Earth Sciences, Tartu, Estonia
[9]Museo Nacional de Ciencias Naturales-CSIC Ecología Evolutiva, Madrid, Spain
[10]Lund University Department of Animal Ecology, Lund, Sweden
[11]Estación Biológica de Doñana-CSIC, Department of Evolutionary Ecology, Sevilla, Spain
[12]University of Oslo Department of Biology, Oslo, Norway

14-37 Poster Assessing the implications of metapopulation dynamics for selection in recently established grayling populations

CLAUDIA JUNGE[1], NICOLA J. BARSON[1], THROND O. HAUGEN[2], ERICA H. LEDER[3], CRAIG R. PRIMMER[3], GLENN-PETER SÆTRE[1], ASBJØRN L. VØLLESTAD[1]

[1]University of Oslo, Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Oslo, Norway
[2]Norwegian Institute for Water Research (NIVA) Unit for Fish Ecology and Aquaculture, Oslo, Norway
[3]University of Turku Department of Biology, Turku, Finland

14-38 Poster Ecological differentiation between coexisting sexual and asexual strains of *Daphnia pulex*

MIKKO LEHTO

University of Fribourg, Department of Biology, Fribourg, Switzerland

14-39 Poster Morph bias of balanaced polymorphisms in subdivided populations with an example from chiral tree snails

PAUL G. CRAZE

University of Sussex, Department of Biology and Environmental Science, Brighton, United Kingdom

14-40 Poster **Reliability of the detection of loci under selection using genome scans**

SAMUEL NEUENSCHWANDER[1], FREDERIC HOSPITAL[2], JEROME GOUDET[1]

[1]University of Lausanne, Department of Ecology & Evolution, Lausanne, Switzerland
[2]UMR Genetique et Diversite Animales INRA, Jouy-en-Josas, France

14-41 Poster **Does phytochrome a contribute to local adaptation in *Arabidopsis lyrata*?**

TUOMAS TOIVAINEN, ANNE NIITTYVUOPIO, TANJA PYHÄJÄRVI, OUTI SAVOLAINEN

University of Oulu, Department of Biology, Oulu, Finland

14-42 Poster **Variation in Inbreeding Effects Resulting from Inter-demic Processes in an Age-Structured Metapopulation of *Silene latifolia***

PETER D. FIELDS, DOUGLAS R. TAYLOR

University of Virginia, Department of Biology, Charlottesville, United States

14-43 Poster **Exploring differential flavonoid production as a mechanism of increased competitive ability in plant invasion**

ANDREA E. BERARDI

University of Virginia, Department of Biology, Charlottesville, United States

14-44 Poster **Local adaptation maintains clinal variation in melanin-based coloration in the European barn owl (*Tyto alba*)**

SYLVAIN ANTONIAZZA, RETO BURRI, LUCA FUMAGALLI, JÉRÔME GOUDET, ALEXANDRE ROULIN

University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

14-45 Poster **Genetic structure of fresh water Atlantic salmon (*Salmo salar*) in Russian Karelia and priorities for conservation**

MIKHAIL YU. OZEROV[1], ALEXEY JE. VESELOV[2], JAAKKO LUMME[3], CRAIG R. PRIMMER[1]

[1]University of Turku, Department of Biology, Turku, Finland
[2]Karelian Research Centre Institute of Biology, Petrozavodsk, Russia
[3]University of Oulu Department of Biology, Oulu, Finland

14-46 Poster **Population Genetic Structure of an Invasive Mixed-Mating Freshwater Snail in the Native and Introduced Range**

KIRSTIN KOPP[1], KIRSTEN WOLFF[2], JUKKA JOKELA[1]

[1]Eawag, Department of Aquatic Ecology, Dübendorf, Switzerland
[2]University of Newcastle School of Biology, Newcastle upon Tyne, United Kingdom

14-47 Poster **The role of gene flow for local adaptation and phenotypic plasticity in island populations of the common frog**

MARTIN I. LIND, FRANK JOHANSSON, DAVID HALL, PÄR K. INGVARSSON

Umeå University, Department of Ecology & Environmental Science, Umeå, Sweden

14-48 Poster **Ecological adaptation of a fresh water snail on Iceland - or is it speciation?**

KIRSTEN KLAPPERT, JUKKA JOKELA

Eawag, Department of Aquatic Ecology, Duebendorf, Switzerland

14-49 Poster **Contrasting quantitative trait and mtDNA divergence in antlion populations along a steep Mediterranean to hyper-arid climatic gradient**

OFER OVADIA, MOR BUCHSHTAV, VADIM KHASDAN
Ben-Gurion University of the Negev, Department of Life Sciences, Beer Sheva, Israel

14-50 Poster **Comparison of genome-wide methods for the detection of selection in subdivided populations**

SIMON BOITARD, CLAUDE CHEVALET
INRA, Department of Animal Genetics, Toulouse, France

14-51 Poster **Are migrations necessary in a recently diverged metapopulation? Outbreeding depression and heterosis in *Triticum aestivum* populations**

YVES ROUSSELLE[1], MATHIEU THOMAS[1], NATHALIE GALIC[1], ISABELLE BONNIN[2], ISABELLE GOLDRINGER[1]
[1]*INRA - CNRS - Université Paris Sud - AgroParisTech, Plant Genetics, Gif sur Yvette, France*
[2]*FRB, Paris, France*

14-52 Poster **Testing the carnivore connection hypothesis in Central Asia**

LAURE SÉGUREL[1], PATRICK PASQUET[1], TATIANA HEGAY[2], ALMAZ ALDASHEV[3], RENAUD VITALIS[1], EVELYNE HEYER[1]
[1]*CNRS - MNHN - Université Paris 7, Department of Ecoanthropology and Ethnobiology, Paris, France*
[2]*Institute of Immunology Uzbek Academy of Sciences, Tashkent, Uzbekistan*
[3]*Institute of Molecular Biology and Medicine National Center of Cardiology and Internal Medicine, Bishkek, Kyrgyzstan*

14-53 Poster **Small-scale spatial and temporal heterogeneity of soil water availability affects floral variation and phenotypic selection on floral traits in *Madia chilensis* (Asteraceae)**

LORENA H. SUAREZ[1], FERNANDA PÉREZ[2]
[1]*Intituto de Ecología y Biodiversidad, Santiago, Chile*
[2]*P. Universidad Católica de Chile Ecología, Santiago, Chile*

14-54 Poster **Adaptive differentiation and hybrid depression between streambed and forest understory species: the role of ecology in maintaining species boundaries**

YUKI MITSUI, HIROAKI SETOGUCHI
Kyoto University, Graduate School of Human and Environmental Studies, Kyoto, Japan

14-55 Poster **Parallel adaptive evolution in Atlantic cod in response to ocean temperature**

IAN R. BRADBURY[1], SOPHIE HUBERT[2], BRENT HIGGINS[3], SHAREN BOWMAN[3], IAN PATERSON[1], PAUL SNELGROVE[4], COREY MORRIS[5], ROBERT GREGORY[5], DAVID HARDIE[6], JEFF HUCTHINGS[7], PAUL BENTZEN[1]
[1]*Dalhousie University, Marine Gene Probe Lab, Halifax, Canada*
[2]*Atlantic Genome Center, Halifax, Canada*
[3]*National Research Council Cod Genome Project, Halifax, Canada*
[4]*Memorial University Ocean Sciences Center, St. John's, Canada*
[5]*Department of Fisheries and Oceans Canada, St. John's, Canada*
[6]*Dalhousie University Oceanography, Halifax, Canada*
[7]*Dalhousie University Biology Department, Halifax, Canada*

14-56 Poster **Molecular evolution of phytochromes in *Cardamine nipponica* (Brassicaceae) suggests involvement of PHYE in local adaptation**

HAJIME IKEDA[1], HIROAKI SETOGUCHI[1], NORIYUKI FUJII[2]
[1]Kyoto University, Graduate school of Human and Enviromental Studies, Kyoto, Japan
[2]Kumamoto University Graduate School of Science and Technology, Kumamoto, Japan

14-57 Poster **A comparison between desert and Mediterranean populations in two antlion species: morphological and life-history aspects**

INON SCHARF[1], IDO FILIN[2], OFER OVADIA[1]
[1]Ben-Gurion University of the Negev, Department of Life Sciences, Beer-Sheva, Israel
[2]University of Helsinki Department of Mathematics and Statistics, Helsinki, Finland

14-58 Poster **Signature of a Selective Sweep in European *Drosophila melanogaster***

ANNEGRET WERZNER[1], LINO OMETTO[2], WOLFGANG STEPHAN[1]
[1]Ludwig-Maximilians-University Munich, Section of Evolutionary Biology, Munich, Germany
[2]University of Lausanne Department of Ecology and Evolution , Lausanne , Switzerland

14-59 Poster **Balancing selection in G-protein coupled receptors of modern humans**

GERALD HECKEL, DANIEL WEGMANN
University of Bern, Institute of Ecology and Evolution, CMPG, Bern, Switzerland

14-60 Poster **Selection on a disease resistance gene in natural populations of self-compatible and self-incompatible *Arabidopsis***

TOVE H. JORGENSEN, BRENT C. EMERSON
University of East Anglia, School of Biological Sciences, Norwich, United Kingdom

Evolutionary transcriptomics

eseb •
12th Congress
Turin 2009

15

Program

Thursday August 27 - **Symposium 15**

Location: Room 4

Evolutionary transcriptomics

Organizers:	*John Parsch, University of Munich, Germany* *Lino Ometto, University of Lausanne, Switzerland*

9.45 - 10.15	**SERGEY V. NUZHDIN** (invited) Evolution of Transcriptome
10.15 - 10.45	**DUCCIO CAVALIERI** (invited) Evolution of transcriptional regulatory networks in yeast populations
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**MEHMET SOMEL** Role of miRNAs in human brain evolution
11.35 - 11.55	**PATRICIA J. WITTKOPP** Using next-generation sequencing to examine cis- and trans-regulatory divergence over evolutionary time
11.55 - 12.15	**CARLOS A. MACHADO** Transcriptome studies of species divergence and hybrid dysfunction in *Drosophila pseudoobscura* and close relatives
12.15 - 12.35	**SÉBASTIEN RENAUT** The ontogeny of adaptive gene expression and hybrid misexpression in whitefish species pairs (*Coregonus* spp. Salmonidae)
12.35 - 12.55	**YANNICK WURM** Caste-specific gene expression during metamorphosis of queen, worker and male fire ants
12.55 - 13.55	*Lunch*

15-1 Oral

EVOLUTION OF TRANSCRIPTOME

Sergey V. Nuzhdin [1]

[1]*University of Southern California,Department of Molecular and Computation Biology, Los Angeles, United States*

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Transcript levels vary among genotypes and diverge between species due to complex interplay of mutation and selection. Here, we describe how transcriptional networks shape this intraspecific variation and result in additive (heritable) and non-additive genetic variances and covariances in transcriptome. We focus on cis and trans components of variation and show how apparent preponderance of trans effects in intraspecific variation but cis effects in interspecific divergence is explained by purely statistical, rather than selection arguments. With *Drosophila* data, we report associations between polymorphisms segregating in cis regulatory regions onto allele-specific expression. With natural *Arabidopsis* allotetraploids, we show how Hill-Robertson effect and Dobzhansky-Muller incompatibilities affect long-term evolution of allele-specific expression.

15-2 Oral

EVOLUTION OF TRANSCRIPTIONAL REGULATORY NETWORKS IN YEAST POPULATIONS

Duccio Cavalieri [1]

[1]*Università degli Studi di Firenze, Dipartimento di Farmacologia, Firenze, Italy*

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The wealth of genomic data generated in the last decade has offered unprecedented opportunities for our understanding of the ecological and evolutionary forces acting on genes on a genomic scale. It is now possible to address how evolution shapes the functional architecture of genomes and how this architecture relates to the evolution of the regulatory networks regulating the expression of genes that make up an organism. Our work focuses on the evolution of gene expression in the wine yeast *S. cerevisiae* comparing intra-specific gene expression with inter-specific gene expression variation. The integration of genetic and genomic data in an ecological perspective shows that most genetic variation in gene expression is dependent on genotype-by-environment interaction. Genes that are not essential for yeast survival and that have paralogs in the genome show at a greater extent genetic variation for transcriptional plasticity. We also show that elimination of some paralogous genes, i.e. *SCO2*, the paralog of *SCO1*, increases yeast fitness in respiratory conditions and is associated with a more efficient utilization of glucose, showing that the lack of selective pressure for respiration allowed the accumulation of potentially harmful mutation in *S.cerevisiae* respiratory genes.

Finally we associate gene expression to fitness and show that extensive genomic rearrangements and mutations in specific metabolic genes can provide an accelerated evolution and allow colonization of new environments and speciation. We speculate that these effects, moving genes from silenced to expressed regions, rather than concerted mutations in gene regulatory sequences, shape transcriptional evolution in a condition dependent manner.

15-3 Oral

ROLE OF miRNAs IN HUMAN BRAIN EVOLUTION

Mehmet Somel [1,2], Hai Y. Hu [1], Yuan Yuan [1], Song Guo [1], Yan Zheng [1], Ying Xu [1],
Michael Lachmann [2], Wei Chen [3], Svante Paabo [2], Philipp Khaitovich [1]

[1]*CAS-MPG Partner Institute for Computational Biology, Shanghai, China*
[2]*Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany*
[3]*Max Planck Institute for Molecular Genetics, Berlin, Germany*

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Micro RNAs (miRNAs) are small RNA species that repress gene expression by interfering with messenger RNA (mRNA) stability and/or translation. While miRNA sequences are highly conserved among species, conservation of miRNA expression profiles and their regulatory functions is yet unknown. We investigated miRNA expression divergence and its influence on the predicted target genes during postnatal brain development and ageing in humans, chimpanzees and rhesus macaques. Using 12 individuals from each species, with ages spanning the respective species' lifespan, we measured miRNA profiles using high-throughput sequencing, and mRNA profiles using microarrays. We find that miRNA expression is on average, more conserved between species, compared to mRNAs. Still, approximately one-third of all miRNAs expressed in brain show significant expression change during lifetime. Notably, for both miRNAs and their mRNA targets, we find a significantly greater expression divergence on the human evolutionary lineage compared to the chimpanzee lineage. Our results suggest that miRNAs may have played an important role in shaping the human specific phenotype.

15-4 Oral

USING NEXT-GENERATION SEQUENCING TO EXAMINE CIS- AND TRANS-REGULATORY DIVERGENCE OVER EVOLUTIONARY TIME

Patricia J. Wittkopp [1], Joseph Coolon [1], Jonathan Gruber [1]

[1]*University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, United States*

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Variable gene expression is a common source of intra- and interspecific diversity. Our research focuses on understanding the genetic mechanisms underlying changes in gene expression and how these mechanisms evolve over time. To a first approximation, variation affecting gene expression can be divided into two classes: *cis* and *trans*. *cis*-regulatory variation affects expression of the gene harboring the variation whereas *trans*-regulatory variation affect expression of one or more other genes in the genome. Previously, we developed an experimental strategy that uses allele-specific expression to distinguish between *cis*- and *trans*-regulatory changes, and used this approach to compare sources of regulatory variation within and between *Drosophila melanogaster* and *Drosophila simulans*. Analysis of 78 genes (using gene-specific Pyrosequencing assays) showed that that *cis*-regulatory divergence explains a much greater proportion of total expression differences between than within species, suggesting that *cis*-regulatory variants may accumulate preferentially over time. To further explore this hypothesis, we are using next-generation sequencing technology to obtain estimates of allele-specific expression that allow us to compare the relative contribution of *cis*- and *trans*-regulatory changes to expression differences genome-wide between strains and species with divergence times ranging from 10,000 to 4 million years ago, replicated in two independent lineages. We are also investigating the mutational sources of regulatory variation by empirically calculating the per-gene “regulatory mutation rate”, assessing dominance of individual regulatory mutations, and elucidating distributions of mutational effects on transcript levels. The latest findings from this research will be presented and discussed.

15-5 Oral

TRANSCRIPTOME STUDIES OF SPECIES DIVERGENCE AND HYBRID DYSFUNCTION IN *DROSOPHILA PSEUDOOBSCURA* AND CLOSE RELATIVES

Carlos A. Machado [1]

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Changes in the timing and level of gene expression have long been suggested to be fundamental for generating evolutionary change and to play a major role in adaptation. Studies of the transcriptome using microarrays and RNA-sequencing are giving us the opportunity to test those suggestions. We have conducted transcriptome studies of species divergence and hybrid dysfunction in *Drosophila pseudoobscura* and its close relatives (*D. persimilis* and *D. p. bogotana*), three classic species for the study of the genetics of speciation that diverged in the last 0.5 Myr. We have uncovered fundamental differences in gene expression and genomic divergence that coupled with physiological studies suggest that ecological differences may have been fundamental for the divergence of *D. pseudoobscura* and *D. persimilis*. Further, we show that in this species group hybrid dysfunction at the transcriptome level does not follow Haldane's rule in three out of four reciprocal hybrid comparisons. An explanation for that pattern is proposed. Finally, we will describe results of sex-biased transcriptome divergence that support sex-specific phenotypic evolution between species.

15-6 Oral

THE ONTOGENY OF ADAPTIVE GENE EXPRESSION AND HYBRID MISEXPRESSION IN WHITEFISH SPECIES PAIRS (*COREGONUS* SPP. SALMONIDAE)

Sébastien Renaut [1], Arne W. Nolte [2], Louis Bernatchez [1]

[1]*Université Laval, Department of Biology, Quebec, Canada*
[2]*Max Planck Institute for Evolutionary Biology, Plon, Germany*

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Genome-wide analyses of the transcriptome have revealed that the interaction of divergent genomes in inter-specific hybrids may cause gene misexpression and consequently underlie reproductive isolation mechanisms. Here, using a 16,006 features cDNA microarray, we compared and contrasted gene expression divergence at two ontogenetic stages in incipient species of normal and dwarf whitefish *(Coregonus clupeaformis)*, to that of first generation (normal X dwarf) and second generation hybrid crosses [backcross: (normal X dwarf) X normal]. Very few transcripts (5 out of 4950 expressed) differed in mean expression level between parental forms at the embryonic stage, in contrast to 16-week old juvenile fish for which 617 out of 5359 transcripts differed significantly. We also found greater evidence for gene misexpression in backcross hybrids whereby non-additivity explained a larger fraction of inheritance patterns in backcross (54%) compared to F1-hybrids (9%). Gene expression was generally more variable in hybrids than in pure crosses and transgressive patterns of expression were ubiquitous in hybrids. In backcross embryos in particular, the expression of three key developmental genes involved in protein folding and mRNA translation was severely disrupted. Accordingly, gene misexpression acting both early in ontogeny on key developmental genes and later, in juvenile fish, on candidate adaptive genes may contribute to the reproductive isolation of incipient species of lake whitefish.

15-7 Oral

CASTE-SPECIFIC GENE EXPRESSION DURING METAMORPHOSIS OF QUEEN, WORKER AND MALE FIRE ANTS

Yannick Wurm [1], John Wang [1], Michael Nicolas [1], Laurent Keller [1]

[1]*University of Lausanne, Department of Ecology & Evolution , Lausanne, Switzerland*

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Ants are among the most successful animals on earth, with societies of a complexity that rivals our own. These societies are characterized by reproductive division of labor between female queens that can live several years and lay thousands of eggs per day, workers that live only a few months and are sterile, and males that live only a few weeks and do not participate in colony tasks. These striking differences in lifespan and roles are echoed by extensive morphological and physiological divergence.

Using the fire ant, *Solenopsis invicta*, we conduct the first genome-wide survey of developmental gene expression levels over 20 time-points from larval to adult stages in workers, queens and males. The degree of caste- and sex-specific gene expression patterns increases during development. This increasing differentiation appears to be linked to caste-specific pulses of gene expression, and we find evidence that Juvenile Hormone (JH) and Ecdysone drive some of these pulses. We characterize the genes putatively regulated by JH and Ecdysone to understand how the roles of these hormones change between castes and during development. Furthermore we identify 20 genes that appear exclusively expressed either in queens or in workers or in males. We propose that some of these genes may be involved in maintaining the caste-differentiated state of cells. Finally, the analysis of recently duplicated genes reveals several cases of genes having evolved caste-specific expression. There is also evidence for positive selection of some of these duplicated genes, suggesting they underwent subfunctionalization and neofunctionalization.

15-1 Poster Expression and molecular evolution of singleton versus duplicate genes in the tetraploid frog *Xenopus laevis*: genomic transitions after genome duplication

FREDERIC JJ. CHAIN, BEN J. EVANS
McMaster University, Department of Biology, Hamilton, Canada

15-2 Poster Of chips and tags - Gene expression studies in New Zealand allopolyploid *Pachycladon*

CLAUDIA VOELCKEL[1], OLIVER DEUSCH[2], PATRICK BIGGS[1], PETER J. LOCKHART[1]
[1]Allan Wilson Centre for Molecular Ecology and Evolution, Palmerston North, New Zealand
[2]Heinrich Heine University Institut fuer Botanik III, Duesseldorf, Germany

15-3 Poster Divergence in gene expression between the closely related plant species *Silene latifolia* and *S. dioica* and their hybrids

ARIA M. MINDER, ALEX WIDMER
ETH Zuerich, Institute of Integrative Biology, Zuerich, Switzerland

15-4 Poster Transcriptional divergence between incipient species of lake whitefish (*Coregonus clupeaformis*, Salmonidae) as seen by massively parallel pyrosequencing

JULIE JEUKENS[1], SÉBASTIEN RENAUT[1], JÉRÔME ST-CYR[1], ARNE W. NOLTE[2], LOUIS BERNATCHEZ[1]
[1]University Laval, Department of Biology, Quebec, Canada
[2]Max Planck Institute for Evolutionary Biology, Plön, Germany

15-5 Poster Digital analysis of adaptive gene expression in two different ecotypes of the three-spined stickleback

TOBIAS L. LENZ[1], CHRISTOPHE EIZAGUIRRE[1], MARTIN KALBE[1], ANNE PLÖTNER[2], MANFRED MILINSKI[1]
[1]Max Planck Institute for Evolutionary Biology, Department of Evolutionary Ecology, Ploen, Germany
[2]GenXPro, Frankfurt Main, Germany

15-6 Poster Role of expression differentiation in adaptation and speciation: comparative analysis of *Drosophila simulans* and *Drosophila sechellia*

FRANÇOIS WURMSER[1], DAVID OGEREAU[1], TRISTAN MARY-HUARD[2], DOMINIQUE JOLY[1], CATHERINE MONTCHAMP-MOREAU[1]
[1]CNRS-UPR9034, Evolution, Genomes and Speciation Laboratory, Gif-sur-Yvette, France
[2]AgroParisTech Statistics and Genomes, Paris, France

15-7 Poster Gene expression variation in African and European populations of *Drosophila melanogaster*

JOHN PARSCH, SARAH SAMINADIN-PETER, STEPHAN HUTTER, WOLFGANG STEPHAN
University of Munich, Department of Biology, Munich, Germany

15-8 Poster **Investigating variation in the transcriptome among human populations**

DAVID A. HUGHES[1], GENEVIEVE L. FAIRBROTHER[2], CARLOS MORENO[3], PHILIPP KHAITOVICH[4], MARK STONEKING[1]

[1]Max Planck Institute for Evolutionary Anthropology, Evolutionary Genetics, Leipzig, Germany
[2]Obstetrics & Gynecology of Atlanta, Atlanta, United States
[3]Emory University School of Medicine Department of Pathology & Laboratory Medicine, Atlanta, United States
[4]CAS-MPG Partner Institute for Computational Biology Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China

15-9 Poster **Selection for transcriptional robustness in the human genome**

BRIAN P. CUSACK[1], PETER F. ARNDT[1], LAURENT DURET[2], HUGUES ROEST-CROLLIUS[3]

[1]Max-Planck Institute for Molecular Genetics, Department Vingron, Berlin, Germany
[2]Université Claude Bernard - Lyon 1 Laboratoire De Biométrie et Biologie Évolutive, UMR CNRS 5558, Lyon, France
[3]Ecole Normale Supérieure Département de Biologie, CNRS UMR 8541, Paris, France

15-10 Poster **Adaptive evolution of male-biased genes in *Drosophila ananassae***

SONJA GRATH, JOHN PARSCH, JOHN F. BAINES

University of Munich (LMU), Section of Evolutionary Biology, Department of Biology, Planegg-Martinsried, Germany

15-11 Poster **Molecular evolution of caste-biased genes in fire ants (*Solenopsis*)**

LINO OMETTO[1], DEWAYNE SHOEMAKER[2], KENNETH G. ROSS[3], LAURENT KELLER[1]

[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland
[2]United States Department of Agriculture, Center for Medical, Agricultural and Veterinary Entomology, Gainesville, United States
[3]University of Georgia Department of Entomology, Athens, United States

15-12 Poster **Sex chromosome evolution and male germline X-inactivation in *Drosophila***

CLAUS KEMKEMER, WINFRIED HENSE, JOHN F. BAINES, JOHN PARSCH

LMU University, Department of Evolutionary Biology, Munich, Germany

15-13 Poster **Z chromosome gene content in birds is shaped by different selective forces in somatic and germ cells**

RADKA STORCHOVA[1], JIRI HEJNAR[2], JIRI PLACHY[2], LIBOR MORKOVSKY[1], PETR DIVINA[3], ROBERT IVANEK[4]

[1]Charles University in Prague, Department of Zoology, Prague 2, Czech Republic
[2]Institute of Molecular Genetics ASCR Department of Cell and Viral Genetics, Prague 4, Czech Republic
[3]Institute of Molecular Genetics ASCR Center for Information Technology, Prague 4, Czech Republic
[4]Institute of Molecular Genetics ASCR Department of Functional Genomics and Bioinformatics, Prague 4, Czech Republic

15-14 Poster **The transcriptomics of the queen's primary sex ratio in invasive fire ants**

MICHIEL B. DIJKSTRA, LAURENT KELLER

University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

15-15 Poster **Transcriptional basis associated with queen acceptance and execution in *Solenopsis invicta***

MINGKWAN NIPITWATTANAPHON, JOHN WANG, LAURENT KELLER

University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

15-16 Poster **Genomic Signatures of Social Evolution in East African Cichlid Fish**

ANNA K. SESSA[1], NINA DUFTNER[1], MICHAEL R. KIDD[1], SUSAN C.P. RENN[2], HANS A. HOFMANN[3]

[1]*University of Texas at Austin, Program in Ecology, Evolution, Behavior, Section of Integrative Biology, Austin, United States*

[2]*Reed College Department of Biology, Portland, OR, United States*

[3]*University of Texas at Austin Program in Ecology, Evolution and Behavior, Section of Integrative Biology; Institute for Cellular and Molecular Biology, Institute for Neuroscience, Austin, United States*

15-17 Poster **Transcriptomics of diet change in herbivorous woodrats *Neotoma***

ELODIE MAGNANOU[1], JAËL MALENKE[2], DENISE M. DEARING[2]

[1]*Laboratoire Arago, FRE 3247 CNRS - Université Paris 6, Banyuls sur Mer, France*

[2]*University of Utah, Biology Department, Salt Lake City, United States*

15-18 Poster **Gene expression analysis identifies functional changes associated with extended longevity in starvation resistant *Drosophila melanogaster***

AGNIESZKA DOROSZUK-VAN DER WURFF[1], MARTIJS J. JONKER[2], NICOLIEN PUL[1], TIMO M. BREIT[2], BAS J. ZWAAN[1]

[1]*Leiden University, Department of Evolutionary Biology, Leiden, Netherlands*

[2]*Universiteit van Amsterdam MicroArray Department, Amsterdam, Netherlands*

15-19 Poster **Old long lived flies retain a young gene expression profile**

PERNILLE SARUP

Aarhus University, Department of Biology, sektion of Genetics and Ecology, Aarhus, Denmark

15-20 Poster **Bgee: integrating ontology and homology for the study of gene expression evolution**

FREDERIC B. BASTIAN[1], GILLES PARMENTIER[1], JULIEN ROUX[1], SEBASTIEN MORETTI[1], VINCENT LAUDET[2], MARC ROBINSON-RECHAVI[1]

[1]*University of lausanne - Swiss Institute of Bioinformatics, Department of Ecology and Evolution, Lausanne, Switzerland*

[2]*Université de Lyon, Institut de Génomique Fonctionnelle de Lyon, ENS Lyon, Université Lyon 1, CNRS, INRA, Institut Fédératif 128 Biosciences Gerland Lyon Sud , Lyon, France*

15-21 Poster **Experimental Design: *in silico* cDNA-AFLPs in Eukaryotes**

KAI N. STÖLTING[1], GERRIT GORT[2], CHRISTIAN WÜST[1], ANTHONY B. WILSON[1]

[1]*University Zürich, Zoological Museum, Zürich, Switzerland*

[2]*Wageningen University & Research Center, Department of Biometris, Wageningen, Netherlands*

15-22 Poster **Evolutionary dynamics of "functional" processed pseudogenes that stabilize Makorin1 mRNAs in mammals**

SATOKO KANEKO[1], YOKO SATTA[2], NAOYUKI TAKAHATA[2]

[1]*Ochanomizu University, Center for Informational Biology, Tokyo, Japan*

[2]*The Graduate University for Advanced Science (Sokendai) Department of Evolutionary Studies of Biosystems, Hayama, Japan*

15-23 Poster **Comparison of gene expression in *Drosophila* embryogenesis: evidence for the hourglass model of development**

ALEX KALINKA, KAROLINA JASTRZEBOWSKA, STEPHAN PREIBISCH, PAVEL TOMANCAK

Max Planck Institute for Molecular Cell Biology and Genetics, Dresden, Germany

Recent advances in macroevolutionary approaches to evolutionary studies

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12th Congress
Turin 2009

16

Program

Thursday August 27 - **Symposium 16**

Location: Room 5

Recent advances in macroevolutionary approaches to evolutionary studies

Organizers: *Francesco Santini, University of California at Los Angeles, United States*

9.45 - 10.15	**JOHN WIENS** (invited) Phylogenies and paradigm shifts in evolutionary biology
10.15 - 10.45	**MICHAEL ALFARO** (invited) Integrating taxonomic and phylogenetic data from incompletely sampled trees in macroevolutionary studies
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**GAVIN H. THOMAS** Patterns and processes of phenotypic diversification
11.35 - 11.55	**MARCIO R. PIE** Intriguing macroevolutionary patterns in large-scale phylogenies
11.55 - 12.15	**JURRIAAN M. DE VOS** Does heterostyly promote rates of diversification in flowering plants? A case study from the primrose family, Primulaceae
12.15 - 12.35	**NIKLAS WAHLBERG** Near demise of nymphalid butterflies at the Cretaceous/Paleogene boundary and subsequent radiation
12.35 - 12.55	**TIM BARRACLOUGH** Species interactions and diversification in the Cape flowering plant biodiversity hotspot
12.55 - 13.55	*Lunch*

16-1 Oral

PHYLOGENIES AND PARADIGM SHIFTS IN EVOLUTIONARY BIOLOGY

John Wiens [1]

[1]*Stony Brook University, Department of Ecology and Evolution, New York, United States*

wiensj@life.bio.sunysb.edu

A major goal of evolutionary biology is to understand the processes that gave rise to the great diversity of life. However, much research in evolutionary biology is focused exclusively on variation within species, and is only indirectly related to explaining patterns of diversity among species. In this talk, I will argue that phylogenies reveal many of the basic evolutionary patterns that we wish to explain. Most importantly, phylogenies can suggest new and unanticipated patterns and thereby lead to new conceptual questions and research program. In this talk, I will try to illustrate these general ideas with examples from my phylogenetic studies of reptiles and amphibians, focusing on the topics of sexual selection, speciation, patterns of species diversity, and morphological character evolution.

16-2 Oral

INTEGRATING TAXONOMIC AND PHYLOGENETIC DATA FROM INCOMPLETELY SAMPLED TREES IN MACROEVOLUTIONARY STUDIES

Michael Alfaro [1], Luke Harmon [2]

[1]*University of California at Los Angeles, Department of Ecology and Evolutionary Biology, Los Angeles, United States*
[2]*University of Idaho, Department of Biological Sciences, Idaho, United States*

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The growing wealth of dated phylogenetic trees has spurred an increase in studies of lineage diversification. Many broad-scale phylogenetic studies adequately resolve splits among major clades but provide poor tip resolution. We introduce MEDUSA (modeling evolutionary diversification using stepwise AIC), a method that integrates the resolved backbone of phylogenetic trees with taxonomic richness data for unresolved tip clades to test macroevolutionary hypotheses. We illustrate the application of this method using several examples from vertebrate macroevolution.

16-3 Oral

PATTERNS AND PROCESSES OF PHENOTYPIC DIVERSIFICATION

Gavin H. Thomas [1]

[1]*Imperial College, NERC Centre for Population Biology, Ascot, United Kingdom*

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Why does phenotypic diversity vary between lineages? Advances in phylogenetics and comparative methods have led to a recent burgeoning of studies on variation in rates of species diversification. By contrast, studies addressing the analogous issue of phenotypic diversification have lagged behind. Powerful new methods, developed by myself and others, provide new insight into the processes that drive extant patterns of morphological, ecological, and behavioural diversity. I will discuss these recent advances with particular reference to variation in rates of phenotypic diversification between clades, and between lineages with different geographic histories, ecology, life-history or behaviour. I will describe several examples of my empirical research including geographic variation in rates of body size diversification in *Anolis* lizards, and ecologically driven increases in the rate of diversification in bill size and shape in hummingbirds. I will conclude by highlighting key avenues for future research into the processes that determine phylogenetic and geographic patterns in phenotypic diversity.

16-4 Oral

INTRIGUING MACROEVOLUTIONARY PATTERNS IN LARGE-SCALE PHYLOGENIES

Marcio R. Pie [1]

[1]*Universidade Federal do Paraná, Departamento de Zoologia, Curitiba, Brazil*

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The availability of comprehensive phylogenies of a variety of animal and plant taxa in recent years has provided unprecedented opportunities to investigate macroevolutionary phenomena. In particular, there has been considerable effort to use phylogenies to identify key adaptations that have promoted the adaptive radiation of different groups, following a tradition that dates back at least to G. G. Simpson and his notion of the occupation of adaptive zones. In this study, we use maximum likelihood methods to demonstrate that shifts in diversification rates do not necessarily result in increases in diversity. Rather, negative shifts seem to be a very pervasive feature during the diversification of a variety of taxa, including flowering plants, ruminants, ants, birds, and frogs. In addition, GLM methods are used to demonstrate a statistically significant phylogenetic signal in diversification rates during the radiation of different organisms, suggesting that diversification potential is itself a biological trait that evolves over time. Moreover, the rate of evolution of diversification potential seems to accelerate over time and might help explain the poor fit of real phylogenies to constant-rate Markov diversification models. These results indicate that considerable insight can be gained from the study of comprehensive phylogenies, including several intriguing and poorly-understood patterns at the interface between micro- and macroevolutionary studies.

16-5 Oral

DOES HETEROSTYLY PROMOTE RATES OF DIVERSIFICATION IN FLOWERING PLANTS? A CASE STUDY FROM THE PRIMROSE FAMILY, PRIMULACEAE

Jurriaan M. de Vos [1], Brian R. Moore [2], Gerald M. Schneeweiss [3], Elena Conti [1]

[1]University of Zurich, Institute for Systematic Botany, Zurich, Switzerland
[2]University of California at Davis, Section of Evolution and Ecology, Davis, United States
[3]University of Vienna, Department of Biogeography, Vienna, Austria

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Understanding the extent to which morphological innovations have contributed to the spectacular radiation of flowering plants has long fascinated evolutionary biologists. Here we adopt a phylogenetic approach to explore the impact of heterostyly on the diversification of Primulaceae. Heterostyly is a reproductive syndrome characterized by species with two (or three) floral morphs that differ in the reciprocal position of male (anther) and female (stigma) reproductive organs. This floral arrangement facilitates outcrossing via precise pollen transfer between morphs: when a pollinator probes a flower of one morph, pollen is deposited on its body at a position that closely matches the position of the stigma in the reciprocal morph. Small differences in anther and stigma height are predicted to increase the probability of speciation via pollinator-mediated isolation, while elevated levels of outcrossing simultaneously reduce extinction risk associated with prolonged periods of selfing. We analyzed chloroplast DNA for 300 species of Primulaceae to test the hypothesis that the evolution of heterostyly is correlated with increased rates of diversification. Our analysis adopts a recently developed Bayesian method that accommodates several inherent sources of uncertainty. This study, representing the first investigation of the evolutionary effects of heterostyly on species diversity, has broad implications across angiosperms, where this trait occurs in 26 families.

16-6 Oral

NEAR DEMISE OF NYMPHALID BUTTERFLIES AT THE CRETACEOUS/PALEOGENE BOUNDARY AND SUBSEQUENT RADIATION

Niklas Wahlberg [1], Julien Leneveu [1], Ullasa Kodandaramaiah [2], Carlos Peña [2], Sören Nylin [2],
André Freitas [3], Andrew V.Z. Brower [4]

[1]*University of Turku, Department of Biology, Turku, Finland*
[2]*Stockholm University, Department of Zoology, Stockholm, Sweden*
[3]*Universidade Estadual de Campinas, Departamento de Zoologia, Campinas, Brazil*
[4]*Middle Tennessee State University, Department of Biology, Murfreesboro, United States*

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The butterfly family Nymphalidae comprises some 6000 species distributed worldwide, with many species familiar to the layperson such as the monarch and the flashy blue morphos. The family contains some of the most important non-drosophilan insect model systems for evolutionary and ecological studies, yet the evolutionary history of the group has remained shrouded in mystery. We have generated a data matrix comprising sequences of 10 protein coding genes and 235 morphological characters for exemplars of 400 of the 540 valid nymphalid genera representing all subfamilies and tribes of the family, based on which we have inferred a robust phylogenetic hypothesis for the family. Using 6 butterfly fossils and the ages of 6 larval food plant families to respectively constrain minimum and maximum clade ages, we infer that Nymphalidae originated in the Cretaceous some 90 million years ago (mya), but that subfamilies began diversifying only after the Cretaceous/Paleogene boundary (KT-boundary; 65 mya). A dispersal-vicariance analysis strongly implies that the common ancestor of Nymphalidae as well as the progenitors of the subfamilies were found in the Neotropical and Oriental regions, suggesting that the common ancestors were widespread on the planet, but that the common ancestors of 10-12 lineages survived the end-Cretaceous catastrophe only in the Neotropical and Oriental regions. Evidence in the shape of the lineages through time plot suggests that the KT-event caused widespread extinction also in nymphalid butterflies.

16-7 Oral

SPECIES INTERACTIONS AND DIVERSIFICATION IN THE CAPE FLOWERING PLANT BIODIVERSITY HOTSPOT

Tim Barraclough [1]

[1]*Imperial College London, Department of Biology, London, United Kingdom*

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The role of competition, pollination and mycorrhizal symbioses in driving diversification of flowering plants are explored using examples from the Cape region of South Africa. Evidence is presented that competition does shape the assembly of local communities, whereas speciation mostly involves geographical isolation and adaptation to new environments. Of several environmental parameters explored, pollinators are shown to be of particular importance. Diversity in mycorrhizal fungal partners is associated with niche partitioning within communities and is evolutionarily conserved, rather than playing a role in speciation events. The findings are placed in the context of how Cape taxa have managed to diversify and persist at such narrow spatial scales.

16-1 Poster **Uniting phylogeography and ecological niche modeling: a case study on the Southern Crested Newt *Triturus karelinii* (Amphibia: caudata)**

BEN WIELSTRA[1], A.G. TOXOPEUS[2], A.K. SKIDMORE[2], J.W. ARNTZEN[1]

[1] *National Museum of Natural History Naturalis, Department of Terrestrial Zoology, Leiden, Netherlands*
[2] *International Institute for Geo-Information Science and Earth Observation, ITC Department of Natural Resources, Enschede, Netherlands*

16-2 Poster **The distribution and coexistence of cryptic amphipod species in Switzerland**

ANJA WESTRAM, IRENE KELLER, JUKKA JOKELA

EAWAG - the Swiss Federal Institute of Aquatic Science and Technology, Department of Aquatic Ecology, Duebendorf, Switzerland

16-3 Poster **Phylogenetic relationships and peri-Tyrrhenian phylogeography in the land snail *Solatopupa* (Gastropoda, Chondrinidae)**

VALERIO KETMAIER[1], FOLCO GIUSTI[2], GIUSEPPE MANGANELLI[2], RALPH TIEDEMANN[1]

[1] *University of Potsdam, Department of Biochemistry and Biology, Potsdam, Germany*
[2] *Università di Siena, Dipartimento di Scienze Ambientali "G.Sarfatti", Siena, Italy*

16-4 Poster **Life history trait evolution in a rapidly radiating Neotropical genus**

ANNE DUPUTIÉ, DOYLE MCKEY[1], JAN SALICK[2]

[1] *CEFE/CNRS UMR5175, Montpellier, France*
[2] *Missouri Botanical Garden Ethnobotany, Saint Louis, United States*

16-5 Poster **Relic population of the moose, Alces alces in the Biebrza valley – analysis of different classes of molecular markers**

MAGDALENA SWISLOCKA[1,2]

[1] *University of Bialystok, Department of Vertebrate Zoology, Bialystok, Poland*
[1] *University of Bialystok, Institute of Biology, Bialystok, Poland*

16-6 Poster **Phylogenetic analyses and mitochondrial gene evolution of the gibbon taxa based on the complete mitochondrial genome sequences**

YI-CHIAO CHAN[1], CHRISTIAN ROOS[2], MIHO INOUE-MURAYAMA[3], EIJI INOUE[4], CHIH-CHIN SHIH[5], KURTIS J.-C. PEI[6], LINDA VIGILANT[1]

[1] *Max Planck Institute for Evolutionary Anthropology, Department of Primatology, Leipzig, Germany*
[2] *German Primate Center , Göttinge , Germany*
[3] *Kyoto University Wildlife Research Center , Kyoto, Japam*
[4] *Kyoto University Graduate School of Science, Kyoto, Japan*
[5] *Taipei Zoo , Taipei, Taiwan*
[6] *National Pingtung University of Science and Technology, Pingtung Rescue Center of Endangered Wild Animals, Pingtung, Taiwan*

16-7 Poster **Phylogeny and biogeography of mammals in Madagascar: a comparative approach**

LUCA POZZI[1,2]

[1] *New York University, Department of Anthropology, New York, United States*
[2] *NYCEP - New York Consortium for Evolutionary Primatology, New York, United States*

16-8 Poster **Explaining patterns of diversity within ray-finned fish**

FRANCESCO SANTINI[1], GIORGIO CARNEVALE[2], LUKE HARMON[3], MICHAEL ALFARO[1]
[1]*University of California, Department of Ecology and Evolutionary Biology, Los Angeles, United States*
[2]*Universita di Pisa, Dipartimento di Scienze della Terra, Pisa, Italy*
[3]*University of Idaho, Department of Biology, Moscow, United States*

16-9 Poster **Positive selection of vertebrate protein coding genes**

MARC ROBINSON-RECHAVI, ROMAIN A. STUDER
Universite de Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

16-10 Poster **Distinct evolutionary patterns of brain and body size during the Tanganyikan cichlid adaptive radiation**

ALEJANDRO GONZALEZ VOYER[1], SVANTE WINBERG[2], NICLAS KOLM[1]
[1]*University of Uppsala, Department of Animal Ecology, Uppsala, Sweden*
[2]*University of Uppsala, Department of Neuroscience, Uppsala, Sweden*

16-11 Poster **Comparing adaptive radiations of cichlid fishes within and across tribes and lakes**

MORITZ MUSCHICK, WALTER SALZBURGER
University of Basel, Zoological Institute, Basel, Switzerland

16-12 Poster **Sources and distribution of the genetic variation in the radiation of Lake Victoria cichlids**

ETIENNE BEZAULT[1,2], SALOME MWAIKO[2,3], OLE SEEHAUSEN[1,2]
[1]*University of Bern, Institute of Ecology and Evolution, Bern, Switzerland*
[2]*EAWAG Centre of Ecology, Department of Evolution and Biogeochemistry, Kastanienbaum, Switzerland*
[3]*Tanzanian Fisheries Research Institute, Dar Es Salaam, Tanzania*

16-13 Poster **Molecular Phylogeny and Node Age Estimation of Lantern Sharks (Elasmobranchii: Etmopteridae)**

NICOLAS STRAUBE[1,2], SAMUEL P. IGLESIAS[3], DANIEL Y. SELLOS[2], JÜRGEN KRIWET[1], ULRICH SCHLIEWEN[2]
[1]*Staatliches Museum für Naturkunde Stuttgart, Palaeontology, Stuttgart, Germany*
[2]*Muséum national d'Histoire naturelle Milieux et Peuplements aquatiques, Concarneau, France*
[3]*Zoologische Staatssammlung München Ichthyology, München, Germany*

16-14 Poster **Old diversity and young species: the Alpine lake whitefish radiation**

ALAN G. HUDSON[1,2], PASCAL VONLANTHEN[1,2], OLE SEEHAUSEN[1,2]
[1]*Universität Bern Division of Aquatic Ecology & Macroevolution, Zoologisches Institut, Bern, Switzerland*
[2]*EAWAG, Centre of Ecology, Evolution and Biogeochemistry, Kastanienbaum, Switzerland*

16-15 Poster **Sturgeon phylogeography in the Ponto-Caspian region: a recent migrations, hybridization, and speciation in the ancient group of vertebrates**

NIKOLAI S. MUGUE[1,2], ANNA BARMINTSEVA[1], NATALIA TIMOSHKINA[3]
[1]*Russian Institute of Fisheries and Oceanography (VNIRO), Laboratory of Molecular genetics, Moscow, Russia*
[2]*Institute of Developmental Biology RAS, Moscow, Russia*
[3]*AzNIRCh, Rostov, Russia*

16-16 Poster **Evolution of plant dispersal abilities on islands: differences between endemic and non-endemic species**

KRISTYNA VAZACOVA[1,2], ZUZANA MÜNZBERGOVA[1,2]
[1]Academy of Sciences of the Czech Republic, Institute of Botany, Pruhonice, Czech Republic
[2]Charles University in Prague, Deparment of Botany, Prague, Czech Republic

16-17 Poster **Rdna- its2 identification of *Hyalomma, Rhipicephalus, Dermacentor* and *Boophilus* spp. (Acari: Ixodidae) collected from different geographical regions of Iran**

MOHAMMAD ABDIGOUDARZI[1], ULRIKE SEITZER[2], JABBAR S. AHMED[2]
[1]Razi Vaccine and Serum Research Institute, Department of Parasitology, Karadj, Iran
[2]Borstel Research Center, Department of Veterinär Infektiologie und Immunologie, Borstel, Germany

16-18 Poster **Social phylogeography of penduline tits: the implications of sexual conflict and parental cooperation**

RENÉ E. VAN DIJK[1], SANDER BOT[2], MARTIN IRESTEDT[3], ÁKOS POGÁNY[4], JAN KOMDEUR[2], PER ERICSON[5], TAMÁS SZÉKELY[1]
[1]University of Bath, Department of Biology and Biochemistry, Bath, United Kingdom
[2]University of Groningen, Animal Ecology Group, Haren, Netherlands
[3]Swedish Museum of Natural History, Laboratory of Molecular Systematics, Stockholm, Sweden
[4]Eotvos Loránd University, God Biological Station, God, Hungary
[5]Swedish Museum of Natural History, Department of Vertebrate Zoology, Stockholm, Sweden

16-19 Poster **Do population genetics processes control diversification rates?**

YAEL KISEL[1,2]
[1]Imperial College London, Department of Life Sciences, London, United Kingdom
[2]Royal Botanic Gardens, Kew, Richmond, United Kingdom

16-20 Poster **Indirect adaptive responses mediated through changes in resource availability by an invasive species**

PHILIPP P. HIRSCH, RICHARD SVANBÄCK, PETER EKLÖV
Uppsala University, Department of Ecology and Evolution, Limnology, Uppsala, Sweden

16-21 Poster **The geographic structure of hybridization in crested newts**

AMY B. BAIRD, GONÇALO E. THEMUDO, J.W. ARNTZEN
Naturalis National Museum of Natural History, Deparment of Terrestrial Zoology, Leiden, Netherlands

16-22 Poster **Cryptic Speciation of Hormogastrid Earthworms in Central Iberian Peninsula is not Related to Soil Properties but to Biogeography**

MARTA NOVO, ROSA M. FERNANDEZ, DOLORES TRIGO, ANA ALMODOVAR, DARIO J. DIAZ COSIN
Universidad Complutense de Madrid, Departamento de Zoologia y Antropologia Fisica, Madrid, Spain

16-23 Poster **Varying rates of diversification in the genus *Melitaea* (Lepidoptera: Nymphalidae) during the past 20 million years**

JULIEN LENEVEU, NIKLAS WAHLBERG
University of Turku, Department of Biology, Turku, Finland

16-24 Poster **Inferring the History of Speciation from Multilocus Sequence and Microsatellite data: the case of the *Microbotryum violaceum* species complex**

PIERRE GLADIEUX, FREDERIC AUSTERLITZ, MICHAEL C. FONTAINE, ELODIE VERCKEN, TATIANA GIRAUD

Université Paris Sud, CNRS, Department of Ecologie Systematique Evolution, Orsay, France

16-25 Poster **Ancient DNA evidence implicates climate, rather than humans, as the driving force behind late Pleistocene musk ox *(Ovibos moschatus)* population dynamics**

PAULA F. CAMPOS[1], BETH SHAPIRO[2], ESKE WILLERSLEV[1], THOMAS P.M. GILBERT[1]

[1]University of Copenhagen, Natural History Museum of Denmark , Copenhagen, Denmark
[2]The Pennsylvania State University, Department of Biology, Pennsylvania, United States

16-26 Poster **Social parasitism in *Myrmica* ants – comparative phylogeography of sister species *M. rubra* and *M. ruginodis***

JENNI M. LEPPÄNEN, RIITTA SAVOLAINEN, KARI VEPSÄLÄINEN

University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland

16-27 Poster ***Ponto-Caspian corophiids (Crustacea, Amphipoda, Corophiidae, Corophiinae):* relationships in the light of molecular phylogeny, morphology, ecology and biogeography**

EKATERINA URYUPOVA[1], NIKOLAI S. MUGUE[2]

[1]Moscow State University, Department of Biology, Moscow, Russia
[2]Koltzov Institute of Developmental Biology RAS, Moscow, Russia

16-28 Poster **New approaches for detecting the causes of differential diversification**

RICHARD G. FITZJOHN, SARAH P. OTTO, WAYNE P. MADDISON

University of British Columbia, Department of Botany and Zoology, Vancouver, Canada

16-29 Poster **Contact zones and phylogeographic break hotspots in the United States**

LESLIE J. RISSLER, WALLY SMITH

University of Alabama, Department of Biological Sciences, Alabama, United States

16-30 Poster **Phylogenetic analysis of actin genes in vascular plants and functional analysis of actin isoforms in the Norway spruce *(Picea abies)* somatic embryogenesis**

ERICA BELLINVIA, LUCAŠ FISCHER, PETRA BOŘÍKOVÁ, ZDENĚK OPATRNÝ

Charles University, Department of Plant physiology, Prague, Czech Republic

16-31 Poster **Does the endemic bat *Myotis goudoti* support the evolution of Madagascar microendemic biota?**

NICOLE WEYENETH[1], STEVEN M. GOODMAN[2], MANUEL RUEDI[1]

[1]Natural History Museum, Department of Mammalogy and Ornithology, Geneva, Switzerland
[2]Field Museum of Natural History Department of Zoology, Chicago, United States

16-32 Poster **Divergence rules in *Aquilegia* radiation: contrasting patterns between North American and Eurasian columbines**

JESUS Mª. BASTIDA, RAFAEL JAIME, JULIO M. ALCÁNTARA, PEDRO J. REY

University of Jaen, Departamento de Biologia Animal, Biologia Vegetal y Ecologia, Jaen, Spain

16-33 Poster **Dating a morphological phylogeny using likelihood-based analysis of its historical biogeography. The Tertiary evolution of the genus *Raymondionymus* (Coleoptera Raymondionymidae)**

DANIELE SILVESTRO[1], MASSIMO MEREGALLI[2], GIUSEPPE OSELLA[3]

[1]*Senckenberg Research Institute,Department of Botany and Molecular Evolution, Frankfurt am Main, Germany*
[2]*Università degli studi di Torino Dipartimento di Biologia Animale e dell'Uomo, Torino, Italy*
[3]*Università de L'Aquila, Department of Environmental Sciences, L'Aquila, Italy*

16-34 Poster **The potential of a new approach to the historical biogeography: an application of *PhyloMapper* method to the genus *Trypocopris* (Coleoptera, Scarabaeidae)**

DANIELE SILVESTRO[1], ASTRID PIZZO[2], CLAUDIA PALESTRINI[2], ANTONIO ROLANDO[2]

[1]*Senckenberg Research Institute, Department of Botany and Molecular Evolution, Frankfurt am Main, Germany*
[2]*Università degli Studi di Torino, Dipartimento di Biologia Animale e dell'Uomo, Torino, Italy*

16-35 Poster **Division Bryophyta: phylogeny and use of DNA barcoding for reconstruction of past ecosystems and modern biodiversity**

ALFONSO ESPOSITO[1,2]

[1]*University of Oslo, Department of Natural History Museum, Oslo, Norway*
[2]*University of Trondheim, Trondheim, Norway*

16-36 Poster **Evolution of trilobite ontogenies**

GIUSEPPE FUSCO[1], GENE HUNT[2], THEODORE GARLAND JR[3], NIGEL C. HUGHES[4]

[1]*University of Padova, Department of Biology, Padova, Italy*
[2]*National Museum of Natural History, Smithsonian Institution, Department of Paleobiology, Washington, United States*
[3]*University of California, Department of Biology, Riverside, United States*
[4]*University of California, Department of Earth Sciencies, Riverside, United States*

16-37 Poster **Morphological and molecular diversity of Transcaucasian Niphargids (Crustacea, Amphipoda)**

DIMITRY M. SCHEPETOV[1], NIKOLAI S. MUGUE[2], STANISLAV I. LJOVUSHKIN[1]

[1]*Moscow State University, Invertebrate Zoology Department, Moscow, Russia*
[2]*Russian Academy of Sciences, Koltzov Institute of Developmental Biology, Moscow, Russia*

16-38 Poster **Evolution of RPCS, the major satellite DNA in rodents from the genus *Ctenomys* (Rodentia, Octodontidae) from the Iberá wetland, Corrientes province, Argentina**

DIEGO A. CARABALLO[1], PABLO M. BELLUSCIO[1], MABEL D. GIMÉNEZ[2], CLAUDIO J. BIDAU[3], PATRICIA M. MIROL[4], JEREMY B. SEARLE[2], MARÍA S. ROSSI[1]

[1]*Facultad de Ciencias Exactas y Naturales, UBA, IFIBYNE-CONICET, LFBM - IFIBYNE, Buenos Aires, Argentina*
[2]*University of York, Department of Biology, York, United Kingdom*
[3]*Instituto Oswaldo Cruz, Departamento de Medicina Tropical, Rio de Janeiro, Brasil*
[4]*Museo Argentino de Ciencias Naturales Bernardino Rivadavia, Sección de Mastozoología, Buenos Aires, Argentina*

16-39 Poster **Diversification of the chamois (genus *Rupicapra*). Discordance between microsatellite and mt-DNA phylogenies**

FERNANDO RODRÍGUEZ, TRINIDAD PÉREZ[1], SABINE HAMMER[2], JESÚS ALBORNOZ[1], ANA DOMÍNGUEZ

[1]*Universidad de Oviedo, Departamento de Biología Funcional, Oviedo, Spain.*
[2]*University of Veterinary Medicine Vienna, Department of Clinical Immunology, Vienna, Austria*

Integrating ecology with parasite evolution

eseb •
12th Congress
Turin 2009

17

Program

Friday August 28 - **Symposium 17**

Location: Room 1

Integrating ecology with parasite evolution

Organizers: *Sarah Reece, University of Edinburgh, United Kingdom*
Jacobus de Roode, Emory University, Atlanta, United States

9.45 - 10.15	**ANNA-LIISA LAINE** (invited) Parasite evolution: the disease triangle re-visited
10.15 - 10.45	**MIKE BOOTS** (invited) Host-parasite coevolutionary dynamics: evolutionary branching and defence against sterilization
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**LAURA C. POLLITT** Responses to competition in the transmission strategies of malaria parasites
11.35 - 11.55	**PEDRO F. VALE** Context dependent virulence-transmission relationships and the evolution of virulence
11.55 - 12.15	**ROMAIN GARNIER** Evolutionary implications of a trasngenerational defence strategy: the maternal transfer of antibodies
12.15 - 12.35	**CLARE L. KINNEAR** Suboptimal typhoid vaccines alter within-host competition dynamics
12.35 - 13.35	*Lunch*
13.35 - 13.55	**MICHAEL BROCKHURST** Coevolution in space: Hotspots, coldspots and pacemakers in experimental selection mosaics
13.55 - 14.15	**CARITA LINDSTEDT** Predation on multiple trophic levels shapes the evolution of pathogen virulence
14.15 - 14.35	**CALDWELL HAHN** Ecological conditions favoring the evolution of stronger immune defenses
14.35 - 14.55	**AMY B. PEDERSEN** Cross species pathogen transmission and disease emergence in primates
14.55 - 15.25	*Coffee break*

17-1 Oral

PARASITE EVOLUTION: THE DISEASE TRIANGLE RE-VISITED

Anna-Liisa Laine [1,2]

[1]*University of Helsinki, Department of Applied Biology, Helsinki, Finland*
[2]*University of Helsinki, Metapopulation Research Group, Department of Biological and Environmental Sciences, Helsinki, Finland*

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While the importance of the environment on infection outcome (infected or not, and severity of infection) was already captured by the classic disease triangle, we have tended to ignore environmental variation in studies of host-parasite coevolution. Long-term studies of the interaction between host plant *Plantago lanceolata* and its obligate fungal parasite, *Podosphaera plantaginis*, coupled with epidemiological data collected annually for nine years from over 3000 host populations, are beginning to show how fundamentally environmental variation may affect trajectories of parasite evolution across all levels. Specific G^H x G^P -interactions are far from being constant as temperature and nutrient availability alter the infection outcome, often through $G^{H/P}$ x E-interactions. As genotype rankings change along environmental gradient, we can better understand how polymorphism is maintained in parasite population. When several parasite strains infect the same host, possibly a major mechanism driving parasite evolution, we find that the outcome of multiple infection is highly context dependent for this interaction. At the metapopulation level, parasite evolution is tightly coupled with its epidemiological dynamics and environment to the extent that parasite adaptation to its host mediated by its adaptation to the local temperature regime. Hence, to fully understand maintenance of genetic diversity in parasite populations, we need to consider parasite dynamics over scales ranging from processes taking place within hosts to metapopulation scales, accounting also for the impact of the environment.

17-2 Oral

HOST-PARASITE COEVOLUTIONARY DYNAMICS: EVOLUTIONARY BRANCHING AND DEFENCE AGAINST STERILIZATION

Mike Boots [1], Alex Best [1], Andy White [2]

[1]*University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom*
[2]*Heriot - Watt University, Mathematics department, Edinburgh, United Kingdom*

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I will present the results of a number of theoretical models that highlight the importance that ecological feedbacks play in evolution of host defence and highligh when co-evolution of the parasite is also vital to the outcome. I will contrast the co-evolutionary dynamics of quantitative resistance in the host and transmission in the parasite with that of infection range and resistance range. Considerable diversity in host defence can be generated and maintained because of the ecological feedbacks in the system and this is much more likely when there is coevolution. In general parasite life-history is highly dependent on that of the host. I will also argue that tolerance rather than resistance is the only method of defence to sterilizing parasites. Throughout I will assume that defence is costly, but I will make the point that the shapes of the trade-off relationships assumed in the models are crucial to the evolutionary outcomes. We have very little information on the shapes of any trade-off in nature and I will argue that this is a crucial gap in our knowledge.

17-3 Oral

RESPONSES TO COMPETITION IN THE TRANSMISSION STRATEGIES OF MALARIA PARASITES

Laura C. Pollitt [1], Nicole Mideo [2], Sarah E. Reece [1]

[1]*University of Edinburgh, Institute of evolutionary biology, Edinburgh, United Kingdom*
[2]*Queen's University, Department of Biology, Kingston, Canada*

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Like all organisms, malaria parasites should maximise fitness by balancing their growth and survival strategies. The best solution to this trade-off is predicted to depend on the social environment and specifically, whether parasites are competing with unrelated strains. While in the vertebrate host malaria parasites must invest in the production of both asexual forms which establish and maintain the infection within the host and gametocytes which provide the potential for transmission. We test theory predicting that parasites should reduce their investment into sexual- relative to asexual-stages when competing with unrelated strains. Our data support this prediction, across several malaria parasite genotypes, revealing that by facultatively lowering investment into reproduction, parasites may be investing more in survival to better compete for red blood cell resources. More broadly, our data provide evidence for the importance of parasites social environment in shaping their life-history trade-offs and how variation in resource availability may explain plasticity in reproductive effort.

17-4 Oral

CONTEXT DEPENDENT VIRULENCE-TRANSMISSION RELATIONSHIPS AND THE EVOLUTION OF VIRULENCE

Pedro F. Vale [1], Tom J. Little [1]

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Predicting how the degree of harm parasites cause their hosts (virulence) evolves is of central importance to studies of coevolution and for the success of some disease control programs. Models consider that virulence evolution is constrained by a trade-off that parasites face between transmission between hosts and growth within hosts. A central assumption is that parasite growth is positively correlated with virulence, and generally, the form of the relationship will critically shape the longer-term evolution of virulence. It has rarely been tested, however, if the nature of the parasite growth and virulence relationship could be context dependent, specifically, whether environmental variation might markedly change the form of the relationship. Yet this seems plausible, given recent work showing pervasive genotype-by-environment interactions in host-parasite systems, for example where the resistance characteristics of particular host genotypes are environment dependent. We tested the assumption of virulence evolution models regarding the expected relationship between growth and virulence under environmental variation. We exposed 8 genotypes of the freshwater crustacean *Daphnia magna* to its bacterial parasite *Pasteuria ramosa* at 15ºC, 20ºC, and 25ºC under limiting or abundant food, and measured host fecundity, mortality and time to castration, and parasite lifetime transmission potential. We demonstrate that under these conditions, the strength and even the direction of parasite growth - virulence relationship can change direction. These results illustrate that the environment-dependent nature of parasitism may limit predictions about the evolutionary outcomes of virulence based on models that assume constant environments.

17-5 Oral

EVOLUTIONARY IMPLICATIONS OF A TRASNGENERATIONAL DEFENCE STRATEGY: THE MATERNAL TRANSFER OF ANTIBODIES

Romain Garnier [1], Thierry Boulinier [1], Sylvain Gandon [1]

[1]*Centre d'Ecologie Fonctionnelle et Evolutive (CEFE), CNRS UMR 5175, Montpellier, France*

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In vertebrate species, mothers can transfer key immunoactive compounds of the acquired immune response, i.e. antibodies, to their offspring. This transfer, and especially the temporary and specific protection it can provide against some parasites, can have profound effects on the phenotype of the offspring. This maternal effect thus has the potential to strongly influence the evolution of host-parasite interactions.

Using a theoretical approach based on a Susceptible Infected Recovered model modified to account for maternal transfer of antibodies, we explored what characteristics of the parasites can explain the evolution of the maternal transfer of antibodies. We show that transgenerational protection of newborns can be an evolutionarily stable strategy depending on both intrinsic and induced costs of this transfer for host individuals and on the characteristics of the parasite. We particularly illustrate the existence of an epidemiological feedback of the virulence of the parasite on the evolution of the maternal transfer of antibodies. We also demonstrate that the maternal transfer of antibodies can interfere with the evolution of a genetic resistance strategy. Finally, our results allow us to outline the potential consequences of the evolution of the maternal transfer of antibodies on the evolution of parasites.

17-6 Oral

SUBOPTIMAL TYPHOID VACCINES ALTER WITHIN-HOST COMPETITION DYNAMICS

Clare L. Kinnear [1], Mark A. Elgar [1], Richard A. Strugnell [2]

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[2]*University of Melbourne, Department of Microbiology and Immunology, Melbourne, Australia*

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The impact of vaccines on the evolution of pathogens, and on the overall effect this may have on the host population is poorly understood. The use of suboptimal vaccines, which offer limited protection, may generate variation in the host environment and consequently alter selective pressures on pathogens. Furthermore, vaccines that prevent host death but not infection may alleviate the high cost of pathogen reproduction on the host. This new selective pressure may influence the pathogen's optimal virulence. Typhoid fever, caused by the intestinal bacterium *Salmonella enterica* serovar Typhi, has been subject to medical interventions for over 100 years, and effective vaccines are regarded as a key feature of disease management. Current typhoid vaccines provide between 33-96% protection, which coupled with different vaccination methods, creates the potential for highly variable host environments. Thus, the host-pathogen interactions in *S. enterica* offer a unique model to investigate the effect of suboptimal vaccination. Experiments using the typhoid mouse model (*Salmonella enterica* serovar Typhimurium) show that mice vaccinated against *S. typhimurium* survive longer post infection than their unvaccinated counterparts, but may develop chronic gut infections, resulting in extended shedding of the bacterium and increased transmission potential. We investigate experimentally how vaccination affects competition dynamics within a single host, and whether vaccination changes the transmission potential to new hosts and the composition of the strains transmitted. Further to this, we have investigated whether different routes of vaccination (either intravenous or oral) produce different outcomes in this system.

17-7 Oral

COEVOLUTION IN SPACE: HOTSPOTS, COLDSPOTS AND PACEMAKERS IN EXPERIMENTAL SELECTION MOSAICS

Michael Brockhurst [1], Andy Fenton [1], Angus Buckling [2], Michael E. Hochberg [3], Tom Vogwill [1]

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Natural populations of hosts and parasites are often spatially structured with patches that vary in the strength of reciprocal selection, so-called coevolutionary hotspots and coldspots with strong or weak reciprocal selection respectively. Theory predicts that dispersal from hotspots should intensify coevolution in coldspots, whereas dispersal from coldspots should weaken coevolution in hotspots, however there have been few empirical tests. We addressed this using paired populations of the bacterium *Pseudomonas fluorescens* and the phage SBW25Φ2 linked by one-way dispersal. Within each population, the strength of reciprocal selection was manipulated by altering the bacteria-phage encounter rate, which changes the rate of coevolution without affecting environmental productivity. We observed that dispersal from hotspots accelerated coevolution in coldspots, while dispersal from coldspots decelerated coevolution in hotspots. These results confirm theoretical predictions of the Geographic Mosaic Theory and suggest that source populations can act as coevolutionary "pacemakers" for recipient populations, overriding local conditions.

17-8 Oral

PREDATION ON MULTIPLE TROPHIC LEVELS SHAPES THE EVOLUTION OF PATHOGEN VIRULENCE

Carita Lindstedt [1], Ville Petri Friman [1], Teppo Hiltunen [1], Jouni Laakso [2], Johanna Mappes [1]

[1]University of Jyväskylä, Department of Bio- and Environmental Science, Centre of Excellence in Evolutionary Research, Jyväskylä, Finland
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The pathogen virulence is traditionally thought to co-evolve through reciprocal selection with its host organism. However, in natural communities, pathogens and hosts are typically embedded within a web of interactions with other species, which could affect indirectly the pathogen virulence and host immunity through trade-offs. Here we show that exposing opportunistic bacterial pathogen, *Serratia marcescens*, to protozoan predation by *Tetrahymena thermophila* decreases its virulence when measured as host moth, *Parasemia plantaginis*, survival. This was probably because the bacterial anti-predatory traits and virulence factors were negatively correlated. However, the host moth survival depended also on its allocation to warning signal used against avian predation. When infected with most virulent ancestral bacterial strain, host larvae with a small warning signal survived better than those with an effective large signal. This suggests that larval immune defence could be traded off with effective defence against bird predators. Our results demonstrate that predation can be important indirect driver of the evolution of both pathogen virulence and host immunity in communities with multiple species interactions. Thus, the pathogen virulence should be viewed as a result of both past evolutionary history, and current ecological interactions.

17-9 Oral

ECOLOGICAL CONDITIONS FAVORING THE EVOLUTION OF STRONGER IMMUNE DEFENSES

Caldwell Hahn [1], Michael H. Kogut [2], William K. Reisen [3]

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The parasitic cowbirds experience intense selection on their immune system as a result of their ecological niche and life history strategy. This New World genus (*Molothrus* spp, Icteridae) includes shiny and brown-headed cowbirds, two generalist brood parasites that lay their eggs in the nests of 200+ species, manipulating other birds to raise their young. Consequently young cowbirds face unique exposure to the diverse species-specific parasites of their foster parents and strong selection on their immune defenses. We show that young cowbirds are exposed to a greater diversity of ectoparasites and blood parasites than are young of non-parasitic species, and we demonstrate that the immune defenses of cowbirds are significantly more effective than those of their non-parasitic relatives. First, we challenged the cowbirds' immune systems with experimental infection with a virulent pathogen, the non-native West Nile virus, and showed that cowbirds are significantly more resistant to WNV than related, non-parasitic birds. Next, we profiled the mechanism of cowbird immunity, their functional innate responses, since innate immunity is responsible for attacking pathogens in the earliest stages of infection and is a critical determinant of a species' disease resistance and susceptibility. We showed that leukocytes isolated from brown-headed cowbirds have significantly greater functional activities than leukocytes from a related non-parasitic species. The cowbirds' niche as brood parasites entails exposure to a parasite-dense environment — the nests and bodies of their foster parent species — and these ecological conditions have shaped the evolution of an enhanced immune system in the cowbirds.

17-10 Oral

CROSS SPECIES PATHOGEN TRANSMISSION AND DISEASE EMERGENCE IN PRIMATES

Amy B. Pedersen [1], Jonathan T. Davies [2]

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Many of the most virulent emerging infectious diseases in humans, e.g. AIDS and Ebola, are zoonotic, having shifted from wildlife populations. A critical question is what determines when and where a disease will first cross from one species to another, and which factors facilitate emergence following a successful host shift. In wild primates, infectious diseases are most often shared between species which are closely related and inhabit the same geographic region. Therefore, humans may be most vulnerable to diseases from the great apes, which include chimpanzees and gorillas, because these species represent our closest relatives. Geographic overlap may provide the ecological opportunity for cross species transmission, but successful infection and establishment will be determined by the biology of both the host and pathogen. Here, we extrapolate the evolutionary relationship between pathogen sharing and divergence time between primates to generate 'hotspot' maps, highlighting regions where the risk of disease transfer between wild primates and from primates to humans is greatest. We find that central Africa and Amazonia are hotspots for cross species transmission events in primates, due to a high diversity of closely related primate species. Hotspots of future emerging infectious diseases in humans will be most likely where humans come into frequent contact with their wild primate relatives, for example, in the forests of central and west Africa. These areas are also likely to sustain a novel epidemic due to their rapidly growing human populations, close proximity to apes, and population centers with high density and contact rates among individuals.

17-1 Poster **Effects of shortened host life span on the evolution of parasite life history and virulence in a microbial host-parasite system**

THIBAULT NIDELET[1], JACOB C. KOELLA[2], OLIVER KALTZ[3]
[1]Universitè Paris Sud/INRA/CNRS/INAPG, UMR de Génétique Végétale, Paris, France
[2]Imperial College London, Division of Biology, London, United Kingdom
[3]Université de Montpellier 2, Institut des Sciences de l'Evolution, UMR 5554, Montpellier, France

17-2 Poster **Genetic diversity in a trypanosome parasite infecting key pollinators**

MARTINA TOGNAZZO, REGULA SCHMID-HEMPEL, PAUL SCHMID-HEMPEL
Institute of Integrative Biology, Department of Environmental Sciences, Zurich, Switzerland

17-3 Poster **The geographic mosaic of the Red Queen: more sex in coevolutionary hotspots**

KAYLA C. KING[1], LYNDA F. DELPH[1], JUKKA JOKELA[2,3], CURTIS M. LIVELY[1]
[1]Indiana University, Department of Biology, Bloomington, United States
[2]EAWAG, Swiss Federal Insitute of Aquatic Science and Technology, Dübendorf, Switzerland
[3]ETH-Zürich, Institute of Integrative Biology, Zürich, Switzerland

17-4 Poster **Effect of temperature fluctuations on dengue virus transmission by *Aedes aegypti***

LOUIS LAMBRECHTS[1,2], LAURA D. KRAMER[3], MATTHEW B. THOMAS[4], THOMAS W. SCOTT[1]
[1]University of California, Department of Entomology, Davis, United States
[2]Centre National de la Recherche Scientifique, Montpellier, Frances
[3]Wadsworth Center, New York State Department of Health Arbovirus Laboratories, Slingerlands, United States
[4]Penn State University, Center for Infectious Disease Dynamics and Department of Entomology, Pennsylvania, United States

17-5 Poster **Comparitive population genetics between bumblebees and their trypanosomatid parasites *Crithidia* reveals frequent horizontal transmission**

SILVIO ERLER, MARIO POPP, MICHAEL G.H. LATTORFF
Martin-Luther-Universität, Institut für Biologie-Zoologie, molek. Ökologie, Halle, Germany

17-6 Poster ***Daphnia* – parasite interactions in a mesocosm metacommunity world**

DINO VERREYDT[1], STEVEN DECLERCK[1], LUC DE MEESTER[1], ELLEN DECAESTECKER[2]
[1]K.U. Leuven, Laboratory of Aquatic Ecology and Evolutionary Biology, Leuven, Belgium
[2]K.U. Leuven, Campus Kortrijk Aquatic Biology, Science & Technology, I.R.C, Kortrijk, Belgium

17-7 Poster **Genotype by environment interactions in the diatom *Asterionella formosa***

ALENA GSELL, BAS IBELINGS, LISETTE DE SENERPONT DOMIS, ELLEN VAN DONK
Netherlands Institute of Ecology, Centre for Limnology, Aquatic Food Web Studies, Nieuwersluis, Netherlands

17-8 Poster **Is the population genetic structure of complex life cycle parasites determined by the geographic range of the most motile host?**

KATJA-RIIKKA LOUHI[1], ANSSI KARVONEN[1], CHRISTIAN RELLSTAB[1], JUKKA JOKELA[2,3]
[1]University of Jyväskylä, Centre of Excellence in Evolutionary Research, Department of Biological and Environmental Science, Jyväskylä, Finland
[2]Eawag, Swiss Federal Institute of Aquatic Science and Technology , Dübendorf, Switzerland
[3]ETH-Zürich, Institute of Integrative Biology, Zürich, Switzerland

17-9 Poster Mixed-Species Parasite Infections in the Mosquito *Aedes aegypti*

ALISON DUNCAN, PHILLIP AGNEW, YANNIS MICHALAKIS, VALERIE NOEL
GEMI, Institute of Research and Development, Montpellier, France

17-10 Poster Parasites modify the host sex-ratio in a bloodsucking insect

CAREZZA BOTTO-MAHAN
Universidad de Chile, Departamento de Ciencias Ecológicas, Facultad de Ciencias, Santiago, Chile

17-11 Poster Host-associated structure as a diversifying mechanism in parasitic organisms; an example involving the seabird tick, *Ixodes uriae*

MURIEL DIETRICH[1], ELENA GOMEZ-DIAZ[1], FLORENT KEMPF[1], JACOB GONZALEZ-SOLIS[2], KAREN D. MCCOY[1], THIERRY BOULINIER[3]
[1]Genetique et Evolution des Maladies Infectieuses, GEMI UMR 2727 CNRS-IRD, Montpellier, France
[2]Universitat de Barcelona, Departamento de Biologia Animal, Barcelona, Spain
[3]Centre d'Ecologie Fonctionnelle et Evolutive, UMR 5175 CNRS, Montpellier, France

17-12 Poster Resource allocation strategies in five species of *Asobara* parasitoid wasps

MAJEED ASKARI SEYAHOOEI
Leiden University, Institute of Biology, Deparment of Animal Ecology, Leiden, Netherlands

17-13 Poster Insecticide resistance as a selective pressure for malaria transmission

JULIEN VEZILIER[1], SYLVAIN GANDON[2], ANTOINE NICOT[1], ANA RIVERO[1]
[1]CNRS Laboratoire de Genetique et Evolution des Maladies Infectieuses (GEMI), Montpellier, France
[2]CNRS Centre d'Ecologie Fonctionnelle et Evolutive (CEFE), Montpellier, France

17-14 Poster Interactions between coinfecting *Borrelia afzelii* strains in wild bank voles *(Myodes glareolus)*

MARTIN ANDERSSON, LARS RÅBERG
Ecology Institution, Department of Animal Ecology, Lund, Sweden

17-15 Poster Ant ecology and the evolution of their *Maculinea* social parasites

LUCA P. CASACCI, FRANCESCA BARBERO, SIMONA BONELLI, EMILIO BALLETTO
Università degli Studi di Torino, Dipartimento di Biologia Animale e dell'Uomo, Torino, Italy

17-16 Poster Local adaptation between a manipulating parasite and its host: contrasted patterns between different components of parasite fitness

THIERRY RIGAUD, NATHALIE FRANCESCHI, STEPHANE CORNET, FRANÇOIS-XAVIER DECHAUME-MONCHARMONT, ALEXANDRE BAUER, LOIC BOLLACHE
Université de Bourgogne, Laboratoire Biogeosciences, UMR CNRS 5561, Dijon, France

17-17 Poster Host-parasite coevolution in an amphipod-acanthocephalan system - susceptibility differences between host populations and species

IRENE KELLER, CAROLINE BAUMGARTNER, ANJA WESTRAM, JUKKA JOKELA
Eawag, Department of Aquatic Ecology, Duebendorf, Switzerland

17-18 Poster Parasite infectivity, virulence and fitness in a multiple-host system

MIKE KELLY[1], MARK BROWN[1,2]
[1]Trinity College Dublin, School of Natural Sciences, Department of Zoology, Dublin, Ireland
[2]University of London, Royal Holloway, School of Biological Sciences, Egham, United Kingdom

17-19 Poster Interaction among temperate phages in polylysogens has strong effects on their fitness and virulence

DOMINIK REFARDT
ETH, Department of Integrative Biology, Zürich, Switzerland

17-20 Poster Maintenance of polymorphism in host-parasite interactions: role of ecological, epidemiological and genetic factors

AURELIEN TELLIER[1], JAMES K.M. BROWN[2]
[1]LMU University of Munich,Department of Evolutionary Biology, Planegg-Martinsried, Germany
[2]John Innes Centre, Department of Disease and Stress Biology, Norwich, United Kingdom

17-21 Poster The Evolution of Diverse Dispersal Mechanisms in *Pseudomonas aeruginosa*

TIFFANY B. TAYLOR
University of Oxford, Department of Zoology, Oxford, United Kingdom

17-22 Poster Nested modelling in evolutionary epidemiology: the case of vector-borne parasites

SAMUEL ALIZON[1], MINUS VAN BAALEN[2,3]
[1]ETH, Institut of Integrative Biologie, Zurich, Switzerland
[2]CNRS UMR 7625, Paris, France
[3]Université Pierre et Marie Curie, ENS, Paris, France

17-23 Poster Coevolution between a plant pathogenic bacteria, *Pseudomonas syringae*, and its local phage population

BRITT KOSKELLA[1], ANGUS BUCKLING[1], JOHN THOMPSON[2]
[1]University of Oxford, Department of Zoology, Oxford, United Kingdom
[2]University of California, Department of Biology, Santa Cruz, United States

17-24 Poster Climate change and disease risks in aquatic systems

ANSSI KARVONEN[1], PAIVI RINTAMAKI[2], JUKKA JOKELA[3], TELLERVO E. VALTONEN[1]
[1]University of Jyvaskyla, Department of Biological and Environmental Science, Jyvaskyla, Finland
[2]University of Oulu, Department of Biology, Oulu, Finland
[3]Institute of Integrative Biology (IBZ), EAWAG, ETH-Zurich, Department of Aquatic Ecology, Zurich, Switzerland

17-25 Poster The parasite-induced cost of being common varies across environments: evidence from natural *Daphnia* populations

JUSTYNA WOLINSKA[1], JAROMIR SEDA[2], PIET SPAAK[3], ADAM PETRUSEK[4]
[1]Ludwig-Maximilians-University, Department of Evolutionary Ecology, Munich, Germany
[2]Biological Centre AS CR, Institute of Hydrobiology , Ceské Budejovice, Czech Republic
[3]Eawag, Department of Aquatic Ecology, Duebendorf, Switzerland
[4]Charles University, Department of Ecology, Prague, Czech Republic

17-26 Poster Navigating a complex life cycle: when should parasites move between hosts?

DANIEL BENESH
Max Planck Institute for Evolutionary Biology, Department of Evolutionary Ecology, Plön, Germany

17-27 Poster Immunodepression and virulence in a crustacean host-acanthocephalan parasite system

STEPHANE CORNET
Université de Bourgogne, UMR CNRS 5561, Biogeosciences Ecologie Evolutive, Dijon, France

17-28 Poster **Genetic response of host-parasitoid insect populations to climate change**

PATRICIA GIBERT, FREDERIC FLEURY, ROLAND ALLEMAND
University Lyon1, CNRS UMR 5558, Biometrie Biologie Evolutive, Villeurbanne, France

17-29 Poster **The effects of predation on a host's life-history and on its ectoparasites**

MICHAEL COSLOVSKY
University of Bern, Institute of Ecology and Evolution, Bern, Switzerland

17-30 Poster **Living with the Consequences - The Maintenance of Variation in Host Tolerance**

ALEX BEST[1], ANDY WHITE[2], MIKE BOOTS[1]
[1]University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom
[2]Heriot-Watt University, Department of Mathematical Sciences, Edinburgh, United kingdom

17-31 Poster **Antagonistic coevolution in a heterogeneous environment: impact of multiple stresss on bacteria-bacteriophage coevolution**

TIMOTHÉE POISOT, MICHAEL E. HOCHBERG
CNRS Université Montpellier 2 Génétique et environnement, Institut des sciences de l'évolution, Montpellier, France

17-32 Poster **Strain-specific interactions among co-infecting parasites: a mechanism maintaining genetic variation?**

OTTO SEPPÄLÄ[1], ANSSI KARVONEN[2], KATJA-RIIKKA LOUHI[2], CHRISTIAN RELLSTAB[2], TELLERVO VALTONEN[2], JUKKA JOKELA[1]
[1]EAWAG / ETH-Zuerich, Department of Aquatic Ecology, Duebendorf, Switzerland
[2]University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland

17-33 Poster **Maternal antibody transmission in the zebra finch *(Taeniopygia guttata)***

SANDRA CHIRIAC
Lund University, Department of Animal Ecology, Lund, Sweden

17-34 Poster **To defeat your enemy, defeat your parasites first - divergence in prevalence to malaria parasites in competing flycatcher species**

KATARZYNA KULMA, ANNA QVARNSTRÖM
Uppsala Universitet, Department of Animal Ecology, Uppsala, Sweden

17-35 Poster **Evolution of virulence in a spore-producing pathogen: a resource allocation dilemma**

AUDREY ANDANSON[1,2], FABIEN HALKETT[1], VIRGINIE RAVIGNÉ [2]
[1]INRA UMR 1136, Nancy, France
[2]CIRAD UMR BGPI, Montpellier, France

17-36 Poster **Strain 'filtering' and transmission of a mixed infection in a social insect**

YUKO ULRICH, PAUL SCHMID-HEMPEL
ETHZ D-UWIS, Zurich, Switerland

17-37 Poster **Recent evidence for the maintenance of autumn colours by host-parasite signaling**

MARCO ARCHETTI[1,2]
[1]University of Oxford, Department of Zoology, Oxford, United Kingdom
[2]Harvard University, Cambridge, United States

17-38 Poster **Host range determinants of a microsporidian parasite**

BENJAMIN LANGE[1,2], DIETER EBERT[1]
[1]*Universität Basel, Zoologisches Institut, Basel, Switzerland*
[2]*K.U. Leuven Campuskortrijk, Department of Science and Technology, I.R.C., Leuven, Belgium*

17-39 Poster **Genetic diversity in the SIR model of pathogen evolution**

ISABEL GORDO[1], GABRIELA GOMES[1], DANIEL REIS[1], PAULO R. CAMPOS[2]
[1]*Instituto Gulbenkian de Ciencia, Oeiras, Portugal*
[2]*Universidade Federal Rural de Pernambuco, Departamento de Fisica, Pernambuco, Brazil*

17-40 Poster **Maintenance of genetic polymorphism in a host-parasite system: an experimental evolution approach**

CAMILLO BERENOS, MATHIAS K. WEGNER, PAUL SCHMID-HEMPEL
ETH Zuerich Experimental Ecology, IBZ, Zuerich, Switzerland

17-41 Poster **Population genetics of an epidemic in a natural plant-pathogen system**

CONSTANCE XHAARD[1], BENOIT BARRES[2], FABIEN HALKETT[1], PASCAL FREY[1]
[1]*INRA, UMR 1136, Interaction Arbres-Microorganismes, Champenoux, France*
[2]*CIRAD BGPI, Montpellier, France*

17-42 Poster **Genetics and adaptation of *Fasciola hepatica* to its intermediate hosts**

ANA C. CORREA, SYLVIE HURTREZ-BOUSSÈS
GEMI UMR 2724 CNRS-IRD, Institute de Recherche pour le Développement, Montpellier, France

17-43 Poster **Temperature dependent infectivity and virulence**

DESIREE E. ALLEN, TOM V. LITTLE
University of Edinburgh, Department of Ecology Evolution and Behaviour, Edinburgh, United Kingdom

17-44 Poster **Clinal variation in Triatomine bugs: studies between urban and rural populations of *Panstrongylus geniculatus***

MARCOS A. MANZANARES
Universidad Central de Venezuela, Facultad de Ciencias, Instituto de Zoología Tropical, Caracas, Venezuela

17-45 Poster **Informative collage in a molecular phylogeny of mosquito vectors using mitochondrial and ribosomal DNA: speciation and co-evolution virus-vector**

JUAN-CARLOS NAVARRO-CASTRO[1], GABRIELA RANGEL-DIA[1], CAMILA HERNANDEZ[1], SCOTT WEAVER[2]
[1]*Universidad Central de Venezuela, IZT, Laboratorio de Biología de Vectores Unidad de Entomologia Molecular, Caracas, Venezuela*
[2]*University of Texas, Medical Branch Center for Biodefense and Emerging Infectious Diseases, Galveston, United States*

17-46 Poster **Ecological and Evolutionary Determinants of Disease Distribution in a Natural Host-Pathogen System**

JESSICA L. ABBATE
University of Virginia, Department of Biology, Charlottesville, United States

17-47 Poster **Relating the liver damage with hepatitis C virus polymorphism in HIV-1-coinfected patients**

JOSÉ A. CASTRO[1], ANDRÉS MOYA[2], ANTONI PAYERAS[3], ANTONI BASSA[3], ANTONIA PICORNELL[1], CARMEN CIFUENTES[3], FRANCISCO X. LÓPEZ-LABRADOR[2], MARIA M. RAMON[1], MARINA MATAS[1], FRANCESC HOMAR[3]
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[2]Universitat de València, Institut Cavanilles de Biodiversitat i Biologia Evolutiva, València, Spain
[3]Hospital Son Llàtzer, Unitat de malalties infeccioses, Palma de Mallorca (Illes Balears), Spain

17-48 Poster **Sex-specific adaptation of the parasite *Pasteuria ramosa* and female weakness of its host *Daphnia magna***

DAVID DUNEAU, PEPIJN LUIJCKX, DIETER EBERT
University of Basel, Zoological institute, Basel, Switzerland

17-49 Poster **Distribution and prevalence of avian malaria in European blue tit populations**

ESZTER SZÖLLÖSI[1], MARIUSZ CICHOŃ[2], MARCEL EENS[3], DENNIS HASSELQUIST[4], BART KEMPENAERS[5], SANTIAGO MERINO[6], JAN-ÅKE NILSSON[4], BALÁZS ROSIVALL[1], SEPPO RYTKÖNEN[7], JÁNOS TÖRÖK[1], MATT WOOD[8], LÁSZLÓ Z. GARAMSZEGI[3]
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[2]Jagiellonian University, Institute of Environmental Sciences, Kraków, Poland
[3]University of Antwerp, Department of Biology, Wilrijk, Belgium
[4]Lund University, Department of Animal Ecology, Lund, Sweden
[5]Max Planck Institute for Ornithology Behavioural Ecology and Evolutionary Genetics, Seewiesen, Germany
[6]Museo Nacional de Ciencias Naturales, Departamento de Ecología Evolutiva, Madrid, Spain
[7]University of Oulu, Department of Biology, Oulu, Finland
[8]Edward Grey Institute of Field Ornithology, Department of Zoology, Oxford, United Kingdom

17-50 Poster **Influence of ecological specialisation in an insect on the genetic diversity and structure of its parasitoid**

EMILIE DION, JEAN-CHRISTOPHE SIMON, YANNICK OUTREMAN
Agrocampus Ouest -Université de Rennes 1, UMR 1099, Biologie des Organismes et des Populations appliquée à la Protection des Plantes, Le Rheu, France

17-51 Poster **The effect of environmental conditions on two measures of immunity in the Indian meal moth, *Plodia interpunctella***

ALISON M. TRIGGS
Queen Mary University of London, School of Biological and Chemical Sciences, London, United Kingdom

17-52 Poster ***Daphnia magna* infected by *Pasteuria ramosa* regain reproduction: a negative correlation between parasite and host fitness**

JON MAGEROY, ELDFRID J. GREPPERUD
University of Bergen, Institute of Biology, Bergen, Norway

17-53 Poster **The influence of a non-natural stress factor on parasite susceptibility**

CLAUDIA BUSER[1,2], MIEKE JANSEN[3], LUC DE MEESTER[3], PIET SPAAK[1]
[1]Eawag, Department of Aquatic Ecology and Evolution, Duebendorf, Switzerland
[2]ETH, Zürich, Switzerland
[3]Katholieke Universiteit Leuven, Aquatic Ecology & Evolution, Leuven, Belgium

17-54 Poster **What makes a host profitable? Parasites balance host nutritive resources against immunity**

PIERRE BIZE

University of Lausanne, Department of Ecology & Evolution, Lausanne, Switzerland

17-55 Poster **Environment matters: temperature and nutrients modify host-parasite interactions in hybridizing *Daphnia***

CORINE SCHÖBEL[1,2], JUSTYNA WOLINSKA[3], PIET SPAAK[1,2]

[1]Eawag, Department of Aquatic Ecology & Evolution, Dübendorf, Switzerland
[2]ETH- Zürich, Institute of Integrative Biology, Zürich, Switzerland
[3]LMU Munich Institute of Ecology, Department of Biology II, Planegg-Martinsried , Germany

17-56 Poster **Limited dispersal helps preserve genetic polymorphism in coevolving plant-pathogen recognition genes**

SAM DOBBIE, JAMES K.M. BROWN

John Innes Centre, Department of Disease and Stress Biology, Norwich, United Kingdom

17-57 Poster **Does host resistance modulate parasite investment in sexuality by altering its virulence components?**

JULIE CLEMENT, BRUNO MARQUER, HÉLÈNE MAGALON, DIDIER ANDRIVON

INRA UMR 1099, Rennes, France

17-58 Poster **MHC II diversity and parasite load in Collared Flycatcher *Ficedula albicollis***

MAGDALENA M. ZAGALSKA-NEUBAUER[1,2], JACEK RADWAN[1], KATARZYNA KULMA[3], LARS GUSTAFSSON[3], MARIUSZ CICHON[1], WIESLAW BABIK[1]

[1]Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland
[2]Museum and Institute of Zoology, PAS, Warsaw, Poland
[3]Uppsala University, Department of Animal Ecology, Uppsala, Sweden

17-59 Poster **Host exploitation strategies in two strains of the rodent malaria, *Plasmodium chabaudi***

NICOLE MIDEO[1], ANDREW F. READ[2], PETRA SCHNEIDER[3], SARAH E. REECE[3], TROY DAY[4]

[1]Queen's University, Department of Biology, Kingston, Canada
[2]Pennsylvania State University, Department of Biology and Entomology, University Park, United States
[3]University of Edinburgh School of Biological Sciences, Edinburgh, United Kingdom
[4]Queen's University, Department of Mathematics and Statistics, Kingston, Canada

17-60 Poster **Blunt egg pole characteristics as a signature of bird species identity**

LENKA POLACIKOVA, TOMAS GRIM

Palacky University, Department of Zoology and Laboratory of Ornithology, Olomouc, Czech Republic

17-61 Poster The life of a dead ant - expression of an adaptive extended phenptype

SANDRA B. ANDERSEN[1], SYLVIA GERRITSMA[2], KALSUM M. YUSAH[3], DAVID MAYNTZ[4], NIGEL L. HYWEL-JONES[5], JOHAN BILLEN[6], JACOBUS J. BOOMSMA[1], DAVID P. HUGHES[7,8]

[1]*University of Copenhagen, Centre for Social Evolution, Department of Biology, Copenhagen, Denmark*
[2]*University of Groningen, Centre for Ecological and Evolutionary Studies, Groningen, Netherlands*
[3]*University of Cambridge, Insect Ecology Group, Cambridge, United Kingdom*
[4]*University of Aarhus, Department of Biological Sciences, Aarhus, Denmark*
[5]*National Centre for Genetic Engineering and Biotechnology Mycology Laboratory, Pathum Thani, Thailand*
[6]*University of Leuven, Zoological Institute, Leuven, Belgium*
[7]*University of Exeter, School of Biosciences, Exeter, United Kingdom*
[8]*Harvard University, Cambridge, United States*

17-62 Poster Role of biotic interactions in microbial adaptation

MIGLA MISKINYTE[1], IRIS CARAMALHO[2], SARA MAGALHÃES[3], ISABEL GORDO[1]

[1]*Instituto Gulbenkian de Ciência, Department of Evolutionary Biology, Oeiras, Portugal*
[2]*Instituto Gulbenkian de Ciência, Centro de Biologia Ambiental, Lisbon, Portugal*
[3]*Universidade de Lisboa Faculdade de Ciências, Centro de Biologia Ambiental, Lisbon, Portugal*

17-63 Poster The Consequences of Double Infections on the Expression and Evolution of Virulence

FRIDA BEN-AMI[1], THIERRY RIGAUD[2], DIETER EBERT[1]

[1]*Universität Basel, Zoologisches Institut Evolutionsbiologie, Basel, Switzerland*
[2]*Université de Bourgogne, Equipe Ecologie Evolutive, Laboratoire Biogéosciences, Dijon, France*

Frontiers in speciation research: proximal and causal mechanisms of behavioural divergence

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12th Congress
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18

Program

Friday August 28 - **Symposium 18**

Location: Room 2

Frontiers in speciation research: proximal and causal mechanisms of behavioural divergence

This Symposium is supported by the European Networking Programme on Frontiers in Speciation Research (FroSpects) coordinated by the European Science Foundation (ESF).

Organizers: *Carole Smadja, University of Sheffield, United Kingdom*
Anneli Hoikkala, University of Jyväskylä, Finland
Roger Butlin, University of Sheffield, United Kingdom
Co-organizer: *Axel Meyer, University of Konstanz, Germany*

9.45 - 10.15	**JEFFREY L. FEDER** (invited) On the Scent of Speciation: Fruit Odor Discrimination and Sympatric Host Race Formation in the Apple Maggot Fly
10.15 - 10.45	**MARK BLOWS** (invited) Microevolutionary Approaches to Understanding how Sexual Selection Generates Phenotypic Divergence
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**KATIE PEICHEL** (ESF – FroSpects invited speaker) Sex chromosome turnover and the evolution of behavioral isolation in a stickleback species pair
11.35 - 11.55	**GLENN-PETER SÆTRE** (ESF – FroSpects invited speaker) Mating behaviour in a flycatcher hybrid zone - divergence, convergence and the process of speciation
11.55 - 12.15	**FLORIAN P. SCHIESTL** (ESF – FroSpects invited speaker) Floral signals, pollinator behaviour, and floral isolation in plants
12.15 - 12.35	**GENEVIEVE M. KOZAK** Learned conspecific mate preference in a species pair of sticklebacks
12.35 - 13.35	*Lunch*
13.35 - 13.55	**ASTRID T. GROOT** What role does phenotypic plasticity play in intraspecific variation in moth pheromone communication signals?

13.55 - 14.15	**RICHARD M. MERRILL** Genetic linkage of speciation genes in *Heliconius* facilitates ecological speciation
14.15 - 14.35	**AMANDA J. MOEHRING** Variation in behavioral isolation loci in *Drosophila*
14.35 - 14.55	**THOR VEEN** Conflict between sexual selection signals and species recognition
14.55 - 15.25	*Coffee break*

18-1 Oral

ON THE SCENT OF SPECIATION: FRUIT ODOR DISCRIMINATION AND SYMPATRIC HOST RACE FORMATION IN THE APPLE MAGGOT FLY

Jeffrey L. Feder [1,2], Charles Linn [3], Andrew A. Forbes [1], Wendell Roelofs [3]

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Speciation occurs as inherent barriers to gene flow evolve between previously interbreeding populations. To elucidate the origins of species therefore requires understanding how and why new traits arise that reproductively isolate taxa. In this seminar, I will discuss how chemical ecology and the evolution of olfactory discrimination for fruit volatiles have played major roles in a textbook example of incipient speciation happening in real time in our own backyards. The *Rhagoletis pomonella* sibling species complex is a model for sympatric speciation via host plant shifts. The recently derived apple *(Malus pumila)*-infesting population of *R. pomonella*, which originated via a shift from hawthorn (*Crataegus* spp.) in the mid-1800s in the northeastern United States, represents an example of host race formation in action, the hypothesized initial stage of sympatric speciation. Host specific mating is a critical feature of *Rhagoletis* biology since these flies mate exclusively on or near the unabscised fruit of their respective host plants. Differences in host preference translate therefore directly into mate choice and premating reproductive isolation. Studies on the characterization of host fruit volatiles for apple-, hawthorn-, and flowering dogwood-infesting populations of *Rhagoletis* have shown that the flies use fruit odor as a key olfactory cue to help distinguish among their respective plants. In flight-tunnel assays and field tests, apple, hawthorn, and flowering dogwood flies all preferentially oriented to, and were captured with, chemical blends of their natal fruit volatiles. The flies also were antagonized by the blends of their non-natal host fruit, suggesting that both preference and avoidance behaviors evolve quickly following host shifts. Flies of mixed apple and hawthorn ancestry were also tested to investigate the genetics and physiological bases for odor preferences. A major unexpected result from these studies was that F1 hybrids do not respond to the volatiles of any parental race. The lack of hybrid behavioral response suggests the possibility that the evolution of avoidance behavior may represent a previously unrecognized post-zygotic barrier to gene flow during sympatric speciation; hybrids formed if and when flies cross mate in nature may be behaviorally sterile and suffer reduced fitness because they have an impaired ability to find and locate host fruit for mating and oviposition. A remaining outstanding question is whether changes in the odor receptors in the antenna or in the way that input signals are integrated and interpreted in the brain underlies the evolution of chemosensory discrimination of *Rhagoletis* flies for their respective fruit volatiles.

18-2 Oral

MICROEVOLUTIONARY APPROACHES TO UNDERSTANDING HOW SEXUAL SELECTION GENERATES PHENOTYPIC DIVERGENCE

Mark Blows [1]

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Phenotypic divergence resulting from sexual selection is an important component of a number of possible mechanisms of speciation, and the intensity of sexual selection predicts diversity within some taxonomic groups. In particular, female preference for arbitrary male traits, in combination with genetic drift, has the potential to generate a diverse array of phenotypic outcomes. Sexual selection has consequently been thought to be particularly effective at generating phenotypic divergence. A framework based on quantitative genetic theory is outlined that allows the empricial determination of the effectiveness of sexual selection in generating phenotypic divergence among populations. This framework is applied to nine natural populations of *Drosophila serrata*, a species in which females exhibit mating preferences for male cuticular hydrocarbons (CHCs). The null hypothesis that male CHCs have diverged among populations solely as a consequence of genetic drift can be rejected for these populations based on a multivariate Q_{st}/F_{st} comparison. Female preferences have also diverged among populations, and can be attributed mainly to the process of reinforcement. Although the divergence in female preference explains a considerable proportion of the divergence in male CHCs among populations, the direction of population divergence has been substantially biased by the underlying genetic variance-covariance structure of the male traits. The general conclusion from these works is that male traits and female preferences have diverged among these natural populations, but have done so in response to a specific selective force and in a manner that is constrained by the available patterns of genetic variation, rather than in arbitrary directions.

18-3 Oral

SEX CHROMOSOME TURNOVER AND THE EVOLUTION OF BEHAVIORAL ISOLATION IN A STICKLEBACK SPECIES PAIR

Katie Peichel [1], Jun Kitano [1], Joseph A. Ross [1], Seiichi Mori [2]

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Threespine sticklebacks (*Gasterosteus aculeatus*) are well suited for identifying the selective forces and genetic mechanisms that underlie the evolution of reproductive isolation between species. Throughout the range of this small teleost fish, there are multiple, independent pairs of recently diverged populations that share overlapping habitats, yet are reproductively isolated. In Japan, there is a unique stickleback species pair, consisting of the Pacific Ocean and Japan Sea species, which have diverged within the past two million years. These two species can be found breeding in overlapping habitats, but rarely hybridize. We have shown that striking differences in male mating behaviors as well as hybrid male sterility contribute to reproductive isolation between this species pair. Recently, we have used SNP genotyping arrays and genetic linkage analysis to identify genomic regions that contribute to reproductive isolation between the Japan Sea and Pacific Ocean sticklebacks. We mapped hybrid male sterility to the threespine stickleback X chromosome (LG19), while divergence in male mating behaviors maps to chromosome 9 (LG9). Interestingly, one copy of LG9 has fused to the Y chromosome specifically in Japan Sea males, creating an X_1X_2Y sex chromosome system in this species. It has been suggested that sexually antagonistic selection might promote sex chromosome turnover between closely related species. Thus, linkage of male behavioral traits might have actually promoted the spread of the Y-autosome fusion in the Japan Sea population. These data provide the first empirical evidence linking sex chromosome turnover to the evolution of behavioral reproductive isolation between closely related species.

18-4 Oral

MATING BEHAVIOUR IN A FLYCATCHER HYBRID ZONE - DIVERGENCE, CONVERGENCE AND THE PROCESS OF SPECIATION

Glenn-Peter Sætre [1]

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The Central European hybrid zone of the collared flycatcher *(Ficedula albicollis)* and the pied flycatcher *(F. hypoleuca)* has become known to provide a convincing example of the process of reinforcement in speciation. A sympatric divergence in male plumage traits helps species recognition and reduces the frequency of maladaptive hybridization. In this talk I present published and unpublished results on mate advertisement and mate choice behaviour in the two species from sympatric populations and compare these with similar data from allopatric populations. Some behavioral traits, such as female preferences for male pluage traits and male courtship displays appear to have diverged in sympatry as predicted from the reinforcement hypothesis, whereas other traits, including male territorial song, appear to have converged or show a more complex pattern of geographic variation. I discuss to what extent the mixed results may be explained either by differences in proximal control of behavioural traits such as to what degree learning is involved, or by conflicting selection pressures such as mate attraction versus territorial defence. Finally, I discuss whether heterospecific pairing may be adaptive under certain conditions, as has previously been suggested, in light of new and improved multi-generation fitness estimates of hybridizing birds.

18-5 Oral

FLORAL SIGNALS, POLLINATOR BEHAVIOUR, AND FLORAL ISOLATION IN PLANTS

Florian P. Schiestl [1]

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Pollinator behaviour strongly impacts on the strengths and mode of pollinator mediated reproductive isolation in plants. The diversity of pollination systems in plants incorporates a variety of different types of behaviour by pollinators. An important distinction is whether pollinators' visits to flowers are motivated by mating or foraging behaviour. Mating behaviour is characterized by innate preferences for mating signals, mediated by "hard wired" behavioural responses. Sexually deceptive orchids imitate mating signals, typically volatile chemicals, and thus exploit male insects that pollinate flowers through attempted copulations. These plants are primarily isolated prezygotically through ethological pollinator isolation by producing species-specific mating signals. In the Australian genus *Chiloglottis*, single volatile compounds and dual blends thereof mediate species-specific pollinator attraction. In the European genus *Ophrys*, bends of multiple compounds in specific proportions are key for pollinator isolation. In pollination systems with food searching behaviour, learning of floral signals is pronounced, as pollinators establish floral constancy in case of rewarding flowers but quickly avoid non-rewarding deceptive flowers. Food deceptive flowers are characterized by high pollinator sharing, and reproductive isolation is primarily postzygotic. Floral constancy in rewarding flowers can be an important component of reproductive isolation. Even minor modifications in floral signals, such as quantitative difference in single odor compound can mediate assortative pollinator visitation thus contribute to reproductive isolation.

18-6 Oral

LEARNED CONSPECIFIC MATE PREFERENCE IN A SPECIES PAIR OF STICKLEBACKS

Genevieve M. Kozak [1], Janette W. Boughman [2]

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Premating isolation between species often depends on conspecific mate preference. Preference for conspecific mates may be genetically inherited but can also be learned. The process of speciation will be affected by how conspecific mate preferences are determined; recent models suggest that learned conspecific preferences might make speciation more likely. However, we understand little about how conspecific preferences are learned and if learning differs between sexes and species. Previous work suggests when one sex learns, the other may not. In some species, conspecific preference is learned through experience with conspecifics (imprinting); in others by experience with heterospecifics (learning to discriminate). We tested if conspecific mate preference was learned in males and females from two recently diverged threespine stickleback species (benthics and limnetics: *Gasterosteus* spp.). We reared fish with either mostly conspecifics or mostly heterospecifics. We measured the effect of this social experience on conspecific preference. In both sexes, learning enhanced conspecific mate preference but the sexes differed in the type of experience that promoted discrimination. Limnetic females learned from experience with conspecifics; males of both species learned through experience with heterospecifics. We also found species differences: limnetic females learned and benthic females did not. We provide the first evidence that both female and male conspecific mate preference can be learned in a pair of recently diverged species. We also show that non-parental imprinting can affect conspecific preference. Our findings suggest that learning through social experience may contribute to current reproductive isolation between these species and may have promoted their original divergence.

18-7 Oral

WHAT ROLE DOES PHENOTYPIC PLASTICITY PLAY IN INTRASPECIFIC VARIATION IN MOTH PHEROMONE COMMUNICATION SIGNALS?

Astrid T. Groot [1,2], Carlos Blanco [3], David G. Heckel [1], Heike Staudacher [1], Juan D. Lopez Jr. [4], Ollie Inglis [2],
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In visual and acoustic communication systems, mate recognition signals have been shown to differ among populations, which appear related to selection by environmental factors that affect the recognition efficiency of these signals. Even though chemical communication signals also have been shown to be affected by environmental factors, and interspecific competition is recognized as playing a major role in the partitioning of pheromone communication channels in moths, so far local environmental conditions have not been explored as a factor that may cause divergence of chemical communication systems.

Sources of variation in the habitat that likely affect chemical communication systems include the presence and abundance of species with similar chemical cues. These may affect the signal-to-noise ratio or generate communication interference, both of which would select for females with the most distinct pheromone blend, optimized for a particular environment. Such selection would generate heritable variation among popuations. An alternative, more speculative hypothesis to explain variation in chemical communication signals is that females and males exhibit phenotypic plasticity in sexual signaling, and that experience during the larval period or early adulthood shapes the expressed phenotype. Such plasticity would result in largely non-heritable differences between populations.

We explored these hypotheses by sampling two closely related noctuid moth species, *Heliothis virescens* (Hv) and *H. subflexa* (Hs), in five different regions for 2–3 consecutive years. The variation we found suggests that optimization of the pheromonal signal may at least partly be due to within-generation physiological adjustments by the moths in response to their chemical environment. Currently we are conducting laboratory experiments to assess the level and effect of pheromone exposure during the immature and early adult stages on the pheromone composition of females, the results of which will be presented.

18-8 Oral

GENETIC LINKAGE OF SPECIATION GENES IN *HELICONIUS* FACILITATES ECOLOGICAL SPECIATION

Richard M. Merrill [1], Bas van Schooten [2], Chris D. Jiggins [1], Janet A. Scott [1]

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Physical linkage between traits that contribute to reproductive isolation can facilitate speciation in the face of gene flow. *Heliconius* butterflies are well known for brightly coloured mimetic warning colour patterns. Because wing colour patterns are also used as mating cues mimetic shifts can cause both pre- and post-mating isolation. However, shifts in colour pattern cannot drive reproductive isolation alone; rather, they must be accompanied by corresponding mate preferences and associations between trait and preference loci may be broken down by mating and subsequent recombination. We demonstrate a genetic linkage between loci for both male and female mate preference and wing colour pattern in *Heliconius cydno* and *H. melpomene*, two divergent and sympatric sister taxa. In addition, we present evidence for further associations between alleles affecting hybrid sterility and host-plant use and colour pattern loci. All this implies that linkage between traits that contribute to reproductive and ecological isolation is a general phenomenon in *Heliconius* with an underlying adaptive basis. These results expose a genetic mechanism that, by impeding recombination, can facilitate two controversial models of speciation, namely reinforcement and divergence in sympatry; associations such as that described here can also promote hybrid speciation.

18-9 Oral

VARIATION IN BEHAVIORAL ISOLATION LOCI IN *DROSOPHILA*

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Behavioral differences between species can lead to reproductive isolation and speciation. While behavioral isolation is considered to be the preliminary impetus for speciation, very little is known about the individual genetic loci contribute to behavioral isolation, how these loci arise, and whether there is genetic variation within a species for behavioral isolation between species. Here, I show results that shed light on two of these questions. Previous work identified regions of the genome that contribute to behavioral isolation between two closely-related species: *Drosophila simulans* and *D. mauritiana*. I will present an expansion of this work by mapping regions of the genome for behavioral isolation from seven *D. simulans* lines, collected from around the world. I will show how regions of the genome contributing to behavioral isolation from *D. mauritiana* vary widely within *D. simulans*, and that isolation is therefore unlikely to have been caused by a single novel mutation.

18-10 Oral

CONFLICT BETWEEN SEXUAL SELECTION SIGNALS AND SPECIES RECOGNITION

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In many species, mating signals are used to discriminate between partners of different quality. The same signals often also serve a function in species recognition in areas where closely related species overlap. As result of this dual use of signals, individuals may have to compromise the opportunity to select a mate of high genetic quality, in order to avoid the costs associated with hybridization. Indeed, conflict between intraspecific mate choice and species recognition occurs frequently in nature, and various solutions to mitigate the conflict seem to have evolved. Yet, the potential evolutionary consequences of the conflict between good-genes sexual selection and species recognition are not well understood. For that reason we used individual-based simulations to model mate choice and species recognition in a hybrid zone. When only one signal is involved, the conflict might be resolved by one species giving up the good-genes benefit altogether, or by different levels of investment in preference and signal expression in the two species. For multiple signals, a mix of these and good-gene equilibria is found, depending on the cost of hybridization and the amount of information that the signals provide about genetic quality. Our model shows the importance of single versus multiple signals for resolving the signaling conflict and reveals solutions that may help reveal and understand (subtle) species recognition patterns in nature.

18-1 Poster **Ecological speciation in the pea aphid: behavioural and genetic divergence of host-associated populations**

JULIA FERRARI
University of York, Department of Biology, York, United Kingdom

18-2 Poster **The genomics of host plant preferences and adaptive speciation in the pea aphid: a candidate gene approach**

CAROLE SMADJA, ROGER K. BUTLIN
University of Sheffield, Animal and Plant Sciences Department, Sheffield, United Kingdom

18-3 Poster **Sequential parallel ecological speciation in Neotropical crater lake cichlid fish**

AXEL MEYER[1], MARTA BARLUENGA[1], MORITZ MUSCHICK[1], CHRISTOPHER HARROD[2], WALTER SALZBURGER[1]
[1]University of Konstanz, Department of Biology, Konstanz, Germany
[2]Max-Planck-Institute for Limnology, Department of Physiological Chemistry, Jena, Germany

18-4 Poster **Frequency-dependent selection and the evolution of assortative mating**

SARAH P. OTTO[1], MARIA SERVEDIO[2], SCOTT NUISMER[3]
[1]UBC, Department of Zoology, Vancouver , Canada
[2]University of North Carolina, United States
[3]University of Idaho, United States

18-5 Poster **The interplay between speciation and adaptation in *Nasonia* wasps**

LEO W. BEUKEBOOM[1], BERND K. GRILLENBERGER[1], TOSCA KOEVOETS[1], ANIEK B.F. IVENS[1], KIRSTEN M. JALVINGH[1], MAARTJE C.W.G. GIESBERS[1], SALETA PEREZ VILA[1], LOUIS VAN DE ZANDE[1], IDO R. PEN[1], DAVID S. SHUKER[2]
[1]University of Groningen, Centre for Ecological and Evolutionary Studies, Evolutionary Genetics, Haren, The Netherlands
[2]University of St. Andrews, School of Biology, St. Andrews, United Kingdom

18-6 Poster **Adaptation to desiccation resistance fails to generate pre- or postmating isolation in *Drosophila melanogaster***

LUCIA KWAN, HOWARD D. RUNDLE
University of Ottawa, Department of Biology, Ottawa, Canada

18-7 Poster **Quantitative genetic analysis of cuticular hydrocarbons in *Drosophila montana***

PARIS VELTSOS[1], KIRSTEN KLAPPERT[2], CLAUDE WICKER-THOMAS[3], MARIA C. KEAYS[1], MIKE G. RITCHIE[1]
[1]University of St. Andrews, School of Biology, St. Andrews, United Kingdom
[2]Eawag, Department of Aquatic Ecology, Duebendorf, Switzerland
[3]Centre National de la Recherche Scientifique, Laboratoire Evolution, Génomes et Spéciation, Gif-sur-Yvettes, France

18-8 Poster **Evolutionary analysis of the desaturase gene family across 12 *Drosophila* species**

MARIA C. KEAYS[1], MIKE G. RITCHIE[1], DANIEL BARKER[1], CLAUDE WICKER-THOMAS[2]
[1]University of St. Andrews, School of Biology, St. Andrews, United Kingdom
[2]Centre National de la Recherche Scientifique Laboratoire Evolution, Génomes et Spéciation, Gif-sur-Yvette, France

18-9 Poster **Gene expression patterns associated with sexual isolation in Zimbabwean *Drosophila melanogaster***

RICHARD I. BAILEY, PAOLO INNOCENTI, EDWARD H. MORROW, ANNA QVARNSTRÖM
Uppsala University, Department of Animal Ecology, Uppsala, Sweden

18-10 Poster **Differential transcription profiles between *Littorina saxatilis* ecotypes, an example of sympatric speciation**

MONICA MARTINEZ-FERNANDEZ[1], LOUIS BERNATCHEZ[2], EMILIO ROLAN-ALVAREZ[1], HUMBERTO QUESADA[1]
[1]Universidad de Vigo, Departmento de Bioquimica, Genetica e Inmunologia, Vigo, Spain
[2]Université Laval, Department of Biology, Québec, Canada

18-11 Poster **A phylogeographic investigation of the hybrid origin of a swordtail species in Mexico**

JULIA C. JONES[1], JODY L. SHIELDS[2], JUAN A. PEREZ-SATO[3], AXEL MEYER[1]
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[2]University of Windsor Great Lakes, Institute for Environmental Research, Windsor, Canada
[3]Campus Cordoba, Colegio de Postgraduados, Veracruz, Mexico

18-12 Poster **Behavioural isolation in the house mouse hybrid zone**

BARBORA BÍMOVÁ[1], MILOŠ MACHOLÁN[1], PAVEL MUNCLINGER[2], CHRISTINA M. LAUKAITIS[3], ROBERT C. KARN[4], STUART J.E. BAIRD[5], JAROSLAV PIÁLEK[6]
[1]Academy of Sciences of the Czech Republic, Institute of Animal Physiology and Genetics, Laboratory of Mammalian Evolutionary Genetics, Brno, Czech Republic
[2]Charles University at Prague, Department of Zoology, Biodiversity Research Group, Prague, Czech Republic
[3]University of Arizona, Department of General Medicine, Tucson, United States
[4]Butler University, Department of Biological Sciences, Indianapolis, United States
[5]Campus Agrário de Vairão, Centro de Investigação em Biodiversidade e Recursos Genéticos, Vairão, Portugal
[6]ASCR Institute of Vertebrate Biology, Department of Population Biology, Studenec, Czech Republic

18-13 Poster **Testosterone allocation in collared flycatcher eggs: a mechanism for life-history divergence?**

AMBER M. RICE
Uppsala University, Evolutionary Biology Centre, Department of Animal Ecology, Uppsala, Sweden

18-14 Poster **Behaviour, morphology, ecology, and genetics: mismatches in Southern Ocean speciation patterns**

MARC DE DINECHIN[1], FRANCESCO BONADONNA[1], PAVEL ZEHTINDJIEV[2], PETRA QUILLFELDT[3], PIERRE JOUVENTIN[1], RICHARD OTTVALL[4], ROUMIANA METCHEVA[2]
[1]CEFE/CNRS UMR 5175, Behavioural Ecology, Montpellier, France
[2]Bulgarian Academy of Sciences Institute of Zoology, Sofia, Bulgaria
[3]Max-Planck-Institut für Ornithologie Vogelwarte Radolfzell, Radolfzell, Germany
[4]Lund University, Department of Animal Ecology, Lund, Sweden

18-15 Poster **Morphological and behavioural divergence between island populations of Skyros wall lizard *Podarcis gaigeae*: colour morph frequencies and pre-mating isolation**

ANNA RUNEMARK, ERIK I. SVENSSON, BENGT HANSSON
Lund University, Department of Ecology, Lund, Sweden

18-16 Poster **Rapid population divergence, variation in colour and its effect on mating behaviour in Strawberry poison frogs**

ANDREAS RUDH[1], ANNA QVARNSTRÖM[1], BJÖRN ROGELL[2], JACOB HÖGLUND[2], MARTIN BREED[1,4], OLLE HÅSTAD[3]
[1]Uppsala University, Department of Animal Ecology, Uppsala, Sweden
[2]Uppsala University, Department of Population Biology and Conservation Biology, Uppsala, Sweden
[3]Uppsala University, Department of Evolutionary Organismal Biology, Uppsala, Sweden
[4]University of Adelaide, Australian Centre for Evolutionary Biology and Biodiversity, School of Earth and Environmental Science, Adelaide, Australia

18-17 Poster **Host-associated divergence in the seabird tick *Ornithodoros maritimus*: insights from genetic markers and stable isotopes**

ELENA GÓMEZ-DÍAZ[1], JACOB GONZÁLEZ-SOLÍS[2], KAREN D. MCCOY[1]
[1]UMR 2724-CNRS/IRD, Genetique et Evolution des Maladies Infectieuses (GEMI), Montpellier, France
[2]University of Barcelona, Departamento de Biologia Animal, Barcelona, Spain

18-18 Poster **Patterns of prezygotic isolation and costs of hybridization in grasshoppers**

MUNJONG KOLSS
University of Bielefeld, Department of Evolutionary Biology, Bielefeld, Germany

18-19 Poster **Genetic analysis of a chromosomal hybrid zone in the Australian morabine grasshoppers (*Vandiemenella*, *viatica* species group)**

TAKESHI KAWAKAMI[1], ROGER K. BUTLIN[2], MARK ADAMS[3], KATHLEEN M. SAINT[3], STEVEN J.B. COOPER[3]
[1]Kansas State University, Division of Biology, Manhattan, United States
[2]University of Sheffield, School of Biology, Sheffield, United Kingdom
[3]South Australian Museum, Evolutionary Biology Unit, Adelaide, Australia

18-20 Poster **Evolutionary Diversification in Stickleback Affects Ecosystem Functioning**

BLAKE MATTHEWS, LUKE J. HARMON, SIMONE DES ROCHE, JONATHAN M. CHASE, JONATHAN B. SHURIN, DOLPH SCHLÜTER
Eawag, Department of Aquatic Ecology, Duebendorf, Switzerland

18-21 Poster **Competitive environments induce shifts in host fidelity**

EMMA ROVA
Uppsala University, Faculty of Ecology and Evolution, Department of Animal Ecology, Uppsala, Sweden

18-22 Poster **Sexual isolation in a group of sympatric intertidal isopods**

DANIEL V. MIFSUD, STUART B. PIERTNEY
University of Aberdeen, Institute of Environmental and Biological Sciences, Aberdeen, United Kingdom

18-23 Poster **Local adaptation by host specialization and dispersal evolution in *Tetranychus urticae***

ELLYN BITUME[1], CAROLINE NIEBERDING[2], ISABELLE OLIVIERI[1]
[1]University Montpellier II, Metapopulation, Conservation, and Coevolution, Montpellier, France
[2]Catholique Université de Louvain-la-Neuve, Department of Ecology and Biogeography, Louvain-la-Neuve, Belgium

18-24 Poster **Mating ecology of malaria parasites: insights from multiple-species interactions**

RICARDO S. RAMIRO, SARAH E. REECE
University of Edinburgh, Institute of Evolutionary Biology, School of Biological Sciences, Edinburgh, United Kingdom

Genetic trade-offs in fitness-traits: theory, evidence, and implications

eseb
12th Congress
Turin 2009

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Program

Friday August 28 - **Symposium 19**

Location: Room 3

Genetic trade-offs in fitness-traits: theory, evidence, and implications

Organizers:	*Katharina Foerster, University of Lausanne, Switzerland* *Alastair Wilson, University of Edinburgh, United Kingdom*

9.45 - 10.15	**DEREK A. ROFF** (invited) Genetic tradeoffs: Do they really matter?
10.15 - 10.45	**ERIK I. SVENSSON** (invited) Studying genetic trade-offs between fitness-related traits in natural populations: empirical challenges and theoretical considerations
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**DOMINIQUE MAZZI** As far as mum and dad: Direct and indirect responses to artificial selection on mobility in the oriental fruit moth
11.35 - 11.55	**FLORENCE DEBARRE** Evolution of specialization in a continuous habitat
11.55 - 12.15	**SUSAN E. JOHNSTON** The genetic basis of a trait under sexually antagonistic selection
12.15 - 12.35	**AYME SPOR** Experimental evolution of life-history strategies in *Saccharomyces cerevisiae*
12.35 - 13.35	*Lunch*
13.35 - 13.55	**MATTHEW R. ROBINSON** The environmental dependency of genetic trade-offs between fitness-traits in a human population
13.55 - 14.15	**BENJAMIN MAUROY** Don't fall off the adaptation cliff ! When asymmetrical fitness costs select for suboptimal traits
14.15 - 14.35	**ELIZABETH G. KING** Modeling the Evolution of Phenotypic Plasticity in Resource Allocation in Wing Polymorphic Insects
14.35 - 14.55	**TARMO KETOLA** Experimental evolution of prey fitness tradeoffs in low or high resources, with or without predator
14.55 - 15.25	*Coffee break*

19-1 Oral

GENETIC TRADEOFFS: DO THEY REALLY MATTER?

Derek A. Roff [1]

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To what extent do genetic tradeoffs modulate evolutionary trajectories and determine equilibrium trait values? What is more important, physiology or ecology? These questions are central to any justification for the study of trade-offs. In this talk I shall sketch out the areas in which the answers are that such tradeoffs matter and those in which it may be irrelevant.

19-2 Oral

STUDYING GENETIC TRADE-OFFS BETWEEN FITNESS-RELATED TRAITS IN NATURAL POPULATIONS: EMPIRICAL CHALLENGES AND THEORETICAL CONSIDERATIONS

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The study of the genetic trade-offs between fitness-related traits in natural populations is a formidable empirical challenge. Although trade-offs can and have been extensively investigated in laboratory settings using model organisms such as *Drosophila melanogaster*, they should preferably be studied in the natural environments that shaped them. Phenotypic manipulation experiments have their heuristic value and have increased our general understanding about the ecology of trade-offs, but they are of limited utility when it comes to understand the genetic and mechanistic basis of trade-offs. Recently, quantitative genetic approaches, such as the “Animal Model”, have become increasingly popular among evolutionary ecologists interested in trade-offs. Although these quantitative genetic approaches also have great value, their application is limited to the relatively few model systems where parents and offspring can be marked and followed in the wild, such as mammals and birds. For the vast majority of organisms that are of interest to evolutionary ecologists (including most insects) we have to rely on other approaches to study the genetic and mechanistic basis of trade-offs. Here I will argue that a methodologically pluralistic approach is the best way to move this research field forward. I will illustrate my talk with recent examples from both my own research and from other laboratories. I will especially focus on how studies on heritable and conspicuous phenotypic polymorphisms can reveal the mechanistic architecture of genetic trade-offs, especially when combined with new molecular approaches from genomics and transcriptomics.

19-3 Oral

AS FAR AS MUM AND DAD: DIRECT AND INDIRECT RESPONSES TO ARTIFICIAL SELECTION ON MOBILITY IN THE ORIENTAL FRUIT MOTH

Dominique Mazzi [1], Marco V.G. Torriani [1], Silke Hein [1], Silvia Dorn [1]

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The individual ability to move from one place to another is crucial to the persistence of populations in rapidly changing environments. The study of the dispersive tendencies of pest species that compete with men for food resources and threaten sustainable crop production furthers the understanding of their spread dynamics and helps to anticipate future invasions. We performed artificial selection on actograph-measured mobility in the oriental fruit moth *Grapholita molesta*, a major wing-monomorphic lepidopteran pest of fruits worldwide, currently expanding its distribution range polewards. Both sexes rapidly responded to the imposed divergent selection regime. Upward-selected moths died sooner than downward-selected ones, thus providing evidence for a cost of mobility to adult survival. Oppositely selected females had similar reproductive output, but differed in the timing of reproduction. We discuss the implications of our results in the context of life-history trade-offs and of the range expansion of invasive species, and their implications for pest management strategies.

19-4 Oral

EVOLUTION OF SPECIALIZATION IN A CONTINUOUS HABITAT

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Our understanding of the evolution of specialization is grounded in the analysis of metapopulation models with no isolation by distance. Limited range of dispersal, however, may greatly affect the heterogeneity of the habitat experienced by different individuals and, consequently, the evolution of specialization. We study this effect in a spatially continuous (one dimensional) environment divided into two adjacent habitats. The individuals are allowed to move in a diffusive way, which implies some isolation by distance. As a first approximation, we assume that the whole population is at its carrying capacity everywhere, and that this carrying capacity is the same all along the environment. We also assume a generic trade-off function for the level of adaptation in each habitat. The population can end up specialized to one habitat (1 specialist), or reach an intermediate value of the trait and be moderately adapted to both habitats (1 generalist), or even split into two locally adapted subpopulations (2 specialists). We show (analytically) that the fate of the original population greatly depends on the shape of the trade-off (especially on its curvature), but also on the range of migration of the individuals, and on the proportion of each habitat. We also show that a minor change in one parameter of the environment (e.g. the proportion of each habitat) can have dramatic consequences on the local adaptation of the whole population. Finally, we compare our work to previous theoretical results, and we discuss how this framework may help understand and control the evolution of multi-drug-resistant parasites.

19-5 Oral

THE GENETIC BASIS OF A TRAIT UNDER SEXUALLY ANTAGONISTIC SELECTION

Susan E. Johnston [1], Dario Beraldi [2], Allan F. McRae [3], Josephine M. Pemberton [2], Jon Slate [1]

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Sexual selection has long been considered a major driver for the evolution of exaggerated male weaponry in animals. After subsequent generations of apparent directional selection, it is predicted that genetic variation underlying such traits will be reduced. Investigating selection on phenotype provides some explanation for this phenomenon, often suggesting that antagonistic selection or genotype-by-environment interactions play a significant role in maintaining variation. However, identifying the genetic basis of selected traits will ultimately allow us to understand their evolution. Soay sheep have an inherited polymorphism for horn type in both sexes, with males presenting either large, normal horns or small, deformed horns (scurs) and females exhibiting normal horns, scurs or a third hornless phenotype (polled). The polymorphism is controlled by a single locus, *Horns*. In addition, horn length among normal-horned males is heritable. Given that males with scurs cannot win conflicts with normal-horned males, it is unusual that genes conferring scurs should persist in the population. Recent studies indicate that genetic variation in horn type is maintained by sexually-antagonistic selection, while variation in horn length among normal-horned males is maintained by environmental heterogeneity affecting the magnitude and direction of selection. We developed molecular markers within a targeted region of the genome, and found that genomic regions controlling variation in horn type between the sexes also contribute to most of the genetic variance in horn morphology within normal-horned males. We aim to extend previous information of selection on phenotype to examine selection on specific genotypes at *Horns*, which will reveal the mechanisms of selection in this population.

19-6 Oral

EXPERIMENTAL EVOLUTION OF LIFE-HISTORY STRATEGIES IN *SACCHAROMYCES CEREVISIAE*

Ayme Spor [1], Thibault Nidelet [1], Jonattan Simon [1], Aurelie Bourgais [1], Christine Dillmann [1],
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Selection process can not maximised all life-history traits together because there are constraints (either genetic or environmental or both) that prevents from the existence of Darwinian Demon. The different combinations of life-history trait values lead then to so-called « life-history strategies ». We showed that domesticated and natural *Saccharomyces cerevisiae* strains display genetic and plastic variations for lifehistory traits (cell size, reproduction rate, carrying capacity). Genetic correlations between traits define two extreme life-history strategies. The “grasshoppers” consume glucose at high rate, have large cell size and low carrying capacity, while the “ants” consume glucose at low rate have small cell size but reach a high carrying capacity. We then conducted an experimental evolution with 6 strains having contrasted life-history strategies (from the most “Grasshopper” one to the most “Ant” one) to analyse the outcomes of 500 generations of selection in 4 treatments. Replicated populations were propagated in serial transfers in two glucose conditions (1% and 15% glucose) and two different “winter lengths” (48h stationary phase length differences) mimicking seasonal environments. Over the four selection regimes, divergent selection leads to an increase of life-history phenotypic variance. But this “global diversification” is to be opposed to a “local adaptation” of population in a given selection environment. Indeed, in the 1% glucose medium, a significant phenotypic convergence is observed. The study of the proteome variation over generations is underway and may shed light on the metabolic changes that are involved in the evolution of life-history strategies.

19-7 Oral

THE ENVIRONMENTAL DEPENDENCY OF GENETIC TRADE-OFFS BETWEEN FITNESS-TRAITS IN A HUMAN POPULATION

Matthew R. Robinson [1], Virpi Lummaa [1]

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A fundamental assumption underlying life-history theory is that evolution is constrained by universal trade-offs between traits affecting fitness, and genetic correlations have been widely used to measure these trade-offs. However, we might expect that trade-offs in the allocation of resources between traits may depend upon resource availability across life and that individuals of different genotypes may differ in their response to changes in resources. We know that the environment can have direct influence on the quantitative genetic parameters underlying life-history traits and there is increasing evidence to suggest that environmental variation can influence interactions among traits. Here, we examine the environmental dependency of genetic correlations in three fitness traits survival, fecundity, and offspring quality, across a natural gradient of resource availability, using data from a pre-industrial Finnish human population. We show that genetic relationships and thus trade-offs between survival, offspring quantity, and offspring quality, are environmentally dependent. This study provides evidence that the genetic architecture of fitness-related traits is not stable, and thus evolutionary processes may largely depend upon the fluctuating environmental conditions, within and between generations, that are experienced by natural populations.

19-8 Oral

DON'T FALL OFF THE ADAPTATION CLIFF ! WHEN ASYMMETRICAL FITNESS COSTS SELECT FOR SUBOPTIMAL TRAITS

Benjamin Mauroy [1], Elodie Vercken [2], Erik I. Svensson [3], Maren Wellenreuther [3]

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Genotypes can have a range of phenotypic values and this has been verbally addressed in the case of clutch size evolution by Mountford (1968) with the "cliff-edge" hypothesis. Although the cliff-edge hypothesis implicates important consequences on our overall understanding of natural selection, very few studies have tried to widen this theory by extending it to all traits bound to phenotypic variability. In fact, the cliff-edge hypothesis introduces the counterintuitive idea that maximising the fitness for such traits is not necessarily the best strategy, and this should apply whenever the fitness of a trait has an asymmetric function around its maximum value.

We propose a general mathematical model of competition based on phenotypic variation in a genetic trait and show that the best genotype depends on the shape of the fitness function and not only on the position of the fitness maximum. The model gives access to a prediction of the distribution of the trait in a population and most importantly provides an alternative function, which should be maximized instead of the fitness.

In addition, in order to demonstrate the generality of the model assumptions and to describe how it can be applied to data, we tested the predictions of the model for various evolutionary trade-offs; (i) litter size and juvenile survival in guinea pigs originally described by Mountford, (ii) sexual selection and predation in the damselfly *Calopteryx splendens*, and (iii) the geometry of the human lung.

19-9 Oral

MODELING THE EVOLUTION OF PHENOTYPIC PLASTICITY IN RESOURCE ALLOCATION IN WING POLYMORPHIC INSECTS

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In nature, resource availability varies spatially and temporally both within and across generations, leading to variation in the amount of energy available to individuals. The optimal allocation strategy may change depending upon the amount of resources available. If so, selection should favor the evolution of allocation strategies that can be altered in response to variation in environmental resource levels. We address this issue using a quantitative genetic simulation model to predict the optimal reaction norm of allocation of resources between two traits in response to varying resource availability in a model system for studying trade-offs, wing polymorphic insects. In wing polymorphic insects there is typically a trade-off between the allocation of resources to dispersal ability and to reproduction. In our model, we focus on allocation as a genetic trait and model the evolution of phenotypic plasticity in this trait in response to spatio-temporal variation in resource availability. We show that the optimal allocation strategy depends on the predictability of resource levels across time. Specifically, the evolved reaction norm of allocation to flight versus reproduction in response to resource availability variation has a positive slope in unpredictable environments and a negative slope in predictable environments. These results are compared to empirical data for the wing dimorphic cricket, *Gryllus firmus*.

19-10 Oral

EXPERIMENTAL EVOLUTION OF PREY FITNESS TRADEOFFS IN LOW OR HIGH RESOURCES, WITH OR WITHOUT PREDATOR

Tarmo Ketola [1], Ville-Petri Friman [1], Jouni Laakso [1], Lauri Mikonranta [1]

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Available resources in the environment affect the evolutionary potential of organisms by determining the trade offs between traits. In addition, the resource environment where the traits are measured can affect the visibility of the tradeoffs between traits. We explored the evolution and the visibility of tradeoffs in prey's defensive and growth traits by experiment in which *Serratia marcescens* -bacteria evolved ca. 2400 generations with or without its ciliate predator *Tetrahymena thermophila*, in low or high resource concentration. After the experiment, 192 prey clone's defensive and growth traits were measured in low and high resource concentrations. The effects of evolutionary history and measurement resource on the variance-covariance matrix of the traits were explored by using multivariate statistics. Interestingly, the measurement resource affected the trait variances and the covariances equally strongly, but the evolutionary history due to resource, predator and their interaction, affected especially on the covariances between the traits. This underlines the importance of trade offs contributing to the evolutionary change. However, further analyses pinpointed also that the exploration of traits or trait pairs ("classical" trade offs) in isolation does not sufficiently describe the evolutionary changes that involve multiple traits. This is especially the case in our dataset where measurement resource, and evolutionary history due to predator and resource, changed several but different defensive traits and contributed also differently to several growth traits.

19-1 Poster **Male and female extra-pair paternity are positively genetically correlated**

WOLFGANG FORSTMEIER, KATRIN MARTIN, ELISABETH BOLUND, HOLGER SCHIELZETH, BART KEMPENAERS
Max Planck Institute for Ornithology, Department of Behavioural Ecology and Evolutionary Genetics, Seewiesen, Germany

19-2 Poster **Quantitative genetics of trade-offs in two populations of great tits (*Parus major*): the importance of multiple comparisons**

ARILD HUSBY[1], MARCEL E. VISSER[2], BEN C. SHELDON[3], LOESKE E.B. KRUUK[1]
[1]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom
[2]Netherlands Institute of Ecology , Heteren, Netherlands
[3]Oxford University, Edward Grey Institute Zoology, Oxford, United Kingdom

19-3 Poster **Trade-off between melanisation and fitness in the large white butterfly, *Pieris brassicae***

AUDREY CHAPUT-BARDY, MICHEL BAGUETTE
UMR 7179 CNRS-MNHN, Muséum National d'Histoire Naturelle, Brunoy, France

19-4 Poster **Maintenance of life history polymorphism in seasonal environments: effects of divergent timing of egg-laying and juvenile competition**

SAMI M. KIVELA[1], PANU VALIMAKI[1], ARJA KAITALA[1], VEIJO KAITALA[2], JARI OKSANEN[1]
[1]University of Oulu, Department of Biology, Oulu, Finland
[2]University of Helsinki, Department of Ecology and Evolutionary Biology, Helsinki, Finland

19-5 Poster **Who pay now? Genetically selfish mothers make offspring pay in a species with a conservative reproductive strategy**

JULIEN MARTIN[1,2], MARCO FESTA-BIANCHET[1,2]
[1]Université de Sherbrooke Département de Biologie, Sherbrooke, Canada
[2]Centre d'Estudes Nordiques, Québec, Canada

19-6 Poster **Intra-population heterogeneity in movement throughout the life cycle of a stream-dwelling salmonid fish**

MICHAEL B. MORRISSEY[1], MOIRA M. FERGUSON[2]
[1]University of Edinburgh, Institute of Evolutionary Biology, Edinbrugh, United Kingdom
[2]University of Guelph, Department of Integrative Biology, Guelph, Canada

19-7 Poster **Do genetic correlations constrain adaptation to a novel habitat in northern fringe populations of the natterjack toad, *Bufo calamita?***

BJÖRN ROGELL[1], ANSSI LAURILA[1], JACOB HÖGLUND[1], MAARTEN HOFMAN[2]
[1]Uppsala University, Department of Population biology, Uppsala, Sweden
[2]University of Antwerpen, Department of Biology, Antwerpen , Belgium

19-8 Poster **Divergence in life-history traits facilitates coexistence in *Ficedula* flycatchers**

NICLAS VALLIN, ANNA QVARNSTRÖM
Uppsala University, Animal Ecology /Department of Ecology and Evolution, Uppsala, Sweden

19-9 Poster **Sex-specific paternal effects in morphological and life history traits in *C. maculatus***

LÁRA R. HALLSSON, MATS BJÖRKLUND
Uppsala University, Animal Ecology/Department of Ecology and Evolution, Evolutionary Biology Centre (EBC), Uppsala, Sweden

19-10 Poster **Sexual variation in heritability of cell-mediated immune response**

SZYMON M. DROBNIAK[1], DARIUSZ WIEJACZKA[1], ANETA ARCT[1], ANNA DUBIEC[2], MARIUSZ CICHON[1]
[1]Jagiellonian University, Institute of Environmental Sciences, Kraków, Poland
[2]Polish Academy of Sciences Museum and Institute of Zoology, Warszawa, Poland

19-11 Poster **Male testosterone mediates the immunocompetence handicap – Inter- and intra-sexual genetic trade-offs revealed**

EERO SCHRODERUS[1], ILMARI JOKINEN[1], MINNA KOIVULA[2], ESA KOSKELA[1], TAPIO O. MAPPES[1], SUZANNE C. MILLS[3], TUULA A. OKSANEN[1], TANJA POIKONEN[1]
[1]University of Jyväskylä, Centre of Excellence in Evolutionary Research, Jyväskylä, Finland
[2]Agrifood Research Finland Biotechnology and Food Research, Department of Biometrical Genetics, Jokioinen, Finland
[3]Université de Perpignan Via Domitia, Biologie et Ecologie Tropicale et Mediterranéenne, Perpignan, France

19-12 Poster **Experimental evolution of life history and virulence of a parasite with vertical and horizontal transmission: the impact of host growth conditions**

HELENE MAGALON[1,2], THIBAULT NIDELET[1,3], OLIVER KALTZ[1,4]
[1]Université Pierre et Marie Curie Paris VI , Laboratoire de Parasitologie Evolutive UMR 7103, Paris, France
[2]INRA, UMR BIO3P, Le Rheu, France
[3]Université Paris Sud, INRA CNRS, UMR de Génétique Végétale, Gif sur Yvette, France
[3]Université Montepellier 2, Institut de Science de l'Evolution, UMR 554, Montepellier, France

19-13 Poster **Interaction between immunity and learning in *Drosophila***

AURELIE BABIN, JOEP M.S. BURGER, TADEUSZ J. KAWECKI
University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

19-14 Poster **Genetic trade-off between maternal immunocompetence and offspring survival in zebra finches?**

JOANNA RUTKOWSKA, ANETA ARCT, RAFAŁ MARTYKA, MARIUSZ CICHON
Jagiellonian University, Institute of Environmental Sciences , Kraków, Poland

19-15 Poster **Food restriction and cost of a dual immune activation**

IGOR VUILLEZ, PAUL SCHMID-HEMPEL
ETH Zuerich, Institute of Integrative Biology, Experimental Ecology, Zuerich, Switzerland

19-16 Poster **Evolution and Mechanisms of the Lifespan-Reproduction Trade-Off in *Drosophila***

THOMAS FLATT
Veterinaermedizinische Universitaet Wien, Institut fuer Populationsgenetik, Wien, Austria

19-17 Poster **The mechanistic basis of the defence strategy of the water flea *Daphnia magna* in response to predation**

KEVIN PAUWELS, ROBBY STOKS, LUC DE MEESTER
Katholieke Universiteit, Laboratory of Aquatic, Ecology and Evolutionary Biology, Leuven, Belgium

19-18 Poster **Analysis of candidate gene sequences for basal metabolic rate (BMR) in the light of the "membrane pacemaker" theory**

MAGDALENA CZAJKOWSKA
University of Bialystok, Department of Vertebrate Zoology, Bialystok, Poland

19-19 Poster **Role-reversal of gender-associated mitochondrial dna affects mitochondrial function in *Mytilus edulis* (Bivalvia: Mytilidae)**

SOPHIE BRETON[1], DONALD T. STEWART[2], PIERRE U. BLIER[3]
[1]Kent State University, Department of Biological Sciences, Kent, United States
[2]Acadia University, Department of Biology, Wolfville, Canada
[3]Universite du Quebec a Rimouski, Département de Biologie, Rimouski, Canada

19-20 Poster **Transcriptional regulation of life-history in response to environmental stress: implications for the evolution of senescence in ecological time**

FIONA R. SAVORY, IAN A. HOPE, TIM G. BENTON, STEVE M. SAIT
University of Leeds, Institute of Integrative and Comparative Biology, Leeds, United Kingdom

19-21 Poster **Exploring the intersexual relationship for ageing in *Drosophila***

CHRISTOPHER M. KIMBER, ADAM K. CHIPPINDALE
Queen's University, Department of Biology, Kingston, Canada

19-22 Poster **How much initiator tRNA does *E. coli* need?**

LAASYA SAMHITA
Indian Institute of Science, Department of Microbiology and Cell Biology, Bangalore, India

19-23 Poster **Models of frequency-dependent selection and its implications to the long-term evolution of polygenic traits**

KRISTAN A. SCHNEIDER[1,2]
[1]University of Vienna, Department of Mathematics, Vienna, Austria
[2]Arizona State University, Phoenix, United States

19-24 Poster **Evolution of life-history phenotypes in outcrossing and inbreeding populations during adaptation to a novel environment: insights from an experimental evolution approach**

SARA CARVALHO, HENRIQUE TEOTONIO
University of Oeiras, Instituto Gulbenkian de Ciencia, Evolutionary Genetics Group, Oeiras, Portugal

19-25 Poster **Genetic evidence for symbiotic trade-off in a nematode by experimental selection**

ELODIE CHAPUIS, VANYA EMELIANOFF, JEAN-BAPTISTE FERDY
Université de Montpellier II, ISEM, UMR 5554, Montpellier, France

19-26 Poster **Divergent selection for flowering time in maize inbred lines**

ELEONORE DURAND, CHRISTINE DILLMANN, MAUD TENAILLON, ALAIN CHARCOSSET
Université Paris-Sud, UMR de Génétique Végétale, INRA/CNRS/AgroParistech, Ferme du Moulin, Essonne, Gif sur Yvette, France

19-27 Poster **Understanding the maintenance of genetic variation in two-spotted spider mites: Does oviposition rate trade off with other fitness traits?**

NICOLA S.H. TIEN, MAURICE W. SABELIS, MARTIJN EGAS

University of Amsterdam, IBED, Department of Population Biology, Amsterdam, Netherlands

19-28 Poster **Adaptation of a phytovirus to its environment : experimental evidence for a cost of specialization and contribution of antagonistic pleiotropy mechanism in fitness tradeoffs**

CHIRAZ JRIDI

UMR 385 CIRAD-INRA-ENSAM, Departement de Biologie et Génétique des Interactions Plante-Parasite (BGPI), Montpellier, France

19-29 Poster **Are adaptation costs necessary to build up a local adaptation pattern?**

SARA MAGALHÃES[1,2], ELODIE BLANCHET[3], MARTIJN EGAS[4], ISABELLE OLIVIERI[2]

[1]Faculty of Sciences of the University of Lisbon, Centre for Environmental Biology, Lisbon, Portugal
[2]Université de Montpellier II, Montpellier, France
[3]CIRAD, Montpellier, France
[4]University of Amsterdam, Amsterdam, Netherlands

19-30 Poster **Male courtship behaviour in insulin pathway deficient *Drosophila melanogaster***

VUKASIN ZRELEC, TADEUSZ J. KAWECKI

University of Lausanne, Department of Evolution and Ecology, Lausanne, Switzerland

Selective forces shaping transitions to social life

eseb
12th Congress
Turin 2009

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Program

Friday August 28 - **Symposium 20**

Location: Room 4

Selective forces shaping transitions to social life

Organizers: *Trine Bilde, University of Aarhus, Denmark*
Patrizia d’Ettorre, University of Copenhagen, Denmark

9.45 - 10.15	**JACOBUS J. BOOMSMA** (invited) Strict life-time monogamy as universal condition for transitions towards eusociality
10.15 - 10.45	**ASHLEIGH S. GRIFFIN** (invited) Promiscuity and kin selection in cooperative breeders
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**KEVIN FOSTER** Social interactions in microbes
11.35 - 11.55	**YAEL LUBIN** Loss of natal dispersal in the transition to sociality in spiders–a remaining puzzle
11.55 - 12.15	**BEN HATCHWELL** The evolution of avian societies: how do kin-structured populations develop?
12.15 - 12.35	**MICHEL CHAPUISAT** Social transfer of fungal resistance in ants
12.35 - 13.35	*Lunch*
13.35 - 13.55	**JEREMY FIELD** Environmental and genetic components of a major evolutionary transition: social phenotype in halictid bees
13.55 - 14.15	**LISA A. MCGRAW** Experimental evolution of pair bonding in the prairie vole *(Microtus ochrogaster)*
14.15 - 14.35	**MICHAEL E HOCHBERG** The coevolution of cooperation and dispersal in social groups and its implications for the emergence of multicellularity
14.35 - 14.55	**SOFIA STATHOPOULOS** Sophisticated olfaction and the evolution of social strategies in African mole-rats
14.55 - 15.25	*Coffee break*

20-1 Oral

STRICT LIFE-TIME MONOGAMY AS UNIVERSAL CONDITION FOR TRANSITIONS TOWARDS EUSOCIALITY

Jacobus J. Boomsma [1]

[1]*University of Copenhagen, Department of Biology, Copenhagen, Denmark*

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All evidence currently available indicates that permanently sterile castes could only arise via the association of parents and offspring. I will extend this notion by arguing that strict life-time monogamy of parents characterized the mating systems of all ancestors of permanently eusocial clades. Evolving eusociality via a ‘monogamy window’ is consistent with Hamilton’s rule ($br_S > r_O c$), but implies that relatedness cancels out of the equation as a variable, because average relatedness to sibs (r_S) and relatedness to offspring (r_O) are both predictably 0.5. This implies that any small benefit of helping at the maternal nest (b), relative to the cost in personal reproduction (c) that persists throughout the life-span of entire cohorts of helpers suffices to make the transition, so that group benefits can increase gradually during, but mostly after the transition. The monogamy window can be conceptualized as a singularity comparable with the single zygote commitment of gametes that characterized the first eukaryotic cell. The increase of colony size in ants, bees, wasps and termites is thus analogous to the evolution of multicellularity. The focus on strict life-time monogamy as the universal precondition for eusociality simplifies the theory, suggests explicit ways of conceptualizing superorganismic germ lines, and helps to resolve controversies about the significance of kin selection and group selection. The monogamy window underlines that cooperative breeding and eusociality are different domains of social evolution, characterized by different sectors of parameter space for Hamilton rule.

20-2 Oral

PROMISCUITY AND KIN SELECTION IN COOPERATIVE BREEDERS

Ashleigh S. Griffin [1], Charlie K. Cornwallis [1]

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In cooperatively breeding birds, parents may share the load of caring for their offspring, with other adults. These “helpers” are usually offspring from previous groups that have not dispersed from their natal territory. In the majority of bird species individuals disperse and breed independently so why in cooperative breeders do individuals help? One possibility is that helpers obtain kin selected benefits by increasing the chick production of related individuals. An under-explored prediction of this hypothesis is that selection for helping will be reduced by increased promiscuity and/or breeder turnover rate at the natal nest, as this will decrease relatedness between chicks across broods. We present the results of a study comparing promiscuity rates with investment in indirect fitness benefits across cooperatively breeding species, using meta-analysis.

20-3 Oral

SOCIAL INTERACTIONS IN MICROBES

Kevin R. Foster [1]

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Sociobiology has come a long way. We now have a solid base of theory, centered on principles like inclusive-fitness theory, and a myriad of empirical tests. One major group that remains relatively unexplored, however, is the microbes, whose full spectrum of sociality only recently came to light. We study how social environment affects microbial behavior in a number of model systems, including biofilm-forming bacteria, slime molds and budding yeast. We find that microbes are extremely sensitive to social context - both in real time and over evolutionary time - and use them to better understand the genetic and genomics of social traits; a pursuit that is difficult in the more classic model organisms for social behavior.

20-4 Oral

LOSS OF NATAL DISPERSAL IN THE TRANSITION TO SOCIALITY IN SPIDERS – A REMAINING PUZZLE

Yael Lubin [1]

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Natal dispersal is axiomatic in the majority of organisms. It is typically performed by juveniles and is often sex-specific. The benefits of reaching better habitats or unoccupied territories and avoiding kin competition and inbreeding should strongly favor dispersal. Yet group-living species have lost this trait either partially or completely. In cooperative group-living (social) spiders, dispersal takes two forms: colony fission leads to formation of nearby daughter colonies, while long-distance dispersal is undertaken by mated females. Neither mode of dispersal occurs in related subsocial species with maternal care and delayed offspring dispersal. What might have selected for these two dispersal modes, and are they alternative strategies? We investigated dispersal in African social spiders (genus *Stegodyphus*, Eresidae). We suggest that colony fission is a form of colony expansion that occurs in response to competition for resources within the nest, while long-distance dispersal is a strategy that enables individuals (and colony lineages) to escape from pathogens or parasites. Data supporting this hypothesis include studies of population dynamics, sex ratios, and dispersal in natural colonies. A scenario for the evolution of long-distance dispersal involves initially large benefits to cooperative group living, followed by the appearance of several correlated traits including: loss of male mating dispersal, regular inbreeding and a female-biased sex ratio. The resulting inbred colonies face a greater risk of pathogen attacks with increasing colony size. We suggest that colony-size dependent long-distance dispersal of mated females evolved as part of the syndrome of correlated traits that characterize the transition to inbred sociality.

20-5 Oral

THE EVOLUTION OF AVIAN SOCIETIES: HOW DO KIN-STRUCTURED POPULATIONS DEVELOP?

Ben Hatchwell [1], Andrew P. Beckerman [1], Stuart Sharp [2]

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The evolution of sociality presents a major problem for evolutionary biologists, and despite decades of research into avian cooperative breeding systems, many questions about the evolution of their societies remain unresolved. A review of the structure of avian societies shows that cooperation occurs predominantly within kin groups, which is consistent with the idea that delayed dispersal is a critical process in family formation. However, cooperation also commonly occurs within networks of individuals living in 'kin neighbourhoods'. These kin associations may form through limited rather than delayed dispersal, thus maintaining population viscosity as a key process in the evolutionary route to cooperative breeding. However, there is substantial overlap in the dispersal strategies of social and non-social bird species, and comparative analyses have not differentiated between the viscosity of social and non-social populations, except at a coarse level. Using a demographic simulation model, we consider the roles that demography and life history may play in generating kin-structured populations. We show that other processes, such as adult survival rate and the pattern of offspring mortality, can have profound effects on the mean relatedness of populations. We conclude that a broader perspective that encompasses life history and demographic processes may provide fresh insights into the evolution of avian societies.

20-6 Oral

SOCIAL TRANSFER OF FUNGAL RESISTANCE IN ANTS

Anabelle Reber [1], Michel Chapuisat [1]

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Social evolution and parasites can affect each other in multiple ways. On the one hand, social life may increase the exposure to parasites. The pressure of parasites may also select for more genetically diverse groups, thereby possibly acting as a brake on the evolution of altruism by kin selection. On the other hand, social interactions and collective defences can limit the impact of parasites. Experiments in ants have indicated that group diversity improves the mean resistance of workers exposed to entomopathogenic fungi. We will present results of new experiments examining if a transfer of resistance occurs (1) between genetically diverse ants and (2) between ants that differ in their past exposure to a fungal pathogen. In the first experiment, we found that the survival of *Formica selysi* workers challenged with *Beauveria bassiana* was improved in presence of ants from another genetic lineage. This increase in resistance occurred only if ants were still in contact after infection, which suggests a curative behaviour. In the second experiment, we found that the survival of ants that had not been exposed to the parasite was improved after having been in contact with previously immunized ants. This social transfer of resistance occurred before infection and may thus have a prophylactic effect. Overall, such behavioural interactions and transfers of resistance have the potential to greatly increase disease resistance in social insect colonies. These results also suggest that parasites may select for more complex societies in some cases.

20-7 Oral

ENVIRONMENTAL AND GENETIC COMPONENTS OF A MAJOR EVOLUTIONARY TRANSITION: SOCIAL PHENOTYPE IN HALICTID BEES

Jeremy Field [1], Robert J. Paxton [2], Antonella Soro [2], Cathy Bridge [1]

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The evolution of eusociality is one of the major biological transitions. Instead of each individual reproducing independently, there is a society with a queen and sterile workers. Eusociality involves a complex set of traits including cooperative brood care, a reproductive division of labour, communication and coordinated cooperative behaviours such as foraging and colony defence. Nevertheless, it has been suggested that the transition to eusociality might sometimes be environmentally induced.

Sweat bees (Halictidae) are particularly interesting becaue they include several recent transitions in both directions between eusociality and non-sociality. Almost uniquely among Hymenoptera, there are also 'socially polymorphic' taxa in which different populations of the same species have different social phenotypes. We carried out the first direct test of what underpins social phenotype in sweat bees using the socially polymorphic *Halictus rubicundus. H. rubicundus* is non-social in colder parts of its distribution but eusocial in warmer parts. Do these differences reflect genetic change, or differential expression of the same set of genes? We present results from transplanting bees between sites to test whether they are socially plastic. We also test whether foraging behaviour differs between bees from different sources in a common garden, and use microsatellite markers to examine genetic differentiation among populations that express different social phenotypes.

20-8 Oral

EXPERIMENTAL EVOLUTION OF PAIR BONDING IN THE PRAIRIE VOLE *(MICROTUS OCHROGASTER)*

Lisa A. McGraw [1], Larry J. Young [2]

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The prairie vole (*Microtus ochrogaster*) is a socially monogamous rodent that unlike the majority of mammalian species, forms long-term relationships between sexual partners, or pair bonds. Other vole species such as the meadow vole (*M. pennsylvanicus*) do not form pair bonds and are relatively asocial. Comparative studies between vole species and within species studies of prairie voles have demonstrated that region-specific expression of the vasopressin 1a receptor (V1aR) in the male vole brain is associated with both species differences and intraspecific variation in pair bonding behavior. However, within prairie voles, it is still unclear if variation in V1aR expression is a major source of the heritable diversity in male pair bonding behavior. We hypothesized that male pair bonding behavior is a heritable trait and that through selective breeding, we could generate two lines of prairie voles where males display either a high propensity to form pair bonds or do not form pair bonds at all. If variation in the V1aR system is a major heritable variable leading to diversity in social bonding behavior, then we would predict that male prairie voles from the selected lines would also display different distributions of V1aR binding in the brain. After four generations of experimental evolution, we have already observed a trend towards divergence in behaviors between lines and are examining line differences in the location and density of V1aR in the brain.

20-9 Oral

THE COEVOLUTION OF COOPERATION AND DISPERSAL IN SOCIAL GROUPS AND ITS IMPLICATIONS FOR THE EMERGENCE OF MULTICELLULARITY

Michael E. Hochberg [1,2], Daniel J. Rankin [3], Michael Taborsky [3]

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Recent work on the complexity of life highlights the roles played by evolutionary forces at different levels of individuality. One of the central puzzles in explaining transitions in individuality for entities ranging from complex cells, to multicellular organisms and societies, is how different autonomous units relinquish control over their functions to others in the group. In addition to the necessity of reducing conflict over effecting specialized tasks, differentiating groups must control the exploitation of the commons, or else be out-competed by more fit groups.

We propose that two forms of conflict – access to resources within groups and representation in germ line – may be resolved in tandem through individual and group-level selective effects. Specifically, we employ an optimization model to show the conditions under which different within-group social behaviors (cooperators producing a public good or cheaters exploiting the public good) may be selected to disperse, thereby not affecting the commons and functioning as germ line. We find that partial or complete dispersal specialization of cheaters is a general outcome. The propensity for cheaters to disperse is highest with intermediate benefit:cost ratios of cooperative acts and with high relatedness. An examination of a range of real biological systems tends to support our theory, although additional study is required to provide robust tests.

We suggest that trait linkage between dispersal and cheating should be operative regardless of whether groups ever achieve higher levels of individuality, because individual selection will always tend to increase exploitation, and stronger group structure will tend to increase overall cooperation through kin selected benefits. Cheater specialization as dispersers offers simultaneous solutions to the evolution of cooperation in social groups and the origin of specialization of germ and soma in multicellular organisms.

20-10 Oral

SOPHISTICATED OLFACTION AND THE EVOLUTION OF SOCIAL STRATEGIES IN AFRICAN MOLE-RATS

Sofia Stathopoulos [1], Jacqueline M. Bishop [2], Nigel C. Bennett [3], Colleen O'Ryan [1]

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African mole-rats (Bathyergidae), a unique family of subterranean rodents, display the widest array of sociality among mammals, ranging from solitary to eusocial species. Life underground imposes unusual constraints on social interactions, resulting in a suite of adaptations. In the absence of visual cues, enhanced olfaction is predicted to be fundamental. The olfactory receptor (OR) gene family is the largest in the vertebrate genome. OR polymorphisms reflect the diversity of odorous chemicals that species can detect. The ratio of functional receptor genes to pseudogenes is used as a measure of olfactory aptitude. We hypothesise that well-developed olfaction in African mole-rats results in increased polymorphism at OR loci, driven by strong positive selection. Using genomic data from 14 mole-rat species we identified 116 unique OR sequences and found a 1:1 ratio of OR genes:pseudogenes, which is lower than ratios reported for model rodent species. The number of potentially functional OR genes however is greater, suggesting expansion of the gene repertoire in mole-rats. Phylogenetic relationships among OR sequences suggest that their diversification preceded speciation within the Bathyergidae, and may account for the large number of pseudogenes that have accumulated since the Miocene origins of contemporary bathyergids. Notably, comparable levels of positive selection drive functional OR variability among eusocial, social and solitary lineages, suggesting that a subterranean lifestyle is the major force responsible for OR diversification. Olfaction undoubtedly constitutes a fundamental sense for these subterranean rodents. We propose that enhanced chemo-sensory ability may have predisposed ancestral bathyergids to exploit a range of social strategies.

20-1 Poster The evolution of cooperation and task sharing in *Xyleborina* (Curculionidae: Scolytinae), fungus gardening ambrosia beetles

PETER H.W. BIEDERMANN[1], KIER R. KLEPZIG[2], MICHAEL TABORSKY[1]
[1]University Bern, Institute of Ecology & Evolution, Department of Behavioural Ecology, Bern, Switzerland
[2]USDA Forest Service Southern Research Station, Pineville, United States

20-2 Poster The genetic basis for the evolution of reproductive altruism

AURORA M. NEDELCU
University of New Brunswick, Department of Biology, Fredericton, Canada

20-3 Poster Adoption of an aggregated nesting habit: relative importance of biotic and abiotic factors for a solitary wasp

MANUELA GIOVANETTI
Queen's University Belfast, School of Biological Sciences, Belfast, United Kingdom

20-4 Poster Are there benefits to foraging with kin in an inbred social spider?

REUT BERGER-TAL, YAEL LUBIN
Ben-Gurion University, Blaustein Institutes for Desert Research, Mitrani Department of Desert Ecology, Midreshet Ben-Gurion, Israel

20-5 Poster A gene for queen control: Krüppel homolog 1 is linked to social organization in bees

HAGAI SHPIGLER[1], CHRISTINA M. GROZINGER[2,3], GUY BLOCH[1], HARLAND M. PATCH[2,3], MIRA COHEN[1], YONGLIANG FAN[2]
[1]The Hebrew University of Jerusalem, The Alexander Silberman Insitute of Life Sciences, Department of Evolution, Systematics and Ecology, Jerusalem, Israel
[2]North Carolina State University, Department of Entomology and Genetics, Raleigh, United States
[3]Pennsylvania University, Huck Institutes of the Life Sciences, University Park, United States

20-6 Poster Kin recognition in a primitively eusocial sweat bee

ROBERT J. PAXTON[1], ANTONELLA SORO[1], MARION U. ZOBEL[2], MANFRED AYASSE[3]
[1]Queen's University Belfast, School of Biological Sciences, Belfast, United Kingdom
[2]University of Tübingen, Department of Animal Physiological Ecology, Tübingen, Germany
[3]University of Ulm, Institute of Experimental Ecology, Ulm, Germany

20-7 Poster Evolution of Social Behaviour in the *Egernia* Group of Australasian Skinks

JULIE I. HAGEN[1,2], MICHAEL BULL[1], STEVE DONNELLAN[2]
[1]Flinders University, Department of Biological Sciences, Adelaide, Australia
[2]South Australian Museum, Adelaide, Australia

20-8 Poster Selective forces favoring social life in lower termites

JUDITH KORB
University of Osnabrueck, Department of Biology/Chemistry: Behavioral Biology, Osnabrueck, Germany

20-9 Poster Teasing apart indirect and direct fitness as drivers of helping behaviour

ELLI LEADBEATER, JEREMY FIELD
University of Sussex, Department of Biology and Environmental Science, Brighton, United Kingdom

20-10 Poster A chemical signal of offspring quality affects maternal care in a social insect

FLORE MAS, MATHIAS KÖLLIKER
University of Basel, Zoological Institute, Department of Evolutionary Biology, Basel, Switzerland

Intralocus sexual conflict: detection, resolution and consequences

eseb
12th Congress
Turin 2009

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Program

Friday August 28 - **Symposium 21**

Location: Room 5

Intralocus sexual conflict: detection, resolution and consequences

Organizers:	*Adam Chippindale, Queen's University, Kingston, Canada* *Steve Chenoweth, University of Queensland, Australia*
9.45 - 10.15	**GÖRAN ARNQVIST** (invited) Intralocus sexual conflict and the gender load: correlated evolution between population fitness and sexual dimorphism in seed beetles
10.15 - 10.45	**BARRY SINERVO** (invited) Antagonistic selection and ontogenetic conflict in the wild
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**RYAN CALSBEEK** Sex, Lies, and the resolution of conflict in the brown anole, *Anolis sagrei*
11.35 - 11.55	**CRAIG A. WALLING** Sexually-antagonistic genetic variation in red deer: which traits and at what age?
11.55 - 12.15	**NILS ANTHES** Broadening our view on sexual selection gradients: intralocus conflict over mating in a hermaphrodite
12.15 - 12.35	**JON E. BROMMER** Intersexual genetic antagonism across traits
12.35 - 13.35	*Lunch*
13.35 - 13.55	**ROBERT M. COX** Sexually antagonistic selection, sexual dimorphism, and the resolution of intralocus sexual conflict
13.55 - 14.15	**PAOLO INNOCENTI** Gene expression profiling of intralocus sexual conflict and fitness variation in *Drosophila melanogaster*
14.15 - 14.35	**HOWARD RUNDLE** Sexually-antagonistic genetic variance for fitness in an ancestral and a novel environment
14.35 - 14.55	**ALEXANDRE ROULIN** Intralocus sexual conflict over melanin-based ornament is resolved by sex ratio bias and genomic imprinting of autosomal genes
14.55 - 15.25	*Coffee break*

21-1 Oral

INTRALOCUS SEXUAL CONFLICT AND THE GENDER LOAD: CORRELATED EVOLUTION BETWEEN POPULATION FITNESS AND SEXUAL DIMORPHISM IN SEED BEETLES

Göran Arnqvist [1]

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Intralocus sexual conflict occurs when the direction of selection on an allele depends upon in which sex it is expressed. Such sexually antagonistic loci will in theory cause a gender load in populations, because sex-specific selection in one sex will compromise adaptation in the other. Although recent studies have unveiled intralocus sexual conflict, it is not clear whether it represents a transient evolutionary state, where conflict is rapidly resolved by the evolution of sexual dimorphism, or whether it is a general and chronic impediment to adaptation. Intralocus sexual conflict should manifest itself as correlated evolution between fitness and sexual dimorphism. However, comparative tests of this ultimate prediction have been unfeasible because variation in sexually congruent adaptation obscures the correlation. Using artificial selection, I minimize the impact of such masking variation by comparing fitness and sexual dimorphism across distinct laboratory populations of seed beetles that are all uniformly and well adapted to a shared environment. I show that sexual dimorphism in juvenile development time, a key life-history trait under sexually antagonistic selection in this model system, is positively related to fitness. This effect is due to a correlated evolution between population fitness and development time that is positive in females but negative in males. Apparently, loosening the genetic bind between the sexes have allowed the sexes to approach their distinct adaptive peaks.

21-2 Oral

ANTAGONISTIC SELECTION AND ONTOGENETIC CONFLICT IN THE WILD

Barry Sinervo [1]

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In nature, the expression of phenotypic traits in the sexes due the action of single genes (pleiotropy) is thought to generate conflicting pressure on the development of traits in the sexes. In most organisms, females are under natural selection and males are under intense sexual selection. Moreover, the presence of alternative strategies within each sex should intensify and perhaps multiplicatively affect the intensity of such antagonistic sexual selection. Inferences in the laboratory are crucial to establish the genetic effects. However, all animals (and plants) are functional in nature and methods must be developed to assess the intensity of antagonistic patterns of selection. Using the deep field pedigree of side-blotched lizard (20 generations, currently 7600 links), we analyze patterns of selection on several gene complexes, including: 1) the alternative strategy locus called OBY (named after the three throat color alleles: orange, blue and yellow), 2) genes for clutch size, which are expressed in females, but the genes also affect survival and success of males via genetically correlated male traits related to sexual selection, 3) the expression of immune function genes, and 4) anti-predator strategies that are governed by genes for dorsal patterns and escape behavior. A striking finding of the studies is that antagonistic selection is not just due to pleiotropy, but substantial antagonistic selection arises from gene epistasis. Each of the trait complexes are physically unlinked and yet they interact to generate alternative fitness optima between the sexes. Therefore, antagonistic selection in nature may be due to epistasis.

21-3 Oral

SEX, LIES, AND THE RESOLUTION OF CONFLICT IN THE BROWN ANOLE, *ANOLIS SAGREI*

Ryan Calsbeek [1]

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Males and females share most of their genome yet often experience very different forms of selection. Consequently, traits that are adaptive when expressed in males may often be maladaptive if expressed in females. Recent studies demonstrating negative correlations in fitness between parents and their opposite-sex progeny suggest that natural selection may favor a reduction in trait correlations between the sexes to partially mitigate intralocus sexual conflict. Here we provide evidence that male and female brown anoles, *Anolis sagrei*, experience sex specific selection pressures owing to a large number of traits that are subject to sexual conflict. Our data suggest that females should be confront a conundrum in that any given sire will produce high quality progeny of only one sex. However, negative genetic correlations between the sexes and the ability of females to bias fertilizations both provide mechanisms by which females can resolve this sexual conflict.

21-4 Oral

SEXUALLY-ANTAGONISTIC GENETIC VARIATION IN RED DEER: WHICH TRAITS AND AT WHAT AGE?

Craig A. Walling [1], Josephine M. Pemberton [1], Katharina Foerster [2], Tim H. Clutton-Brock [3], Loeske E. B. Kruuk [1]

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Currently there is considerable interest in the observation that differences in selection pressures acting on the sexes can result in sexually antagonistic genetic variation, where genes that are beneficial when expressed in males are detrimental in females and vice versa. A long term individual study has shown a negative genetic correlation between male and female fitness in a wild population of red deer on the Isle of Rum, Scotland. Understanding this negative genetic correlation requires detailed investigation of the quantitative genetic variation in life history and morphological traits that influence fitness. Importantly, novel random regression animal models have recently demonstrated that genetic variation for a number of such life history traits is not consistent over ontogeny. Here, we use random regression and animal models allowing non-normal distributions to investigate the underlying genetic variation of a number of life history traits important in determining both male and female fitness. These methods allow us to investigate not only which traits may be driving the negative genetic correlation between male and female fitness, but also the role that changes in genetic variation over ontogeny play in mediating or exacerbating these effects. Such information should provide insight into the relative importance of different life history traits in generating sexually antagonistic genetic variance and a unique understanding of ontogenetic variation in their contributions.

21-5 Oral

BROADENING OUR VIEW ON SEXUAL SELECTION GRADIENTS: INTRALOCUS CONFLICT OVER MATING IN A HERMAPHRODITE

Nils Anthes [1], Dennis Sprenger [1]

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The relationship between mating success and reproductive success (‘sexual selection gradient’) provides a common proxy for the overall intensity of sexual selection on male and female characters. Experimental work in vertebrates and insects has established this approach to successfully uncover patterns such as sex role reversal or intralocus sexual antagonism. However, generalizations about the consequences of sexual selection require empirical data from systems beyond the ‘standard’ separate sex organisms. For the first time, we experimentally assess sexual selection gradients for male and female functions in a simultaneous hermaphrodite, the freshwater gastropod *Biomphalaria glabrata*. By measuring mating success at different (pre- and postcopulatory) levels, our novel approach allows disentangling the strength of sexual selection between successive selection episodes and thus improves the precision of the selection gradient methodology. Moreover, our data provide novel information about (i) the sex function experiencing stronger selection in a hermaphrodite, (ii) the ‘conflict load’ between male and female function over mating rate, (iii) the sex role that provides the higher added value of sequestering further mates (i.e., the ‘preferable mating role’), and (iv) candidate traits exposed to sexual selection in this system.

21-6 Oral

INTERSEXUAL GENETIC ANTAGONISM ACROSS TRAITS

Jon E. Brommer [1]

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Traits that are not closely correlated with fitness generally have a high intersexual genetic correlation, whereas evidence is accumulating that fitness-related traits may show sexually antagonistic genetic effects resulting in a low or even negative intersexual genetic correlation. Here, I explore this relationship in a natural population of collared flycatchers *Ficedula albicollis*. I employ an animal model approach, which allows estimation of the genetic correlation across the sexes for a number of morphometric and behavioural traits and for fitness and its components. The findings are consistent with a build-up of intersexual genetic antagonism as one moves across the trait continuum towards fitness. I discuss the extent to which the pattern observed is indicative of sexual conflict. I emphasize that intersexual genetic antagonism may present a considerable force in maintaining genetic variance in fitness-related traits.

21-7 Oral

SEXUALLY ANTAGONISTIC SELECTION, SEXUAL DIMORPHISM, AND THE RESOLUTION OF INTRALOCUS SEXUAL CONFLICT

Robert M. Cox [1], Ryan Calsbeek [1]

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Males and females share most of their genomes and express many of the same phenotypic traits, yet the sexes often have markedly different selective optima for these shared traits. This sexually antagonistic (SA) selection generates intralocus sexual conflict that is thought to be resolved through the evolution of sexual dimorphism. However, we currently know little about the prevalence of SA selection in wild populations, the components of fitness that generate sexual antagonism, or the relationship between sexual dimorphism and current SA selection. We reviewed published selection studies in wild animal populations to address these questions using 424 selection estimates representing 89 traits from 34 species. Males and females often differed substantially in the direction and magnitude of selection on shared traits, although statistically significant SA selection was relatively uncommon. Sexual selection generated stronger sexual antagonism than fecundity or viability selection, and these individual components of fitness tended to reinforce one another to generate even stronger sexual antagonism for net fitness. Traits exhibiting strong sexual dimorphism exhibited greater SA selection than did weakly dimorphic traits, although this pattern was not significant after controlling for the inclusion of multiple traits nested within species. Our results suggest that intralocus sexual conflict may often persist despite the evolution of sexual dimorphism.

21-8 Oral

GENE EXPRESSION PROFILING OF INTRALOCUS SEXUAL CONFLICT AND FITNESS VARIATION IN *DROSOPHILA MELANOGASTER*

Paolo Innocenti [1], Edward H. Morrow [1]

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Conflict between the sexes over allelic variation is thought to have a significant impact on fitness through its effect on a number of loci. However, the identity and number of these sexually antagonistic loci is still unknown. We used a combination of hemiclonal analysis and modern genomics technology (microarrays) to ascertain the existence of intralocus sexual conflict and to investigate its genetic basis in *D. melanogaster*. One hundred hemiclonal lines were established and assayed for both male and female relative fitness in a replicated design under competitive conditions. We found significant genetic variation for both male and female relative fitness, as well as a significant negative genetic correlation between the sexes – thereby confirming the existence of intralocus sexual conflict. The gender-by-genotype interaction was characterized by a strong crossing pattern: some genomes show strong reversals in fitness when expressed in the two sexes (either strongly "masculinized" or "feminized"), while others show average fitness independent of gender. In order to identify which loci contribute to fitness variation and the sexually antagonistic effect we compared gene expression profiles from groups of masculinized, feminized and intermediate genomes. This powerful empirical approach provides an experimentally-derived estimate for the proportion of the transcriptome affected by intralocus sexual conflict and identifies the genes and biological processes associated with the fitness load.

21-9 Oral

SEXUALLY-ANTAGONISTIC GENETIC VARIANCE FOR FITNESS IN AN ANCESTRAL AND A NOVEL ENVIRONMENT

Matthieu Delcourt [1], Mark Blows [2], Howard D. Rundle [1]

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The intersex genetic correlation for fitness (r_W^{fm}), a standardized measure of the degree to which male and female fitness covary genetically, has consequences for important evolutionary processes but few estimates are available and none have explored how it changes with environment. Using a half-sibling breeding design, we estimated the genetic (co)variance matrix (**G**) for male and female fitness, and the resulting r_W^{fm}, in *Drosophila serrata*. Our estimates were performed in two environments: the laboratory yeast-food to which the population was well adapted, and a novel corn-food. The major axis of genetic variation for fitness in the two environments, accounting for 51.3% of the total genetic variation, was significant and revealed a strong signal of sexual antagonism, loading negatively in both environments on males but positively on females. Consequently, estimates of r_W^{fm} were negative in both environments (−0.34 and −0.73 respectively), indicating that the majority of genetic variance segregating in this population has contrasting effects on male and female fitness. The possible strengthening of the negative r_W^{fm} in the novel environment may be a consequence of no history of selection for amelioration of sexual conflict, and may explain why sexual selection may not commonly promote adaptation to novel environments.

21-10 Oral

INTRALOCUS SEXUAL CONFLICT OVER MELANIN-BASED ORNAMENT IS RESOLVED BY SEX RATIO BIAS AND GENOMIC IMPRINTING OF AUTOSOMAL GENES

Alexandre Roulin [1], Res Altwegg [2], Henrik Jensen [3], Ingelin Steinsland [4], Michael Schaub [5,6]

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[3]*Norwegian University of Science and Technology, Department of Biology, Trondheim, Norway*
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Males and females are caught in an evolutionary conflict which stems from their different reproductive interests. Sex-specific selection pressures generate sexual genetic conflicts because selection acting on one sex tends to displace the other sex from its optimum. Theory predicts that the resolution of this conflict selects for genomic imprinting, sex ratio bias and non-random location of sexually antagonistic genes on autosomes or sex chromosomes. We report a unique case for these three mechanisms in a long-term study of the barn owl, a species displaying a heritable melanin-based ornament with females displaying larger black spots on their plumage than males. We show that this ornament is sexually antagonistically selected as juvenile survival strongly increased with spot size in females and weakly decreased in males. In line with the hypothesis of genomic imprinting, sons had high survival only when their mother was small-spotted and daughters only when their father was large-spotted. As expected offspring sex ratio was adaptively biased towards sons when the mother or the father was small-spotted. Finally, intense directional selection on spot size in females resulted in an increase in this trait over the 12-year study period in our population, because of a change in the architecture of autosomal genes. Our results demonstrate that sexually antagonistic selection on autosomal genes coding for an ornament has profound effect not only on the maintenance of sexual dimorphism and genetic variance but also on the evolution of genomic imprinting and sex ratio.

21-1 Poster The paradoxical spread of a new Y chromosome – a role for sexually antagonistic selection

RICHARD A. NICHOLS[1], PARIS VELTSOS[2], IRENE KELLER[3]
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21-2 Poster Inferences on the molecular evolution of sex biased expression in the Drosophilids

CHARLES D. L. MULLON
UCL, GEE, CoMPLEX, London, United Kingdom

21-3 Poster Genetic conflict and non-adaptive selection in *Drosophila simulans*: a population genetics analysis of X chromosomes meiotic drive

HÉLOÏSE BASTIDE[1,2], LUCIE FOUVRY[1,2], MICHEL CAZEMAJOR[1], DAVID OGEREAU[1], CATHERINE MONTCHAMP-MOREAU[1]
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[2]Universite Paris Sud, Orsay, France

21-4 Poster The Hill-Robertson effect on the W chromosome does not explain mtDNA diversity in birds

SHINICHI NAKAGAWA[1], JOANNA RUTKOWSKA[2], MALGORZATA LAGISZ[3]
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Inbreeding depression: from gene expression to population viability

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Program

Saturday August 29 - **Symposium 22**

Location: Room 1

Inbreeding depression: from gene expression to population viability

Organizers:	*Bengt Hansson, Lund University, Sweden* *Sara Naurin, Lund University, Sweden*

9.45 - 10.15	**TORSTEN N. KRISTENSEN** (invited) Inbreeding and environmental stress – investigated on different levels of biological organization using *Drosophila* species as model organisms
10.15 - 10.45	**ERIK POSTMA** (invited) Individual- and population-level causes and consequences of inbreeding depression in the wild
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**SUSANNE ZAJITSCHEK** The relationship between levels of inbreeding, sperm numbers and the environment
11.35 - 11.55	**GABRIELA GLEISER** Inbreeding depression for male fertility in an animal-pollinated plant
11.55 - 12.15	**CHRISTOPH R. HAAG** Population-wide inbreeding favours the invasion of an asexual competitor
12.15 - 12.35	**EMMA VITIKAINEN** Effects of inbreeding on ant colonies - a long term study on a natural population
12.35 - 12.55	**DAN NUSSEY** Inbreeding depression and ageing in island populations of mammals
12.55 - 13.55	*Lunch*

22-1 Oral

INBREEDING AND ENVIRONMENTAL STRESS – INVESTIGATED ON DIFFERENT LEVELS OF BIOLOGICAL ORGANIZATION USING *DROSOPHILA* SPECIES AS MODEL ORGANISMS

Torsten N. Kristensen [1], Kamilla S. Pedersen [1], Ary A. Hoffmann [2], Volker Loeschcke [3]

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Increased rates of inbreeding due to reduced population size are often observed in small populations. We investigate the impact of inbreeding and interactions between inbreeding and environmental stress from the DNA to the fitness level. Recent developments in molecular and systems biology have led to novel approaches in the study of inbreeding, and ‘omics’ technologies can be used to reveal new information on the impact of inbreeding on different levels of biological organization. Results from our laboratory suggest that inbreeding leads to marked changes in gene expression, proteome and metabolic profile and that inbreeding and environmental stress both independently and synergistically affect these traits. Furthermore, we have used SNP markers to show that a slow rate of inbreeding reduces the amount of genetic variation less than a fast rate of inbreeding, despite the same expected absolute level of inbreeding. These results are of interest in relation to explaining the inbreeding-rate dependent levels of inbreeding depression often observed. Finally, we perform experiments under semi-natural conditions to increase our knowledge on the impact of the environment on the level of depression. Results suggest that inbreeding depression is highly dependent on the environmental conditions and seems to be more severe under stressful temperatures.

22-2 Oral

INDIVIDUAL- AND POPULATION-LEVEL CAUSES AND CONSEQUENCES OF INBREEDING DEPRESSION IN THE WILD

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Inbreeding depression, the reduced survival and performance of individuals with related parents, is among the oldest and longest standing topics in evolutionary genetics. This continued interest stems from the fact that it takes a central position in a large number of phenomena in biology, ranging from fundamental biological processes such as mate choice and dispersal to the conservation of endangered species, as well as human and animal health and productivity. Here we will first provide a brief overview of some basic but important concepts related to the quantification of inbreeding, with special reference to the relative merits of molecular and pedigree data. Subsequently, we will discuss the potential deleterious effects of inbreeding, and emphasise the importance of obtaining a better understanding of the genetic basis of such inbreeding depression. We will then illustrate the apparent ubiquity of inbreeding depression in the wild with examples from our own work, but will also highlight a number of important but fascinating complications. Finally, we will discuss and illustrate how inbreeding depression, a phenomenon acting on the level of the individual, can have population-level consequences.

On the whole, we will argue that despite over a century of research, some important aspects of the evolutionary consequences of inbreeding in natural populations remain poorly understood. A number of exciting recent statistical and molecular developments may however have the potential to change this.

22-3 Oral

THE RELATIONSHIP BETWEEN LEVELS OF INBREEDING, SPERM NUMBERS AND THE ENVIRONMENT

Susanne Zajitschek [1,2], Robert C. Brooks [2]

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Inbreeding can have profound impacts on reproductive traits. Here, we present data on inbreeding depression in sperm quantity in the guppy, *Poecilia reticulata*, with sperm numbers decreasing with increasing inbreeding coefficients. Moreover, we report on differences in the magnitude of inbreeding depression under different environmental conditions. Even though the overall effect of decreasing fitness with increasing inbreeding was evident under both experimental conditions, the effect was magnified under more natural conditions: In semi-natural enclosures we found severely elevated inbreeding depression compared to Laboratory conditions. Laboratory experiments generally aim to eliminate factors such as competition for resources and mating partners in order to minimise stress that might be interfering with experimental outcomes. Nevertheless, our study highlights the importance of near-natural conditions in studies examining effects of inbreeding of fitness, as negative fitness consequences of inbreeding might be easily underestimated or even overlooked under standard Laboratory conditions. We also discuss the importance of female preferences for outbred versus inbred males as an adaptive mechanism to avoid the undesirable effects of inbreeding on male reproductive traits in this species.

22-4 Oral

INBREEDING DEPRESSION FOR MALE FERTILITY IN AN ANIMAL-POLLINATED PLANT

Gabriela Gleiser [1], Frederic Austerlitz [2], Giorgina Bernasconi [1]

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Inbreeding can reduce the fitness of inbred relative to outbred offspring (inbreeding depression). However, we have very limited knowledge of inbreeding depression for pollination success via the male function in flowering plants. We tested whether inbred and outbred plants differ in siring success after open pollination in the dioecious white campion, *Silene latifolia* (Caryophyllaceae). To this end, we exposed to natural pollination male and female plants that were issued from crosses in which inbreeding and pollen competition intensity were simultaneously manipulated. We used microsatellite markers to genotype the seeds formed, and analysed male fertility by jointly considering the influence of experimentally controlled factors (inbreeding, pollen competition intensity), as well as spatial, phenotypic and kinship effects, using a neighbourhood model. Inbreeding, pollen competition intensity in the previous generation and several phenotypic traits significantly affected male fertility. While inbreeding depression was already demonstrated to affect several vegetative traits in this species, we show here that the level of biparental inbreeding in males also reduces their success as pollen donors.

22-5 Oral

POPULATION-WIDE INBREEDING FAVOURS THE INVASION OF AN ASEXUAL COMPETITOR

Christoph R. Haag [1]

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Colonization of empty habitat patches in metapopulations often leads to genetic bottlenecks due to low numbers of colonizers. The consequences of such genetic bottlenecks may differ between sexual and asexual species: In sexual species, genetic bottlenecks can lead to inbreeding (increased homozygosity), but in asexual species this does not happen because they do not breed. To test the idea that genetic bottlenecks lead to an increased advantage of asexuals due to inbreeding in sexuals, I performed experiments with cyclical parthenogenetic (“sexual”) and obligate parthenogenetic (“asexual”) *Daphnia pulex* from highly subdivided metapopulations. I compared their relative fitness in different artificial populations, which were either strongly inbred, of natural inbreeding level, or outbred. Asexuals had a much lower fitness when in competition with an outbred sexual population than with either strongly or naturally inbred populations, where they persisted and sometimes drove the sexual populations to extinction. This suggests that asexuals are more easily able to invade habitats such as highly fragmented metapopulations, where sexuals suffer reduced fitness due to inbreeding.

22-6 Oral

EFFECTS OF INBREEDING ON ANT COLONIES - A LONG TERM STUDY ON A NATURAL POPULATION

Emma Vitikainen [1], Cathy Haag-Liautard [2], Liselotte Sundström [1]

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Inbreeding results in lowered fitness, inbreeding depression, in most species studied so far, but information on natural populations is still scarce and limited to few well studied taxa. A particularly important but in this respect poorly known group is the social Hymenoptera - ants, bees and wasps. Their sociality has interesting implications for studies of inbreeding, because both the reproductive females (queens) and their worker offspring may be affected. Furthermore, despite their relative abundancy and apparent dominance of many ecosystems, the effective population sizes of social insects may be small due to the reproductive division of labour within the colonies. Perennial ant colonies provide an excellent study system for gaining insight of the combined effects of inbreeding and environment, as they can be followed from year to another, and their genetic structure and fitness measured with non destructive sampling techniques. Our study is based on a survey of a natural population of the narrow-headed ant *Formica exsecta*, located in the SW coast of Finland. In this study, we found that the inbreeding level of the workers (measured as homozygosity in 10 microsatellite marker loci) influences colony reproductive output in two ways: by decreasing the production of female sexuals, and by reducing male size. We suggest both effects are mediated through the efficacy of the workers. We will also discuss the interactions between the yearly weather conditions and inbreeding, and their significance in determining the reproductive output of the colonies in the long term.

22-7 Oral

INBREEDING DEPRESSION AND AGEING IN ISLAND POPULATIONS OF MAMMALS

Dan Nussey [1]

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Interactions between the effects of inbreeding and the ageing process on fitness may represent an important form of context-dependent inbreeding depression. An increase in inbreeding depression with age is also predicted under the mutation accumulation theory of ageing. Although inbreeding-by-age interactions affecting fitness parameters are well documented in laboratory study systems, very few studies have tested for such interactions in either human populations or in wild vertebrate populations. Here, we test for age-dependent variation in inbreeding depression affecting maternal fitness traits in an inbred human population and two wild mammal populations. Analyses were conducted using historical data from an endogamous human population from Isle aux Coudres, Quebec and life history and pedigree data collected from two island populations of wild ungulates. Our results highlight the potential importance of inbreeding-by-age interactions in natural settings.

22-1 Poster **Do abiotic and biotic environmental stressors differ in their effects on the magnitude of inbreeding depression?**

LARAMY ENDERS, LEONARD NUNNEY

University of California, Department of Ecology, Evolution and Organismal Biology, Riverside, United States

22-2 Poster **Sex-specific consequences of inbreeding in *Drosophila melanogaster* and the maintenance of sexual reproduction**

MARTIN A. MARTIN, SEAN FEAGAN, ADAM K. CHIPPINDALE

Queen's Univeristy, Department of Biology, Kingston, Canada

22-3 Poster **The influence of sexual selection on the rate of extinction and purging in small inbred populations of bulb mite *Rhizoglyphus robini***

MAGDALENA JARZEBOWSKA, JACEK RADWAN

Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland

22-4 Poster **Effects of inbreeding rate on inbreeding depression, population viability, and purging of genetic load**

NINA PEKKALA, MIKAEL PUURTINEN, JANNE S. KOTIAHO

University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland

22-5 Poster **Effects of inbreeding on cognition in *Drosophila***

VIRGINIE NÉPOUX, TADEUSZ J. KAWECKI

University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland

22-6 Poster **Inbreeding depression and phenotypic plasticity in a hermaphrodite: effects of mate availability and predation risk on life-history traits**

JOSH R. AULD[1], PATRICE DAVID[1], PHILIPPE JARNE[1], RICK RELYEA[2]

[1]CEFE - CNRS, Montpellier, France,
[2]University of Pittsburgh, Department of Biological Sciences, Pittsburgh, United States

22-7 Poster **Inbreeding depression and hybrid vigor in different populations of *Daphnia magna***

EVELIN HUERLIMANN

University of Fribourg, Department of Biology, Fribourg, Switzerland

22-8 Poster **Conflict over inbreeding in a poeciliid fish, *Heterandria formosa***

OUTI ALA-HONKOLA[1], ANNIKA UDDSTRÖM[1], BEATRIZ DIAZ PAULI[2], LAURA TUOMINEN[1], KAI LINDSTRÖM[3]

[1]University of Helsinki, Department of Biological and Environmental Sciences, Helsinki, Finland
[2]University of Bergen, Department of Biology, Bergen, Norway
[3]Åbo Akademi University, Department of Environmental and Marine Biology, Turku, Finland

22-9 Poster **Extreme promiscuity: mates relatedness reveals some "order" in a seemingly "free for all" mating system**

PATRICK BERGERON[1], DANY GARANT[1], DENIS RÉALE[2]

[1]Université de Sherbrooke, Département de Biologie, Sherbrooke, Canada
[2]UQAM, Department of Sciences biologiques, Montreal, Canada

22-10 Poster **Adaptive genetic variation and inbreeding in house sparrows**

AASA A. BORG[1], SINDRE A. PEDERSEN[1], ENRIK JENSEN[1], HELENA WESTERDAHL[2]

[1]Norwegian University of Science and Technology, CCB, Department of Biology, Trondheim, Norway
[2]Lund University, Department of Ecology, Lund, Sweden

22-11 Poster **Conservation genetics of *Olearia*, the status of tree daisies in New Zealand**

GARY J. HOULISTON[1], ADELINE BARNAUD[1,2], PETER B. HEENAN[3], PETER J. DE LANGE[4]

[1]Landcare Research, Ecological Genetics, Lincoln, New Zealand
[2]Stellenbosh University, Stellenbosh, South Africa
[3]Landcare Research, Allan Herbarium, Lincoln, New Zealand
[4]Department of Conservation, Research Unit, Auckland, New Zealand

22-12 Poster **Low genetic diversity in a natural cichlid population that shows inbreeding preference**

KATHRIN LANGEN[1], HARALD KULLMANN[2], THEO C.M. BAKKER[1], JULIA SCHWARZER[3], TIMO THUENKEN[1]

[1]University of Bonn, Institute of Evolutionary Biology and Ecology, Bonn, Germany
[2]University of Muenster, Muenster, Germany
[3]University of Bonn, Zool Forschungsmuseum Alexander Koenig, Bonn, Germany

22-13 Poster **Molecular inference of inbreeding: which estimate to use?**

MARCUS LJUNGQVIST, BENGT HANSSON, MIKAEL ÅKESSON

Lund University, Department of Animal Ecology, Lund, Sweden

22-14 Poster **Pedigrees and microsatellites: what do they tell us when species are endangered?**

MARIA J. RUIZ-LÓPEZ[1], EDUARDO R. S. ROLDÁN[1,2], GERARDO ESPESO[3], MONTSERRAT GOMENDIO[1,4]

[1]Museo Nacional de Ciencias Naturales (CSIC), Reproductive Ecology and Biology Group, Madrid, Spain
[2]The Royal Veterinary College, Department of Veterinary Basic Sciences, London, United Kingdom
[3]Estación Experimental de Zonas Áridas (CSIC), Parque de Rescate de la Fauna Sahariana, Almeria, Spain
[4]University of Cambridge, Department of Zoology, Cambridge, United Kingdom

22-15 Poster **What can heterozygosity-fitness correlations tell us about inbreeding depression in threatened species? A case study of the highly endangered takahe**

CATHERINE E. GRUEBER, JONATHAN M. WATERS, IAN G. JAMIESON

University of Otago, Department of Zoology, Dunedin, New Zealand

Ecological consequences of polyploidy in plants and animals

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Program

Saturday August 29 - **Symposium 23**

Location: Room 2

Ecological consequences of polyploidy in plants and animals

Organizers:	*Barbara Mable, University of Glasgow, United Kingdom* *Marc Stift, University of Glasgow, United Kingdom*

9.45 - 10.15	**FRANCE DUFRESNE** (invited) Do extra genome copies enable animal species to adapt to new environmental conditions?
10.15 - 10.45	**BRIAN C. HUSBAND** (invited) Evolutionary dynamics of polyploidy: implications for rapid speciation
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**MARTIN I. TAYLOR** Ecological consequences of polyploidy in *Corydoras* catfishes
11.35 - 11.55	**SANDRINE MAURICE** Self-incompatibility in the *Senecio inaequidens –S. madagascariensis* complex in its native and invaded ranges
11.55 - 12.15	**MATTHIAS STOECK** Genome composition of polyploids and hybrid origin of triploids in a contact zone of diploid and tetraploid vertebrates: Palearctic green toads (*Bufo viridis* subgroup)
12.15 - 12.35	**JANA RAABOVA** Do diploid and hexaploid plants differ in their ability of local adaptation?
12.35 - 12.55	**THOMAS G. D'SOUZA** The importance of rare tetraploids in predominantly triploid parthenogenetic planarians
12.55 - 13.55	*Lunch*

23-1 Oral

DO EXTRA GENOME COPIES ENABLE ANIMAL SPECIES TO ADAPT TO NEW ENVIRONMENTAL CONDITIONS?

France Dufresne [1]

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Despite the important role played by polyploidy in species diversification, very little is known about factors responsible for the evolutionary advantages of newly arisen polyploids. Since polyploids originate in sympatry with diploid species, they must either compete with their progenitors or adapt to new niches. Polyploidy often generate morphological and physiological changes that have the potential of altering habitat and geographical distributions. Transitions to polyploidy are also accompanied by rapid and stochastic processes of differential gene expression providing an additional source of genetic variation that could be important for the successful adaptation of new polyploids. Although there are numerous suggestions of the active role played by polyploidy in promoting adaptive changes, its real influence is still unclear. Past work on polyploid animals has mostly concentrated on elucidating origins of polyploidy and characterizing geographical distribution. The mere presence of polyploids in harsh environments do not necessarily imply that they are more adapted to extreme environmental conditions. Such demonstration can only be done by comparing fitness and tolerance to various environmental factors in the laboratory as well as by conducting reciprocal transplant experiments. I will review evidence for the presence of new adaptive traits in animal polyploids as well as presenting results from my research group on life history, metabolic, and transposon insertion differences in diploid and polyploid *Daphnia*.

23-2 Oral

EVOLUTIONARY DYNAMICS OF POLYPLOIDY: IMPLICATIONS FOR RAPID SPECIATION

Brian C. Husband [1]

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Polyploidy, or genome duplication, has occurred repeatedly throughout the diversification of plants and animals and is widely viewed as a rapid, mechanism of sympatric speciation. However, the specific pathways by which polyploids arise and establish within diploid populations, and the role of genome duplication versus selection in driving phenotypic divergence and reproductive isolation, are poorly understood. Here, I describe an ongoing research program into polyploid evolution and speciation in the perennial plant, fireweed (*Chamerion angustifolium*; Onagraceae). Using field experiments, experimental crosses, phylogeographic analyses and synthesized polyploids, a picture of a very dynamic system is emerging. Polyploid mutations arise at high frequencies but are generally opposed by strong frequency-dependent selection. Assortative mating, coupled with recurrent polyploid formation, favours the establishment of polyploids within diploid populations. However, experimental research on synthesized polyploids suggests that phenotypic divergence and pre-zygotic reproductive isolation are not fully established through genome duplication. Rather, divergence mediated by interactions between ploidies, may also be important. Our results suggest that the common portrayal of polyploid speciation is perhaps an oversimplification and underestimates the importance of the interaction between selection and genome duplication in guiding the evolution of species divergence.

23-3 Oral

ECOLOGICAL CONSEQUENCES OF POLYPLOIDY IN *CORYDORAS* CATFISHES

Martin I. Taylor [1], Markos Alexandrou [1]

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With over 150 species, the armoured catfishes of the genus *Corydoras* amount to a significant proportion of the freshwater ichthyofaunal diversity of South America. They are of particular interest from an evolutionary perspective as they have extraordinary variation in genome sizes and chromosome numbers, suggesting that polyploidy has played an important role in their diversification. At many (>12 known) sites throughout South America, several *Corydoras* species exist in sympatry. These co-occuring species shoal together and have evolved almost identical colour patterns yet differ subtly in morphology. Here we demonstrate using mtDNA and nuclear phylogenies that sympatric species are always from different genetic clades, ruling out the possibility of their evolution via sympatric speciation. We also demonstrate using stable isotope analysis that sympatric species with different genome sizes are ecologically differentiated, with members of a single genetic clade occupying the same trophic level at multiple sites. We suggest that this may enable the long term co-existence of sympatric *Corydoras* species providing the stability for the evolution of identical colour patterns through predation driven natural selection. Although no causal link has yet been established between polyploidy and niche divergence, we demonstrate consistent differences in morphology and niche between species with different genomic complements.

23-4 Oral

SELF-INCOMPATIBILITY IN THE *SENECIO INAEQUIDENS – S. MADAGASCARIENSIS* COMPLEX IN ITS NATIVE AND INVADED RANGES

Sandrine Maurice [1], Lucile Lafuma [1]

[1]*Université Montpellier 2, Institut des Sciences de l'Evolution, Montpellier, France*

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Senecio inaequidens, *S. harveianus* and *S. madagascariensis* are native from South Africa and form a species complex of unclear taxonomy. Populations described as *S. madagascariensis* present only diploid individuals (2n=20) whereas populations described as *S. inaequidens* or *S. harveianus* present diploid or tetraploid (2n=40) individuals. Diploids are invading Australia and South America under the name of *S. madagascariensis* and tetraploids are invading Europe under the name *S. inaequidens*. *S. inaequidens* is known to be self-incompatible. In colonizing species, bottlenecks affect population size and cause losses of allelic variation at the S-locus, reducing both number of individuals and percentage of cross-compatible mates. Moreover, Baker's law invokes the importance of reproductive assurance in selecting for self-fertilization in colonizing plants and animals. We tested if diploids and tetraploids differ in the strength of their self-incompatibility systems in their native range and if these systems have been relaxed during the colonization of new areas.

23-5 Oral

GENOME COMPOSITION OF POLYPLOIDS AND HYBRID ORIGIN OF TRIPLOIDS IN A CONTACT ZONE OF DIPLOID AND TETRAPLOID VERTEBRATES: PALEARCTIC GREEN TOADS (*BUFO VIRIDIS* SUBGROUP)

Matthias Stoeck [1,2], Dunja K Lamatsch [3], Craig Moritz [2], Nicolas Perrin [1], Manfred Schartl [4], Jana Ustinova [2,5]

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[3]*Austrian Academy of Sciences, Institute for Limnology, Mondsee, Austria*
[4]*University of Wuerzburg, Lehrstuhl für Physiologische Chemie I, Theodor-Boveri-Institut, Biozentrum, Am Hubland, Wuerzburg, Germany*
[5]*University of Karlsruhe (TH), Zoologisches Institut I, Lehrstuhl für Zell- und Neurobiologie, Karlsruhe, Germany*

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The rise, nature, and consequences of polyploidy in vertebrates, whose origin was widely driven by genome duplications, may be best studied in populations of naturally occurring diploid and polyploid populations. We investigate Palearctic green toads of three ploidy levels and examine the origin and genetic nature of triploids (3n) and tetraploids (4n) in a diploid 2n/4n contact zone in northern Kyrgyzstan. Since the discovery of gonochoristic 4n forms (1976), 3n individuals have been reported, occurring apparently in a zone of geographic contact between 2n and 4n toads. Previous attempts have failed to elucidate the genetic composition of 3n and 4n. Using mitochondrial sequence, several microsatellite and anonymous nuclear markers in 84 individuals as well as three nuclear sequence markers in one adult representative from each ploidy level, we show that 4n from northern Kyrgyzstan (*B. pewzowi*) represent allopolyploids, whose one ancestral maternal parent is a geographically proximate 2n species (*B. turanensis*). The 3n forms in that contact zone arise through hybridization. Adult 3n mature males (with *B. turanensis* mtDNA) can result from *de novo* hybridizations of female 2n and male 4n. However, these adult 3n males are distinguishable from (partly aneuploid) triploid tadpoles (with *B. pewzowi* mtDNA) by nuclear microsatellites using the program STRUCTURE. This suggests a different than just reciprocal hybrid (2n male x 4n female) origin of these 3n (plus some uneuploid) tadpoles (with *B. pewzowi* mtDNA). Therefore, we favor hypotheses, in which 3n males (with *B. turanensis* mtDNA) backcross with 2n and 4n females to explain the phenomena found in the system. We discuss possible mechanisms explaining how this 2n/3n/4n-system may be maintained and propose future research to test these three major hypotheses. New field data from 2009 may be included.

23-6 Oral

DO DIPLOID AND HEXAPLOID PLANTS DIFFER IN THEIR ABILITY OF LOCAL ADAPTATION?

Jana Raabová [1,2], Zuzana Münzbergová [3,4]

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Polyploidy is common in flowering plants and is considered as an important mechanism of evolutionary novelties in plant populations. Many studies showed that polyploid plants are adapted to a wider range of environmental conditions than diploid plants. However, little is known about possible differences between diploids and polyploids in their ability of local adaptation. We studied local adaptation in six diploid and six hexaploid populations at a small spatial scale in the rare herb *Aster amellus*. We conducted a reciprocal transplant experiment in the field using both seeds and juvenile plants. We tested whether the two ploidy levels differ in performance and in their ability to adapt to local conditions. Hexaploid plants had higher germination percentage, higher survival probability and longer leaves (a correlate of dry mass) than diploid plants. Germination percentage was higher at home than at foreign populations both in diploids and hexaploids and neither diploids nor hexaploids were affected by home population in survival probability. Nevertheless, diploids had significantly larger leaves at foreign populations than at home populations while hexaploids did not differ between home and foreign populations in the leaf length. This indicates that hexaploid plants do not show any local adaptation in plant size while diploid plants show foreign-site advantage. To conclude, ploidy level did not affect local adaptation in early traits but affected local adaptation in plant size, suggesting that polyploidization may influence species ability to cope with changing environments.

23-7 Oral

THE IMPORTANCE OF RARE TETRAPLOIDS IN PREDOMINANTLY TRIPLOID PARTHENOGENETIC PLANARIANS

Thomas G. D’Souza [1], Nico K. Michiels [1]

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The occurrence and geographical distribution of polyploidy is well documented in many species of planarian flatworms. However, less is known about the fitness consequences of polyploidy and its evolutionary and ecological implication for population composition and survival.

Here we investigate the role of tetraploids for the success of supposedly triploid “evolutionary dead-ends” in the parthenogenetic forms of the hermaphroditic freshwater planarian *Schmidtea polychroa*. Among polyploid parthenogenetic *S. polychroa*, triploidy (3x = 12) is the most common type, while tetraploidy (4x = 16) is generally rare. Therefore tetraploid *S. polychroa* have been often neglected in previous studies. However, tetraploids play a key role as a source of genetic variation in parthenogenetic populations. Tetraploids are by-products of a two-step cycle of occasional sex in otherwise parthenogenetic *S. polychroa*. In this cycle, triploids sometimes produce tetraploid offspring (3x to 4x) and *vice versa* tetraploids sometimes produce triploid offspring (4x to 3x). Both steps include syngamy of parthenogenetic eggs with haploid sperm from the functional male line of parthenogenetic conspecifics. Despite low fitness of tetraploids, occasional sex leads to stable co-existence of tetraploids and triploids. Moreover, occasional sex with tetraploids as interstages increases the fitness of triploids at a population level. Hence tetraploid production appears to be of major significance for the long-term survival of triploid parthenogenetic planarians.

23-1 Poster **Asexual range expansions of common ancestry lineages with variable ploidy**

SOFIA ADOLFSSON[1,2], YANNIS MICHALAKIS[2], DOROTA PACZESNIAK[1,3], SASKIA N.S. BODE[3,4], ROGER K. BUTLIN[3], DUNJA K. LAMATSCH[3,5], MARIA J.F. MARTINS[6,7], JUKKA JOKELA[1]

[1]*EAWAG/ETH, Department of Aquatic Ecology, Zurich, Switzerland*
[2]*CNRS/IRD Génétique et Evolution des Maladies Infectieuses, Montpellier, France*
[3]*University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom*
[4]*RBINS Freshwater Biology, Brussels, Belgium*
[5]*Institute for Limnology, Mondsee, Austria*
[6]*University of Gdansk, Department of Genetics, Gdansk, Poland*
[7]*University of Parma, Department of Environmental Sciences, Parma, Italy*

23-2 Poster **Evolution of endosperm ploidy level in angiosperms**

AURELIE C. CAILLEAU, THOMAS LENORMAND, PIERRE-OLIVIER CHEPTOU
CNRS, CEFE, Montpellier, France

23-3 Poster **Breeding barriers between cytotypes maintain a secondary contact zone in the polyploid *Aster amellus***

SÍLVIA CASTRO[1,2], JANA RAABOVÁ[3,4], JOÃO LOUREIRO[5,6], ZUZANA MÜNZBERGOVÁ[1,2]

[1]*Charles University in Prague, Faculty of Science, Department of Botany, Prague, Czech Republic*
[2]*Institute of Botany, Academy of Sciences, Průhonice, Czech Republic*
[3]*National Museum, Department of Botany, Průhonice, Czech Republic*
[4]*Department of Vascular Plants, National Botanic Garden of Belgium, Meise, Belgium*
[5]*University of Coimbra Department of Botany, Coimbra, Portugal*
[6]*University of Coimbra, Centre for Functional Ecology, Coimbra, Portugal*

23-4 Poster **Nuclear DNA content variation and pollen malformation in *Ranunculus parnassifolius* (Ranunculaceae)**

EDUARDO CIRES, CANDELA CUESTA, MARÍA ÁNGELES FERNÁNDEZ CASADO, MARÍA DEL CARMEN FERNÁNDEZ-CARVAJAL ÁLVAREZ, ELENA L. PEREDO, MARÍA ÁNGELES REVILLA, JOSÉ ANTONIO FERNÁNDEZ PRIETO
University of Oviedo, Departamento de Biología de Organismos y Sistemas, Oviedo, Spain

23-5 Poster **The role of polyploid evolution in flowering plants: a case study from the Alpine species *Primula marginata***

LAURA GRANATO[1,2], LUIGI MINUTO[2], GABRIELE CASAZZA[2], ELENA CONTI[1]

[1]*University of Zurich, Institute of Systematic Botany, Zurich, Switzerland*
[2]*Università degli studi di Genova DIP.TE.RIS, Genova, Italy*

23-6 Poster **How duplicated receptor genes create problems for Atlantic salmon residing in polluted environments**

MARIA C. HANSSON[1,2]

[1]*Lund university, Department of Environmental Science, Lund, Sweden*
[2]*Lund university, Department of Ecology, Lund, Sweden*

23-7 Poster **Are outcrossing rates linked to polyploidy levels in congeneric *Vaccinium?***

BENOÎT H. HOST
Catholic University of Louvain La Neuve, BAPA/BENA, Louvain, Belgium

23-8 Poster **Nordihydroguiaretic Acid in the Polyploids of *Larrea tridentata*: Effects of Temperature and Developmental Stage**

KIMBERLY L. HUNTER[1], KATHERINE R. MILLER[2], SHELBY SMITH[1]
[1] *Salisbury University, Department of Biology, Salisbury, United States*
[2] *Salisbury University, Department of Chemistry, Salisbury, United States*

23-9 Poster **Habitat diversification by recurrent polyploidization events in *Cardamine* L. (Brassicaceae)**

HIROKO IWANAGA[1], KENTARO K. SHIMIZU[1], RIE SHIMIZU-INATSUGI[1], HIROSHI KUDOH[2]
[1] *University of Zurich, Institute of Plant Biology, Zurich, Switzerland*
[2] *Kyoto University, Center for Ecological Research, Otsu, Japan*

23-10 Poster **Gene expression regulation and lineage evolution in the polyploid complex *Squalius alburnoides***

IRENE PALA[1], MANFRED SCHARTL[2], MARIA M. COELHO[1]
[1] *Centro de Biologia Animal, Department of Animal Biology, Faculty of Sciencies, Lisbon, Portugal*
[2] *University of Würzburg, Biozentrum Physiologische Chemie I, Würzburg, Germany*

23-11 Poster **Allopolyploidy in the *Sphagnum subsecundum* complex**

MARIANA RICCA[1,2], A. JONATHAN SHAW[1]
[1] *Duke University, Biology Department, Durham, United States*
[2] *Universidate do Porto, Porto, Portugal*

23-12 Poster **Impact of selective logging on gene flow in the intensely exploited Amazonian tetraploid tree *Dipteryx odorata***

CHRISTINA C. VINSON, STEPHEN A. HARRIS, DAVID H. BOSHEIR
University of Oxford, Department of Plant Sciences, Oxford, United Kingdom

23-13 Poster **Enigmatic Sakhalin sturgeon (*Acipenser mikadoi*, Hilgendorf, 1892): ploidy, cytogenetics, molecular phylogeny**

DARIA A. ZELENINA[1], YEGOR E. YEGOROV[2], KHAVA S. VISHNYAKOVA[2], GALINA A. DELONE[3], NIKOLAI S. MUGUE[1,3], EKATERINA V. MIKODINA[1]
[1] *Russian Federal Research Institute of Fisheries and Oceanography (VNIRO), Molecular Genetics of Aquatic Animals, Moscow, Russia*
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Functional analysis of natural variation

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Program

Saturday August 29 - **Symposium 24**

Location: Room 3

Functional analysis of natural variation

Organizers:	*Christian Schlötterer, Universität Wien, Austria* *Alistair McGregor, Universität Wien, Austria* *Jean-Michel Gibert, University of Geneva, Switzerland*

9.45 - 10.15	**VINCENT COUSTHAM** (invited) Linking molecular biology and natural variation to gain insights into *Arabidopsis* adaptation
10.15 - 10.45	**ROWAN BARRETT** (invited) Natural selection on a major armor gene in threespine stickleback
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**LAURA E. ROSE** How does genetic variation translate into functional differences among individuals of interacting hosts and parasites?
11.35 - 11.55	**JIN-YONG HU** Structural variation of ath_miR824 precursors fine-tunes life cycle traits and contributes to the adaptive evolution of *Arabidopsis thaliana*
11.55 - 12.15	**FREDERIC MERY** Natural variation in a cGMP-dependent protein kinase (PKG) gene (for) underlie an adaptive response of memory to environmental heterogeneity
12.15 - 12.35	**JAY F. STORZ** High-altitude adaptation of deer mouse hemoglobins involves parallel functional differentiation at multiple globin gene duplicates
12.35 - 12.55	**JEAN-MICHEL GIBERT** Functional analysis of natural variant of the Polycomb group gene cramped
12.55 - 13.55	*Lunch*

24-1 Oral

LINKING MOLECULAR BIOLOGY AND NATURAL VARIATION TO GAIN INSIGHTS INTO *ARABIDOPSIS* ADAPTATION

Vincent Coustham [1], Amy Strange [2], Peijin Li [1], Clare Lister [1], Magnus Nordborg [3], Caroline Dean [1]

[1]*John Innes Centre, Department of Cell and Developmental Biology, Norwich, United Kingdom*
[2]*Oxford University, Wellcome Trust Centre for Human Genetics, Oxford, United Kingdom*
[3]*University of South California, Department of Biological Sciences, Los Angeles, United States*

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During the life cycle of the plant, the correct timing of flowering is essential to maximize reproductive success. We are studying the molecular control of the timing of flowering, when plants switch from vegetative to reproductive development. We focus on the acceleration of flowering by a long period of cold, a process called vernalization. Vernalization involves the cold-induced repression and epigenetic silencing of the floral repressor FLOWERING LOCUS C (FLC). Analysis of flowering time and vernalization in natural *Arabidopsis* accessions provides a rare opportunity to link mechanistic understanding of a complex trait with fitness consequences of different alleles and their distribution within the population. We have shown that molecular variation at FLC and linked genes underpin a large proportion of the natural variation in accessions selected to represent a wide range of vernalization responses. We are continuing to investigate how cis polymorphism in non-coding regions affects FLC silencing. The data so far indicates that a major contributor to the microevolution of vernalization is recent selection of independent FLC alleles whose epigenetic silencing is subtly altered by a small number of nucleotide changes. The different accessions can also be viewed as a pool of “natural mutants” that help define cis elements mediating vernalization-induced FLC silencing. Dissecting the molecular basis of adaptation is a major goal in evolutionary and ecological genetics and the results from this study are likely to provide important insights into adaptation relevant to many biological systems.

24-2 Oral

NATURAL SELECTION ON A MAJOR ARMOR GENE IN THREESPINE STICKLEBACK

Rowan Barrett [1]

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Experimental estimates of the effects of selection on genes determining adaptive traits add to our understanding of the mechanisms of evolution. We measured selection on genotypes of the *Ectodysplasin* locus, which underlie differences in lateral plates in threespine stickleback fish. A derived allele (low) causing reduced plate number has been fixed repeatedly after marine stickleback colonized freshwater from the sea, where the ancestral allele (complete) predominates. We transplanted marine sticklebacks carrying both alleles to freshwater ponds and tracked genotype frequencies over a generation. The low allele increased in frequency once lateral plates developed, most likely via a growth advantage. Opposing selection at the larval stage and changing dominance for fitness throughout life suggest either that the gene affects additional traits undergoing selection or that linked loci also are affecting fitness.

24-3 Oral

HOW DOES GENETIC VARIATION TRANSLATE INTO FUNCTIONAL DIFFERENCES AMONG INDIVIDUALS OF INTERACTING HOSTS AND PARASITES?

Laura E. Rose [1], Sharon A. Hall [2], Rebecca L. Allen [2], Eric B. Holub [2], Jim L. Beynon [2]

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[2]*University of Warwick, Warwick - HRI, United Kingdom*

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The model plant species, *Arabidopsis thaliana*, is naturally infected by the oomycete pathogen, *Hyaloperonospora parasitica*. Over the last 15 years, we have cloned several genes in the host and parasite that influence the outcome of this interaction. Our initial studies revealed that many of these genes, in both host and parasite, harbored elevated levels of amino acid polymorphism and were subject to balancing selection. In one case, we observed a multi-allelic series in both the host resistance gene, RPP13, and the cognate pathogen gene, ATR13. Using a series of functional studies, including whole-plant inoculations and transgenic co-expression of host and pathogen proteins, we determined which host alleles recognize which pathogen alleles. Furthermore, using site-directed mutagenesis and domain swaps, we were able to determine precisely which amino acid polymorphisms in the pathogen protein triggered a host defense response. To our surprise, only a small subset of the RPP13 alleles present in natural host populations recognized the cognate pathogen protein ATR13. However, alternate alleles of RPP13 were still functional and recognized additional ligands expressed by the pathogen. Using genetic crosses in the pathogen, we mapped these novel genes that encode ligands recognized by RPP13. In parallel, we discovered that some ATR13 alleles are recognized by resistance proteins other than RPP13. In summary, using a battery of functional tests and genetic crosses, we were able to determine that convergent evolution in the host population for pathogen recognition has resulted in a complex network of gene-for-gene interactions between these two interacting species.

24-4 Oral

STRUCTURAL VARIATION OF ath_mir824 PRECURSORS FINE-TUNES LIFE CYCLE TRAITS AND CONTRIBUTES TO THE ADAPTIVE EVOLUTION OF *ARABIDOPSIS THALIANA*

Jin-Yong Hu [1], Juliette de Meaux [1]

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Post-transcriptional regulation of gene expression via miRNAs has been proposed to play a fundamental role in development of life complexity. However, rare report concerning of miRNAs contributing to the organism's adaptation has been found. The *ath_miR824* precursor of *Arabidopsis thaliana* has been previously shown to harbor distinct secondary structural variations. Transcript level assays suggest that these structural differences are very likely associated with the mature miR824 processing efficiency from the precursors. Further functional tests certified that *AGL16*, which is the proved *miR824* target in *Arabidopsis*, takes part in the regulation not only of vegetative growth and floral transition processes, but also in the modulating of seed germination pathway. In addition, the precursor structural change between alleles, which obviously leads to variation of *AGL16* transcripts level, is fine-tuning these key life cycle traits. Our work finally propose one mechanism on how plants fine-tune their genetic switches and adapt to variable environments by modulating small RNAs production through secondary structure variation after partially duplicating their genome.

24-5 Oral

NATURAL VARIATION IN A CGMP-DEPENDENT PROTEIN KINASE (PKG) GENE (FOR) UNDERLIE AN ADAPTIVE RESPONSE OF MEMORY TO ENVIRONMENTAL HETEROGENEITY

Christopher Reaume [1], Marla B. Sokolowski [1], Frederic Mery [2]

[1]*University of Toronto at Mississauga, Department of Biology, Mississauga, Canada*
[2]*CNRS, Lab Evolution Genome and Speciation, Gif sur Yvette, France*

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Natural allelic variation in the *foraging (for)* gene encodes a cGMP-dependent protein kinase (PKG) that contributes to differences in learning and memory in larval and adult *Drosophila melanogaster*. These allelic polymorphisms are pleiotropic for differences in food-related locomotion in larvae and adults and likely have fitness consequences. We investigated if there was a relationship between learning, memory and the adaptive response to environmental heterogeneity in these natural variants by testing their responses to environmental variation using both reversal learning and multiple stimulus learning in a Pavlovian paradigm. We predicted that the rover strain (*for*^{R}) would place greater emphasis on their most recent experience compared to sitter (*for*^{s}) and sitter mutants on a rover genetic background (*for*^{s2}) since they are more likely to encounter environmental variation in nature. As expected, the *for*^{R} strain displayed a greater ability to reverse their response to the stimulus-shock pairing compared to *for*^{s} and *for*^{s2}. When flies were asked to learn multiple stimulus-odour pairings, the rover strain placed more emphasis on the last conditioning while decreasing the strength of the first, whereas the sitter strains placed equal emphasis on both. These data, considered alongside other known *for* pleiotropies, suggest that variation in *for* influences an adaptive response to environmental heterogeneity which may lead to alternative resource-use strategies in adult *D. melanogaster.*

24-6 Oral

HIGH-ALTITUDE ADAPTATION OF DEER MOUSE HEMOGLOBINS INVOLVES PARALLEL FUNCTIONAL DIFFERENTIATION AT MULTIPLE GLOBIN GENE DUPLICATES

Jay F. Storz [1]

[1]*University of Nebraska, School of Biological Sciences, Lincoln, United States*

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In principle, adaptive modifications of heteromeric proteins could involve genetically based changes in single subunits or parallel changes in multiple genes that encode distinct, interacting subunits. Vertebrate hemoglobin (Hb) is an ideal molecule for addressing questions about the functional evolution of allosteric, multimeric proteins. In high-altitude vertebrates, fine-tuned adjustments in Hb-oxygen affinity are known to play a key role in adaptation to hypoxia. These adaptive changes in Hb function may often require coordinated changes in both alpha- and beta-chain subunits of the Hb tetramer, thereby necessitating coordinated changes in two or more unlinked genes. Here we investigate this possibility by conducting a population genetic analysis of duplicated alpha- and beta-globin genes that underlie adaptation to different elevational zones in natural populations of deer mice *(Peromyscus maniculatus)*. We used a simulation-based analysis of multilocus data to evaluate the role of spatially varying selection in shaping observed patterns of altitudinal variation at two alpha-globin paralogs and two beta-globin paralogs. We then evaluated the functional significance of the observed changes in Hb structure by measuring oxygen-binding properties of purified Hbs from mice with known genotypes. Results of the evolutionary/functional analysis revealed that high-altitude adaptation of deer mouse Hbs involves parallel functional differentiation at multiple globin gene duplicates. Our results illustrate the value of integrating evolutionary analyses of sequence variation with mechanistic studies of protein function.

24-7 Oral

FUNCTIONAL ANALYSIS OF NATURAL VARIANT OF THE POLYCOMB GROUP GENE CRAMPED

Jean-Michel Gibert [1], Rob Maeda [1], Christian Schlötterer [2], François Karch [1]

[1]*University of Geneva, Department of Zoology and Animal Biology, Geneva, Switzerland*
[2]*Veterinary University of Vienna, Institute of Population Genetics, Vienna, Austria*

Jean-Michel.Gibert@unige.ch

Several chromatin regulators have been identified as targets of selection during the out of African expansion of *Drosophila melanogaster*. The well characterised thermosensitivity of chromatin regulatory mechanisms suggests that selection on these higly pleiotropic genes have helped *Drosophila melanogaster* populations to adapt to the differences in temperature between the ancestral and derived habitats (average temperature and temperature range). Our study focuses on the Polycomb group gene *cramped (crm)* which was identified as putative target of selection in European populations and show amino acid polymorphisms with highly biased frequencies in Europe and sub-saharan Africa. We have designed sensitive tests to analyse how natural variation in crm affects its regulatory network. Using isogenic backgrounds and mutations in interacting genes we found that *crm* natural variation has functional consequences on several traits not only on the mean of these traits but also in interaction with temperature. This strongly suggests that *crm* has been involved in adaptation to different temperature environments. Presumably, these amino acid polymorphisms modulate interactions with particular cofactors. In order to analyze their effect on the dynamic of CRM interactions we generated fluorescent fusions to compare in vivo the dynamic of different alleles on the chromatin.

24-1 Poster **Ageing in a variable environment: senescence in parasite resistance in wild Soay sheep**

ADAM D. HAYWARD, ALASTAIR J. WILSON, JILL G. PILKINGTON, JOSEPHINE M. PEMBERTON, LOESKE E.B. KRUUK
University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom

24-2 Poster **The genetic basis of trichome density variation in natural *Arabidopsis thaliana* populations**

JULIA HILSCHER[1,2], MARIE-THERES HAUSER[2], CHRISTIAN SCHLÖTTERER[1]
[1]VUW, Institute of Population Genetics, Vienna, Austria
[2]Boku, Department of Applied Genetics and Cell Biology, Vienna, Austria

24-3 Poster **The genomes of distant vertebrates share many conserved positive selection hotspots**

DAVID ENARD[1], FRANTZ DEPAULIS[2], HUGUES ROEST-CROLLIUS[1]
[1]Ecole Normale Supérieure, Dyogen Lab CNRS UM8541, Paris, France
[2]Ecole Normale Supérieure Laboratoire d'Ecologie CNRS UMR7625, Paris, France

24-4 Poster **Footprints of selection and divergence between two closely related and hybridizing plant species, *Silene latifolia* and *S. dioica***

MARIA DOMENICA MOCCIA, ALEX WIDMER
ETH, Zuerich, Plant Ecological Genetics, Zuerich, Switzerland

24-5 Poster **Mitochondrial recombination increases with age**

ANNE D. VAN DIEPENINGEN, DANIEL J. GOEDBLOED, ROLF F. HOEKSTRA, ALFONS J.M. DEBETS
Wageningen University, Laboratory of Genetics, Wageningen, Netherlands

24-6 Poster **Identification of candidate genes involved in skin colouration in *Salmo* sp. by microarray analysis**

ANJA PALANDAČIĆ, URŠKA SIVKA, ALEŠ SNOJ, SIMONA SUŠNIK
University of Ljubljana, Biotechnical faculty, Department of Animal Science, Domzale, Slovenia

24-7 Poster **Signs of selection in and expression analysis of avian immune genes**

ROBERT EKBLOM, LISA FRENCH, JON SLATE, TERRY BURKE
University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom

24-8 Poster **Patterns of genotypic fitness at two hybrid zones indicate functional differentiation among populations of sculpins**

ARNE W. NOLTE
Max-Planck Institute for Evolutionary Biology, Department of Evolutionary Genetics, Ploen, Germany

24-9 Poster **Environmental genomics of the marine gastropod *Nucella lapillus* in response to organotin pollution**

SONIA PASCOAL[1,2], GARY R. CARVALHO[1], ROGER HUGHES[1], NEIL HALL[3], ANDREW COSSINS[3], CARLOS MIGUEZ[2], SONIA MENDO[2], SIMON CREER[1]
[1]Bangor University, School of Biological Sciences, Bangor, United Kingdom
[2]Universidade de Aveiro, Departamento de Biologia, Aveiro, Portugal
[3]University of Liverpool, School of Biological Sciences, Liverpool, United Kingdom

24-10 Poster **Natural selection dynamics on standing genetic variation of *Drosophila melanogaster* experimental populations**

IVO M. CHELO, HENRIQUE TEOTÓNIO
Instituto Gulbenkian de Ciencia, Oeiras, Portugal

24-11 Poster **Identifying the genetic basis for the colour polymorphism in the Common Buzzard (*Buteo buteo*)**

MARIE A. POINTER, OLIVER KRUGER, NICHOLAS I. MUNDY
University of Cambridge, Department of Zoology, Cambridge, United Kingdom

24-12 Poster **Evidence for small scale natural variation in brain structure: mating strategy and sex affect brain structure in wild brown trout**

NICLAS KOLM, ALEJANDRO GONZALEZ-VOYER, SVANTE WINBERG, DANIEL BRELIN
Uppsala University, Faculty of Ecology & Evolution, Evolutionary Biology Centre, Department of Animal Ecology, Uppsala, Sweden

24-13 Poster **Analysis of functional variation in host specificity in a species complex of a pathogenic fungus**

ELODIE VERCKEN[1], BENJAMIN DEVIER[1], FRÉDÉRIC AUSTERLITZ[1], GABRIELA AGUILETA[1,2], TATIANA GIRAUD[1]
[1]Université Paris-Sud XI, laboratoire Ecologie, Systématique, Evolution, Orsay, France
[2]MIG - INRA UR 1077, Jouy en Josas, France

24-14 Poster **Convergent evolution of RuBisCO enzymes from different plant lineages**

MAXIM KAPRALOV[1], DAVID KUBIEN[2], JERONI GALMES[3], DMITRY FILATOV[1]
[1]University of Oxford, Department of Plant Sciences, Oxford, United Kingdom
[2]University of New Brunswick, Department of Biology, Fredericton, Canada
[3]Universitat de les Illes Balears, Departament de Biologia, Palma de Mallorca, Spain

24-15 Poster **A gene duplication/loss event in the otherwise highly conserved Ribulose-1,5-Bisphosphate-Carboxylase/Oxygenase (RuBisCO) small subunit gene family among ecotypes of *Arabidopsis thaliana***

SANDRA SCHWARTE, MADLEN STANGE, FANNY WEGNER, RALPH TIEDEMANN
University of Potsdam, Unit of Evolutionary Biology, Potsdam, Germany

24-16 Poster **Evolution of MHC class I genes in ducks and geese**

INA POKORNY, STEFANIE GROßER, RALPH TIEDEMANN
University of Potsdam, Unit of Evolutionary Biology/Systematic Zoology, Potsdam, Germany

24-17 Poster **Comparative analysis of five immunity-related genes reveals different levels of adaptive evolution in the *virilis* and *melanogaster* groups of *Drosophila***

RAMIRO MORALES-HOJAS, CRISTINA P. VIEIRA, MICAEL REIS, JORGE VIEIRA
Instituto de Biologia Molecular e Celular - IBMC, Molecular Evolution, Porto, Portugal

24-18 Poster **Adaptive divergence between parapatric freshwater and marine sticklebacks: insights from an integrated analysis of candidate gene expression within a quantitative genetics framework**

R.J. SCOTT MCCAIRNS, LOUIS BERNATCHEZ
Université Laval, Institut de Biologie Intégrative et des Systèmes (IBIS), Québec, Canada

24-19 Poster **Evolutionary analysis of four glycosylation pathways in worldwide human populations**

GIOVANNI M. DALL'OLIO, ANNA FERRER-ADMETLLA, FERRAN CASALS, HAFID LAAYOUNI, JAUME BERTRANPETIT, MARTIN SIKORA

Pompeu Fabra University, IBE, Institut de Biologia Evolutiva (UPF-CSIC), CEXS-UPF-PRBB, Spain

24-20 Poster **Mapping of quantitative adaptive traits of the guppy, *Poecilia reticulata***

CHRISTINE DREYER, NAMITA TRIPATHI, EVA-MARIA WILLING, MARGARETE HOFFMANN

Max-Planck-Institute for Developmental Biology, Department of Molecular Biology, Tuebingen, Germany

24-21 Poster **Effects of clutch size on post-hatching growth and physiological stress in Great Tit chicks**

TERJE LISLEVAND[1], RUEDI NAGER[2], PAT MONAGHAN[2]

[1]University of Bergen, Natural History Museum, Bergen, Norway
[2]University of Glasgow Division of Environmental and Evolutionary Biology, Glasgow, United Kingdom

24-22 Poster **A new genetic solution to a colossal problem - resolving *Mesonychoteuthis hamiltonii***

MAANASA RAGHAVAN, THOMAS GILBERT P.M.

University of Copenhagen, Natural History Museum of Denmark, Copenhagen, Denmark

24-23 Poster **Sexual selection and brain size in shorebirds**

GABRIEL E. GARCIA-PEÑA[1,2]

[1]University of Bath, Department of Biology & Biochemistry, Bath, United Kingdom
[2]Consejo Nacional de Ciencia y Tecnologia, Conacyt, Mexico

24-24 Poster **Individual Behaviour in Firebugs (*Pyrrhocoris apterus*)**

ENIKŐ GYURIS, ZOLTÁN BARTA

University of Debrecen, Behaviour Ecology Research Group, Debrecen, Hungary

24-25 Poster **Photosynthetic response and plant performance in relation to drought and irradiance stresses in Iberian columbines**

PEDRO J. REY , CELIA SERICHOL, JESUS M. BASTIDA, JULIO M. ALCANTARA, RAFAEL JAIME

Universidad de Jaen, Departamento de Biologia Animal, Biologia Vegetal y Ecologia, Jaen, Spain

24-26 Poster **Pubescence functionality in relation to herbivory in south Iberian columbines**

RAFAEL JAIME, JESUS M. BASTIDA, JULIO M. ALCANTARA, PEDRO J. REY

Universidad de Jaen, Departamento de Biologia Animal, Biologia Vegetal y Ecologia, Jaen, Spain

24-27 Poster **Sex ratio adjustment in the Collared Flycatcher: the role of corticosterone**

BALÁZS ROSIVALL[1], ESZTER SZÖLLŐSI[1], DOROTTYA KISS[1], SOPHIE RETTENBACHER[2], JÁNOS TÖRÖK[1]

[1]Eötvös Loránd University, Department of Systematic Zoology and Ecology, Budapest, Hungary
[2]Veterinary University Vienna, Institute of Biochemistry, Vienna, Austria

24-28 Poster **Experimental tests of sex allocation theory using the RNAi-knockdown approach**

KIYONO SEKII[1], GEORG KUALES[2], KATRIEN DE MULDER[3], PETER LADURNER[2], LUKAS SCHÄRER[1]

[1]University of Basel, Zoological Institute, Department of Evolutionary Biology, Basel, Switzerland
[2]University of Innsbruck, Institute of Zoology, Department of Ultrastructural Research and Evolutionary Biology, Innsbruck, Austria
[3]University of Ghent, Department of Biology, Ghent, Belgium

24-29 Poster **Genetic variability in the tick *Ixodes ricinus* based on nucleotidic polymorphism of two nuclear and mitochondrial genes sets**

RIM NOUREDDINE[1], OLIVIER PLANTARD[1], ALAIN CHAUVIN[2]

[1]INRA, UMR 1300 BioEpAR, Nantes, France
[2]ENVN, UMR 1300 BioEpAR, Nantes, France

24-30 Poster **Is sex allocation in response to density adaptive?**

REINDER RADERSMA, STEPHANIE P.M. MICHLER, JOOST M. TINBERGEN, JAN KOMDEUR

University of Groningen, Animal Ecology group, Centre for Ecological and Evolutionary Studies, Haren, Netherlands

24-31 Poster **Evolution of floral size control in the genus *Capsella***

ADRIEN SICARD, KATRIN HERMANN, MICHAEL LENHARD, NICOLA STACEY

John Innes Centre, Department of Cell & Developmental Biology, Norwich, United Kingdom

24-32 Poster **Environmental acidity drives adaptive divergence in Swedish moor frog (*Rana arvalis*) populations**

SANDRA HANGARTNER[1,2], ANSSI LAURILA[3], KATJA RÄSÄNEN[2]

[1]EAWAG, Aquatic Ecology, Dübendorf, Switzerland
[2]ETH Zurich, Zurich, Switzerland
[3]Uppsala University, Department of Population and Conservation Biology, Uppsala, Sweden

24-33 Poster **Can nucleotide diversity patterns in *Pinus pinaster* lignification transcription factors be explained by demography or selection?**

CAMILLE LEPOITTEVIN[1,2], FRANÇOIS HUBERT[1], CHRISTOPHE PLOMION[1], PAULINE GARNIER-GÉRÉ[1]

[1]INRA, BIOGECO, Cestas, France
[2]FCBA, Nangis, France

24-34 Poster **Vocal tract morphology shapes vocal communication in lemurs**

MARCO GAMBA, CRISTINA GIACOMA

University of Torino, Department of Animal and Human Biology, Torino, Italy

24-35 Poster **Evolutionary cross-talks between plant growth and innate immunity**

M. MADLEN VETTER[1], SILKE ROBATZEK[2], JULIETTE DE MEAUX[1]

[1]Max Planck Institute for Plant Breeding Research, Plant Breeding and Genetics, Cologne, Germany
[2]Max Planck Institute for Plant Breeding Research, Plant Microbe Interactions, Cologne, Germany

24-36 Poster **Geographic variation of phenotypic traits – response to climate and introgression**

ZBYSZEK BORATYNSKI[1], TAPIO O. MAPPES[1], ESA KOSKELA[2]

[1]University of Jyväskylä, Department of Biological and Environmental Science, Center of Excellence in Evolutionary Research, Jyväskylä, Finland
[2]University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland

24-37 Poster Selection in the tropical rain? Gene-level and trait-level divergence in contrasting water-availability conditions in a Neotropical tree

IVAN SCOTTI, CAROLINE SCOTTI-SAINTAGNE, DAMIEN BONAL, DELPHINE AUDIGEOS

INRA, EcoFoG, Kourou, French Guiana

Recent advances in kin selection

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Program

Saturday August 29 - **Symposium 25**

Location: Room 4

Recent advances in kin selection

Organizers: *Francisco Ubeda, University of Tennessee at Knoxville, United States*
Andy Gardner, University of Edinburgh, United Kingdom

9.45 - 10.15	**STUART WEST** (invited) Evolutionary theory in the social sciences
10.15 - 10.45	**ALAN GRAFEN** (invited) Formalising Darwinism and inclusive fitness theory
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**SÉBASTIEN LION** Habitat saturation and the evolution of fecundity and survival altruism
11.35 - 11.55	**GEOFF WILD** Kin selection, sex-ratio evolution and genomic imprinting
11.55 - 12.15	**MIGUEL DOS SANTOS** Evolution of costly punishment and cooperation through punishment scoring
12.15 - 12.35	**FRANÇOIS ROUSSET** Multilocus social evolution in finite populations
12.35 - 12.55	**SAM P. BROWN** Joint evolution of multiple social traits – an inclusive fitness analysis
12.55 - 13.55	*Lunch*

25-1 Oral

EVOLUTIONARY THEORY IN THE SOCIAL SCIENCES

Stuart West [1]

[1]*Oxford University, Department of Zoology, Oxford, United Kingdom*

stu.west@ed.ac.uk

I will discuss the application of and misunderstandings about evolutionary theory in the social sciences literature.

25-2 Oral

FORMALISING DARWINISM AND INCLUSIVE FITNESS THEORY

Alan Grafen [1]

[1]*Oxford University, Department of Zoology, Oxford, United Kingdom*

alan.grafen@sjc.ox.ac.uk

Inclusive fitness maximisation is a basic building block of social evolution theory. There is a view in mathematical population genetics that nothing is caused to be maximised in the process of natural selection, but this is explained as arising from a misunderstanding about the meaning of fitness maximisation. Current theoretical work on inclusive fitness is discussed, with emphasis on my “formal Darwinism” project. Generally favourable conclusions are drawn about the validity of assuming fitness maximisation, but the need for continuing work is emphasised, along with the possibility that substantive exceptions may be uncovered.

25-3 Oral

HABITAT SATURATION AND THE EVOLUTION OF FECUNDITY AND SURVIVAL ALTRUISM

Sébastien Lion [1], Sylvain Gandon [2]

[1]Royal Holloway, University of London, School of Biological Sciences, Egham, United Kingdom
[2]CNRS, Montpellier, France

Sebastien.Lion@rhul.ac.uk

Hamilton's rule provides a general description of the conditions for the evolution of altruism. But the fact that altruism can take different forms depending on which life history trait is affected by the helping behaviour (fecundity versus survival altruism) has often been overlooked. In particular, these different forms of altruism may have very different demographic consequences, which may feed back on evolution. We examine the interplay between various forms of altruism and demography in viscous populations with empty sites. A key component of our analysis is the local density of empty sites experienced by a focal individual, which provides a measure of habitat saturation. We show that habitat saturation has contrasting effects on the evolution of altruism depending on 1) whether the physiological costs and benefits of helping affect fecundity, survival or both; and 2) whether the costs of helping are paid in a density-dependent or density-independent manner. Our analysis stresses the importance of taking into account the feedback between population demography, life history evolution and kin selection when investigating the selective pressures on altruism.

25-4 Oral

KIN SELECTION, SEX-RATIO EVOLUTION AND GENOMIC IMPRINTING

Geoff Wild [1]

[1]University of Western Ontario, Department of Applied Mathematics, London, Canada

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Kin selection provides a nice framework for modelling intragenomic conflict and the evolution of genomic imprinting. In my talk I will illustrate this point with an example of sex-ratio evolution. Time permitting I will also discuss a toy model of conflict resolution that highlights new avenues of research.

25-5 Oral

EVOLUTION OF COSTLY PUNISHMENT AND COOPERATION THROUGH PUNISHMENT SCORING

Miguel dos Santos [1], Daniel Rankin [2], Claus Wedekind [1]

[1]*University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland*
[2]*University of Zurich, Department of Biochemistry, Zurich, Switzerland*

miguel.dossantos@unil.ch

Costly punishment, defined as incurring a cost to decrease the fitness of uncooperative individuals, has been proposed as an important mechanism for promoting cooperation in humans. While many studies on the evolution of costly punishment assumed that individuals do not have information on the punishing behaviour of others, little attention has been given to the possible deterrence effect of carrying the reputation to punish noncooperators. Here, we use computer simulations to investigate this idea in an indirect reciprocity framework. We take a reputation system used in models of indirect reciprocity (image scoring) and apply it to costly punishment, to form what we call a “punishment score”. We assume that individuals have two loci: one coding for the cooperative behaviour (e. g. always cooperate, cooperate with “good individuals”, cooperate with punishers etc.) and one coding for the punishing behaviour (i.e. never punish, punish defection, punish cooperation or always punish). In total, this gives us between 32 and 64 possible strategies. Allowing all of these strategies to evolve reveals a striking result: only one simple combination of strategies prevails, namely cooperate with punishers of defectors and punish defectors. We argue that this strategy dominates as it fundamentally confers an inclusive fitness advantage on the bearer: they help individuals which have the same punishment allele (i.e. punish defection) and spitefully punish individuals which do not help, and therefore do not have a cooperative allele. Our results show that reputation can promote costly punishment, which in turn promotes cooperation through a combination of direct and indirect fitness benefits.

25-6 Oral

MULTILOCUS SOCIAL EVOLUTION IN FINITE POPULATIONS

Francois Rousset [1], Laurent Lehmann [2]

[1]*CNRS & University of Montpellier 2, Institut des Sciences de l’Evolution, Montpellier, France*
[2]*Stanford University, Department of Biological Sciences, Stanford, United States*

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Social behavioral syndromes may depend on the joint evolution of several traits, each with a distinct genetic basis, as well as on the initial linkage disequilibrium between mutations for each trait in finite populations. In this work we extend preexisting frameworks for both multilocus evolution and for social evolution in finite populations, to derive approximations for fixation probabilities of multilocus combinations of mutations in finite populations. We investigate the ability of these approximations to predict the direction of selection on several social scenarios, e.g. marker-based conditional harming or of joint evolution of helping and punishment.

25-7 Oral

JOINT EVOLUTION OF MULTIPLE SOCIAL TRAITS – AN INCLUSIVE FITNESS ANALYSIS

Sam P. Brown [1], Peter D. Taylor [2]

[1]*Oxford University, Department of Zoology, Oxford, United Kingdom*
[2]*Queens University, Kingston, Canada*

sam.brown@zoo.ox.ac.uk

General models of the evolution of cooperation, altruism and other social behaviours have focused almost entirely on single traits, whereas it is clear that social traits commonly interact. Using an extension of inclusive fitness theory, we show that whenever there are interactions among social traits (whether ecological, genetic, chemical, physical), new behaviours can emerge that are not predicted by one-dimensional analyses. We illustrate our framework with an analysis of the generic two-dimensional social dilemma posed by first, the construction and secondly, the exploitation of a shared public good. We find that, contrary to the separate one-dimensional analyses, evolutionary feedback between the two traits can cause an increase in the equilibrium level of selfish exploitation with increasing relatedness, while both social (production plus exploitation) and asocial (neither) strategies can be locally stable.

25-1 Poster **Co-evolution of soldier allocation and oviposition behaviour in parasitoid polyembryonic wasps**

JOAO ALPEDRINHA, ANDY GARDNER
University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom

25-2 Poster **Female beetles adjust their offspring sex ratio according to their relatedness to neighboring females**

DAPHNA GOTTLIEB[1], AMOS BOUSKILA[1], YAEL LUBIN[2], ALLY R. HARARI [1,3]
[1]Ben-Gurion University of the Negev, Department of Life Sciences, Be'er-Sheva, Israel
[2]Ben-Gurion University of the Negev, Mitrani Department of Desert Ecology, Blaustein Institutes for Desert Research, Be'er-Sheva, Israel
[3]The Volcani Center, Bet Dagan, Israel

25-3 Poster **Production of replacement queens by thelytokous parthenogenesis of workers in the polyandrous ant *Cataglyphis cursor***

BLANDINE CHERON, THIBAUD MONNIN, PIERRE FEDERICI, CLAUDIE DOUMS
Université Pierre et Marie Curie, Laboratoire Ecologie et Evolution, Paris, France

25-4 Poster **Multiple infections by related strains of the anther smut fungus in plant populations**

MANUELA LOPEZ VILLAVICENCIO[1], ODILE JONOT[2], AMÉLIE COANTIC[2], MICHAEL E. HOOD[3], JÉRÔME ENJALBERT[4], AMANDA GIBSON[2], TATIANA GIRAUD[2]
[1]Museum National d'Histoire Naturelle, Systematique et Evolution, Paris, France
[2]Universite Paris XI, Département de Genetique et Ecologie Evolutives, Orsay, France
[3]Amherst College, Department of Biology, Amherst, United States
[4]INRA, Département de Pathologie Végétale, Grignon, France

25-5 Poster **The effect of kinship and density in fire salamander (*Salamandra infraimmaculata*) larvae**

SHAI MARKMAN, DANIEL BERKOWIC
Haifa University - Oranim, Department of Biology, Tivon, Israel

25-6 Poster **Impact of fertility transmission and homogamy in family size in humans**

JEAN-TRISTAN BRANDENBURG[1,2], FRÉDÉRIC AUSTERLITZ[1], BRUNO TOUPANCE[2]
[1]Université Paris Sud, Département d'Ecologie, Sytematique et Evolution, Orsay, France
[2]Université Paris-Diderot, Eco-anthropology and Ethnobiology UMR 7206 CNRS / MNHN, Paris, France

25-7 Poster **Making sense of complex signature odours**

NICKY BOS, FERNANDO J. GUERRIERI, JELLE S. VAN ZWEDEN, PATRIZIA D'ETTORRE
Copenhagen University, Department of Biology, Centre for Social Evolution, Copenhagen, Denmark

25-8 Poster **Parasitic females of black-headed gulls lay eggs in closely related females' nests**

NORBERT DUDA
University of Bialystok, Department of Vertebrate Zoology, Bialystok, Poland

Post-genomic approaches to host-parasite evolution

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Program

Saturday August 29 - **Symposium 26**

Location: Room 5

Post-genomic approaches to host-parasite evolution

Organizers:	*Steve Paterson, University of Liverpool, United Kingdom* *Stuart Piertney, University of Aberdeen, United Kingdom*

9.45 - 10.15	**FRANCIS JIGGINS** (invited) The evolution of insect immunity genes
10.15 - 10.45	**BREGJE WERTHEIM** (invited) Functional genomics of plastic and evolutionary responses to parasitism
10.45 - 11.15	*Coffee break*
11.15 - 11.35	**CHARLOTTE TOLLENAERE** Detecting genetic markers associated with plague resistance in natural populations of *Rattus rattus* though AFLP genome scan
11.35 - 11.55	**JOSEPHINE M. PEMBERTON** Genome-wide association of parasite resistance in a free-living sheep population
11.55 - 12.15	**ELLEN DECAESTECKER** A molecular reconstruction of a *Daphnia*-parasite interaction
12.15 - 12.35	**BENJAMIN DEVIER** Detecting genes involved in host specialisation in fungal pathogens by looking for signals of positive selection in genomic data
12.35 - 12.55	**PAUL SCHMID-HEMPEL** Genetic architecture of resistance genes and implications for sex and recombination
12.55 - 13.55	*Lunch*

26-1 Oral

THE EVOLUTION OF INSECT IMMUNITY GENES

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Animals are faced with an ever changing array of pathogens against which they must defend themselves, and this can result in intense natural selection on their immunity genes. By studying the selection pressures acting on these genes, we can gain insights into how animals adapt to and coevolve with their pathogens. We have resequenced most of the known immunity genes from population samples of *Drosophila melanogaster* and *Drosophila simulans*, and used an extension of the McDonald-Kreitman test to infer their rate of adaptive protein evolution. Compared to the rest of the genome, immunity genes have higher and more variable rates of adaptive evolution, which is primarily due to a small number of genes that are under exceptionally intense selection. At a finer scale, we have identified particular genes and pathways with high rates of adaptive evolution. The most rapidly evolving of all are the antiviral RNAi genes, which is probably because these genes are targeted by viral suppressors of RNAi. Overall our results demonstrate that pathogens are an important cause of adaptive evolution, and that immunity genes tend to be under directional rather than balancing selection.

26-2 Oral

FUNCTIONAL GENOMICS OF PLASTIC AND EVOLUTIONARY RESPONSES TO PARASITISM

Bregje Wertheim [1,2], Alex R. Kraaijeveld [3]

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The parasitoid-host interaction is highly suitable for studying evolution in progress. Parasitoids exert extremely high selection pressures on their hosts, while strong immunological resistance against parasitoids is a costly trait. Hosts can induce a phenotypic plastic response to parasitism (i.e., launch an acute immune response), but there is large genetic variation in the success rate of this resistance. Populations exposed to high levels of parasitism rapidly evolve towards higher resistance. Our aim was to compare the genetics of these plastic and evolutionary responses to parasitoids.

Genome-wide studies are uniquely powerful to detect genetic networks and interactions, and to identify novel putative immunity genes and pathways. To identify the genetic networks involved in evolution of resistance to parasitoids, we described the transcriptional differences between a *Drosophila* strain artificially selected for parasitoid resistance and its control. We profiled expression at 7 timepoints during the development from egg until late second instars, and found a relatively large number of genes (>550) with changed expression levels among the 2 strains. Our study indicated an elaborate interplay of gene regulatory networks. Interestingly, the overlap in genes with changed expression during the acute and evolved responses was significant, but small. This suggests that the plastic and evolutionary responses are modulated partially through the same pathways, while many other processes and pathways are also modulated during the acquiring of parasitoid resistance.

26-3 Oral

DETECTING GENETIC MARKERS ASSOCIATED WITH PLAGUE RESISTANCE IN NATURAL POPULATIONS OF *RATTUS RATTUS* THOUGH AFLP GENOME SCAN

Charlotte Tollenaere [1], Jean-Marc Duplantier [1], Lila Rahalison [2], Carine Brouat [1]

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Understanding the genetic basis of adaptation is a key question of evolutionary biology and population genomics provide a way to address this issue by separating locus-specific effects (mainly natural selection) from genome-wide effects (genetic drift and gene flow). Pathogens, in particular highly virulent ones, can act as strong selective pressure on their hosts, resulting in rapid evolutionary changes. To understand how pathogen selection can drive host genetic variation and to detect markers associated with host resistance to a pathogen, we applied a population genomics approach on *Rattus rattus* Malagasy populations.
In Madagascar, the black rat (*R. rattus*) is the main reservoir of plague (*Yersinia pestis* infection). This disease is endemic in central highlands (above 800 meters) but absent at low-altitude and *R. rattus* populations were shown to be much more plague resistant within plague foci than within plague-free zone (for wild and F1 animals).
This study used eight *R. rattus* natural populations (about 30 individuals per population) resulting in four comparisons of plague focus / plague-free zone populations. Ten AFLP primer combinations (about 250 polymorphic loci) were used. We identified a few loci potentially important in plague resistance. Functional significance and relation with plague of these loci is then investigated through comparison of individuals exhibiting different responses to experimental plague inoculations. Finally, determination of similar sequences in the genome of the close model species *R. norvegicus* could allow identifying the genomic regions that may be involved in plague resistance.

26-4 Oral

GENOME-WIDE ASSOCIATION OF PARASITE RESISTANCE IN A FREE-LIVING SHEEP POPULATION

Josephine M. Pemberton [1], Dario Beraldi [1], Emily Brown [2], John Hopkins [3], Jon Slate [2], Philine Feulner [2],
Peter M. Visscher [4], Allan F. McRae [4], Hong Lee [4]

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Genome-wide association studies (GWAS), usually with case-control format, have become the method of choice for finding genome regions associated with complex disease in human medical genetics. We present one of the first applications of this technique within a free-living non-human population in pursuit of an evolutionary objective: can it be used to locate parasite resistance genes in a free-living population? Following a major genome sequencing effort in 2007-8, the International Sheep Genomics Consortium and Illumina have generated a 60K SNP chip. Pilot analyses suggest that the Soay sheep of St Kilda are polymorphic at some 60% of selected SNPs. We selected for genotyping 566 free-living Soay sheep with extreme estimated breeding values for various phenotypic traits including a measure of parasite resistance, faecal egg count. We present analyses of this data set and lessons learned from the experience.

26-5 Oral

A MOLECULAR RECONSTRUCTION OF A *DAPHNIA*-PARASITE INTERACTION

Ellen Decaestecker [1], Tom J. Little [2], Pierrick Labbé [2]

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In their 'arms race' with fast evolving parasites, there will be selection in *Daphnia* populations against defence mechanisms that are abundant in the momentary interaction, as parasites adapt to the most abundant host genotypes. The resulting antagonism produces an ongoing co-evolutionary dynamic that maintains genetic variation in infectivity traits. It is, however, notoriously difficult to study co-evolutionary dynamics in nature, because time series over many generations are needed. Consequently, empirical evidence for the process of host-parasite co-evolution in natural systems is lacking. An elegant way to bridge this gap is to use aquatic organisms that produce dormant stages. Dormant stages settle in layered pond sediments producing egg banks that can be reactivated after years or decades. An archive of evolutionary change is thus available and we previously used this in a phenotypic reconstruction of a host-parasite co-evolution between the crustacean *Daphnia* and its bacterial parasite, *Pasteuria*. Co-evolution was documented as changes in host and parasite fitness in cross-infection experiments: *Daphnia* clones were exposed to parasites of different depths of a sediment core, and the different sediment depths represented different time frames in the co-evolution. In a recent molecular reconstruction, we used these same temporally spaced samples of interactors to study the mechanism of this *Daphnia*-parasite co-evolution. I here represent the state of the art on the results of the study of evolving genes through massively parallel sequencing of the *Daphnia* transcriptome as it has changed in sediment-archived samples. In this way, we reconstructed the genetic and immunological background that characterizes *Daphnia* -*Pasteuria* co-evolution.

26-6 Oral

DETECTING GENES INVOLVED IN HOST SPECIALISATION IN FUNGAL PATHOGENS BY LOOKING FOR SIGNALS OF POSITIVE SELECTION IN GENOMIC DATA

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Numerous genes involved in host-pathogens interactions have been shown to evolve under positive selection. They are indeed expected to evolve rapidly either because of coevolution with their host, or specialization on novel host species. Looking for genes under positive selection between closely related pathogen species can thus provide new insights on the genes involved in coevolution and host specialization. *Microbotryum violaceum*, responsible for anther smut disease, is a complex of sibling species, each being specialized on a particular Caryophyllaceae plant species. Using a dataset of 40,000 ESTs sequenced from 4 different species of *Microbotryum*, we performed a large analysis on orthologous genes to detect those under positive selection. Around 10% of the 372 predicted orthologous genes were found to evolve under positive selection. Sequencing 16 of these genes in 9 additional *Microbotryum* species, as well as within-species analyses, confirmed that they have indeed been rapidly evolving, in particular in pathogenic species specialized on a given host. These genes under positive selection were putatively involved in putative functions that could be related to pathogenecity, such as nutrient transport, metabolite synthesis and secretion, hyphal growth and differentiation, and regulation of other genes. Such a blind approach, without a priori candidate genes, is thus interesting to investigate the proportion and the nature of the genes involved in host-pathogens interactions and in host specialization.

26-7 Oral

GENETIC ARCHITECTURE OF RESISTANCE GENES AND IMPLICATIONS FOR SEX AND RECOMBINATION

Paul Schmid-Hempel [1,2], Lena Bayer-Wilfert [2]

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Host-parasite interactions are strongly affected by genotypic interactions between the two parties. Recent years have seen a vast increase in genome wide quantitative trait locus (QTL) mapping and association studies identifying the genetic basis of host parasite interactions. We have surveyed the available data and found a number of general patterns in the genetic architecture of host resistance. The accumulating evidence shows that a limited number of loci are typically involved in determining resistance and susceptibility, with epistatic loci playing an important role. We found that studies repeating QTL searches under different environmental conditions are more likely to yield identical loci than studies that are repeated using different genotypes of a host or parasite species. This suggests that strong genotypic interactions prevail over environmental interactions in shaping genetic architecture. Strikingly, epistatic interactions were found to occur predominantly between, rather than within, linkage groups or chromosomes. Thus, segregation and chromosome number rather than recombination via cross-over should be the major elements of sexual reproduction affecting adaptive change in host resistance.

26-1 Poster **Duplication of the MHC class II genes in the bank vole**
KRISTIN SCHERMAN
Lund University, Department of Ecology, Lund, Sweden

26-2 Poster **Rates and patterns of evolution in mutualistic and parasitic endosymbionts**
MEG WOOLFIT
University of Queensland, School of Biological Sciences, Brisbane, Australia

26-3 Poster **Mapping disease resistance genes in *Daphnia magna***
JARKKO ROUTTU, ISABELLE COLSON, DIETER EBERT
University of Basel, Department of Evolutionary Biology, Basel, Switzerland

26-4 Poster **Widespread flux in a host-parasite interaction revealed through comparison of contemporary and historical samples**
EMILY A. HORNETT[1,4], SYLVAIN CHARLAT[2], NINA WEDELL[3], CHRIS D. JIGGINS[4], GREG D. D. HURST[1]
[1]University of Liverpool, School of Biological Sciences, Liverpool, United Kingdom
[2]University of Lyon, Laboratoire de Biometrie & Biologie Evolutive, Villeurbanne, France
[3]University of Exeter, Centre for Ecology & Conservation, Cornwall, United Kingdom
[4]University of Cambridge, Department of Zoology, Cambridge, United Kingdom

26-5 Poster **Host-parasite interactions, immunocompetence and population dynamics in red grouse**
LUCY M. I. WEBSTER[1], FRANÇOIS MOUGEOT[2], JESUS MARTINEZ-PADILLA[1], STEVE PATERSON[3], STUART B. PIERTNEY[1]
[1]University of Aberdeen, Institute of Biological and Environmental Sciences, Aberdeen, United Kingdom
[2]IRES Instituto de Investigacion en Recursos Cinegeticos, Ciudad Real, Spain
[3]University of Liverpool, School of Biological Sciences, Liverpool, United Kingdom

26-6 Poster **Genes Affecting Viral Resistance and Transmission in *Drosophila melanogaster***
MICHAEL M. MAGWIRE
University of Cambridge, Department of Genetics, Cambridge, United Kingdom

26-7 Poster **Selection shapes malaria genomes and drives divergence between pathogens infecting hominids versus rodents**
FRANCK PRUGNOLLE[1], KATE MCGEE[2], JOHN KEEBLER[2], PHILIP AWADALLA[2,3]
[1]CNRS Montpellier, Laboratory Genetics and Evoution of Infectious Diseases, Montpellier, France
[2]North Carolina State University, Department of Genetics, United States
[3]University of Montreal, Department of Pediatric, S.te Justine Hospital Research Center, Montreal, Canada

26-8 Poster **Microarray analysis of experimental evolution in a parasitic nematode**
STEVE PATERSON, HELEN EVANS
University of Liverpool, School of Biological Sciences, Liverpool, United Kingdom

26-9 Poster **Evolution of pathogen resistance pathways in wild tomato**
ANJA C. HOERGER, LAURA E. ROSE, WOLFGANG STEPHAN
Ludwig-Maximilians-University, Department of Evolutionary Biology, Munich, Germany

26-10 Poster **Co-evolving Polymorphisms in an Insect and a Virus**
LENA WILFERT, FRANK JIGGINS
University of Cambridge, Department of Genetics, Cambridge, United Kingdom

26-11 Poster **Pathogen-induced selection on innate immunity genes in wild rodents**

BARBARA TSCHIRREN, LARS RÅBERG, KRISTIN SCHERMAN, MARTIN ANDERSSON, HELENA WESTERDAHL

Lund University, Department of Animal Ecology, Lund, Sweden

26-12 Poster **Co-evolution between sigma viruses and *Drosophila***

BEN LONGDON[1], LENA BAYER WILFERT[2], DARREN J. OBBARD[1], FRANCIS JIGGINS[2]

[1]University of Edinburgh, Institute of Evolutionary Biology, Edinburgh, United Kingdom
[2]University of Cambridge, Genetics Department, Cambridge, United Kingdom

26-13 Poster **Selection and evolution of parasite resistance genes in a free-living mammal population**

EMILY A. BROWN

University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom

Early evolution

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Program

Saturday August 29 - **Symposium 27**

Location: Room 1

Early evolution

Organizers:	*Renato Fani, University of Florence, Italy* *Simonetta Gribaldo, Institut Pasteur, Paris, France*

13.55 - 14.25	**PURIFICACION LOPEZ-GARCIA** (invited) On the origin of eukaryotes
14.25 - 14.55	**PAOLA LONDEI** (invited) Begin at the beginning: an ancestral problem with divergent solutions
14.55 - 15.15	**DAVID MOREIRA** Can viruses be included in the Tree of Life?
15.15 - 15.45	*Coffee break*
15.45 - 16.05	**PETER VAN DER GULIK** The missing link between prebiotic amino acids and early proteins
16.05 - 16.25	**JOEL R. PECK** Is Life Impossible?

27-1 Oral

ON THE ORIGIN OF EUKARYOTES

Purificacion Lopez-Garcia [1,2]

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The origin of the eukaryotic cell is one of the major unsolved questions in evolutionary biology. Molecular phylogeny and comparative genomic analyses have clearly demonstrated the contribution of the alphaproteobacterial ancestor of mitochondria to the making of the eukaryotic cell. However, both, the nature of the host that incorporated the mitochondrial ancestor and the process that led to the formation of the most emblematic eukaryotic feature, the nucleus, remain elusive. Was the proto-mitochondrial host a member of a hypothetical proto-eukaryotic lineage endowed already with the capacity of phagocytosis? Was it a prokaryote and, if so, was it a bacterium or an archaeon? How and why did the nucleus evolve? Did viruses play a role? How did the membrane system evolve? Several mutually exclusive hypotheses have been put forward to try answering these questions. Some of them can be disproved on the basis of comparative genomics and molecular phylogeny. We will discuss some of these questions and revisit them in the light of the syntrophy hypothesis for the origin of eukaryotes.

27-2 Oral

BEGIN AT THE BEGINNING: AN ANCESTRAL PROBLEM WITH DIVERGENT SOLUTIONS

Paola Londei [1]

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Translation, the link between genotype and phenotype, is a key step in gene expression but perhaps the hardest to understand in evolutionary terms. Decoding of a nucleic acid into a polypeptide entails evolving a dictionary (the genetic code) and a specific machinery (tRNA, ribosomes) to actually read the code. A central problem for successful decoding that must have been solved early in evolution is that of setting a precise start site for reading the message. In present-day cells, the landing of the ribosome on the correct translation initiation codon is a complex process that appears to diverge extensively in the bacteria and the eukaryotes. Recently, however, the study of the third primary domain of cell descent, the archaea, has revealed new aspects of the mechanism of translational initiation, giving a more comprehensive view of its conserved and unique features. The most recent data on archaeal translation will be presented and compared with those available for the other two primary domains. The data will be integrated into a speculative model of the ancestral machinery for translation initiation at the LUCA stage of cellular evolution.

27-3 Oral

CAN VIRUSES BE INCLUDED IN THE TREE OF LIFE?

David Moreira [1]

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There is an innate bias in humans to interpret biological diversity as the consequence of a progressive nature of the evolutionary process, so that simple organisms tend to be perceived as necessarily primitive. When viruses were discovered, they were thus rapidly accepted as the missing link between the inert world and living organisms. However, this idea was abandoned long ago when their ultimate molecular parasitic nature was demonstrated during the past 50 years. In recent years, the idea that viruses are living organisms that played a key role as inventors of several essential cellular characters has experienced a renaissance owing to the discovery of unusual complex viruses, such as the Mimivirus, with some typical cellular genes. Nevertheless, it can be demonstrated by phylogenetic analysis that these genes have been acquired by those viruses from their hosts by horizontal gene transfer. This, together with considerations such as the polyphyly of the different viral lineages, impedes to incorporate viruses within the Tree of Life. Moreover, the complete absence of carbon and energy metabolism makes inappropriate to consider viruses as living beings.

27-4 Oral

THE MISSING LINK BETWEEN PREBIOTIC AMINO ACIDS AND EARLY PROTEINS

Peter Van der Gulik [1], Serge Massar [2], Dimitri Gilis [3], Harry Buhrman [1,4], Marianne Rooman [3]

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[2]*Université Libre de Bruxelles, Laboratoire d'Information quantique, Brussels, Belgium*
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One of the big open questions in evolutionary biology is the character of the first coded peptides. Two competing hypotheses concerning this question can be formulated. According to the first hypothesis, the first coded peptides were structural elements, functioning in RNA-peptide complexes, much like polyamines are nowadays functioning in complexes with, among other molecules, tRNAs. From this early, short molecules the evolutionary development would go on towards the first protein domains, which would have played a role as a kind of RNA chaperones. The next stage would be independent proteins, with their own function, developing active sites as a last step. According to the second hypothesis, the first coded peptides were autonomous active sites. Short peptides with a metal ion, bound by carboxyl groups, would have had a fixed conformation, and have provided a rough, chemical activity. The metal-binding active sites would have been the heart of the first protein domains, which would develop when an evolving biochemistry became progressively more complex. As a last step, multi-domain proteins would emerge. To accumulate evidence to support the second hypothesis, a computer program was developed with which short, metal-binding amino acid sequences were extracted from the Protein Data Bank. The sequences which were searched for, are composed of prebiotic amino acids (including the negatively charged Asp) and are bound to a positive metal ion. This program extracted sequences representing the active sites from proteins like kinases, mutases and polymerases. Remarkably, these activities of proteins, all involving the manipulation of phosphate groups, are very much like the activities of ribozymes, which also manipulate phosphate groups with the participation of metal ions. When comparing ribozyme activities with very primitive protein activities (the active site of the mRNA producing polymerase is universally conserved, and thus probably about four billion years old), the two kind of macromolecules seem to converge to a same kind of catalytic repertoire! Considering recent results about the potential of montmorillonite clay to catalyze the production of random oligomers of both RNA and peptide (starting with nucleotides and amino acids), the question can be posed if a role was played by amino acids, dipeptides and short, coded oligopeptides in the RNA world. In other words: did RNA ever exist without protein around?

27-5 Oral

IS LIFE IMPOSSIBLE?

Joel R. Peck [1], David Waxman [1]

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Eigen's Paradox is a logical puzzle concerned with the origin of complex life. It is presumed that, early in the history of life, mutation rates were much higher than they are in contemporary organisms. According to Manfred Eigen, this implies that the maximum amount of information that could have been stably encoded in the genomes of early organisms must have been severely limited. In contemporary organisms, the mechanisms of error prevention and correction are quite complex. This leads to a "chicken-and-egg problem." How could life that is complex enough to allow the suppression of mutation to low levels have evolved while mutation rates were quite high? Eigen's calculations are based on the idea that, if the genome with the best-possible fitness can not be maintained in a population, then "The information ... would slowly seep away until it is entirely lost." However, this idea is not obviously based on any firm information theoretic foundation. What really matters is whether, in a stable population, organisms are able to generate phenotypes that are complex enough to allow for highly effective error prevention and correction mechanisms. Here, we re-analyze the problem using this phenotypic-complexity criterion. We find that there are conditions where much more information can be stably encoded in the genome than would follow from Eigen's criterion, despite the existence of relatively high mutation rates. We find that the highest levels of information content are obtained when recombination occurs, and when each possible phenotype is produced by many different genotypes.

Pollinator-mediated selection in floral evolution

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Program

Saturday August 29 - **Symposium 28**

Location: Room 2

Pollinator-mediated selection in floral evolution

Organizers: *Yuval Sapir, Tel Aviv University, Israel*
Scott Armbruster, University of Portsmouth, United Kingdom and University of Alaska, Fairbanks, United States

13.55 - 14.25	**THOMAS F. HANSEN** (invited) Multivariate constraints and evolvability in floral diversification
14.25 - 14.55	**STACEY D. SMITH** (invited) Macroevolutionary tests of pollination syndromes
14.55 - 15.15	**MARIO VALLEJO-MARIN** Division of labour within flowers
15.15 - 15.45	*Coffee break*
15.45 - 16.05	**CHARLES FENSTER** Correlational selection and the evolution of the hummingbird pollination syndrome in *Silene virginica* (Caryophyllaceae)
16.05 - 16.25	**RODRIGO MEDEL** Ecological and genetic constraints on flower evolution in the Andean monkeyflower *Mimulus luteus*
16.25 - 16.45	**PAUL D. RYMER** Can pollinator foraging behaviour maintain divergent floral morphs in sympatric populations of *Gladiolus longicollis* (Iridaceae)? Insights from a paternity analysis in a natural hybrid zone
16.45 - 17.05	**SILVANA MARTEN-RODRIGUEZ** Evolutionary breakdown of specialization: generalized and autogamous pollination systems provide reproductive assurance in Antillean Gesneriaceae

28-1 Oral

MULTIVARIATE CONSTRAINTS AND EVOLVABILITY IN FLORAL DIVERSIFICATION

Thomas F. Hansen [1]

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The resin-producing inflorescences of *Dalechampia* show a range of variation among species and populations influenced by adaptations to different bee pollinators and by character displacement. In this presentation I discuss the role of variational constraints and evolvability in the diversification within the widely-distributed species complex of *Dalechampia scandens*. Using recently proposed methods for measuring multivariate evolvability I characterize the constraints on diversification and compare these to patterns of among-population diversification with the aim of testing hypotheses about the role of constraints in evolution.

28-2 Oral

MACROEVOLUTIONARY TESTS OF POLLINATION SYNDROMES

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The pollination syndrome concept, which proposes that floral traits form adaptive combinations reflecting specialization for particular pollinators, has had enormous impact on studies of plant ecology and evolution. While the role of pollinators in shaping floral variation has been studied extensively at the population-level, relatively few studies have directly examined how these microevolutionary processes are manifested in macroevolutionary patterns. I will describe several patterns that might be predicted from the pollination syndromes, such as the clustering of species in floral morphospace and correlated evolution among floral traits, and discuss how these patterns might be tested with statistical comparative methods. Using the Andean clade *Iochroma* as an example, I will discuss a phylogenetic test of another prediction, that changes in floral traits are correlated with shifts in pollination system. I estimated phylogenetic correlations among major groups of pollinators and four floral traits, and found that two traits, nectar reward and display size, show significant associations with shifts in both bird and insect pollination. The remaining two traits, corolla length and color, appear to evolve largely independently of changes in pollination system, contrary to the predictions of classic pollination syndromes. This study highlights the utility of comparative approaches for testing adaptive hypotheses and the need for additional macroevolutionary studies of pollination syndromes.

28-3 Oral

DIVISION OF LABOUR WITHIN FLOWERS

Mario Vallejo-Marin [1], Jessamyn S. Manson [2], James D. Thomson [2], Spencer C. H. Barrett [2]

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Nectarless plants often rely on pollen to attract pollinators. Pollen in these species has a dual function: on one hand pollen is the carrier of male gametes and on the other is food consumed by pollinators. Heteranthery, the production of two or more stamen types by individual flowers, reconciles these contrasting fates of pollen by allowing different stamens to specialize in "pollinating" and "feeding" functions. Using a combination of experimental manipulations, pollinator observations, and theoretical models we investigate this "division-of-labour" hypothesis. We present evidence indicating that although feeding anthers are preferentially manipulated by bees, pollinating anthers export more pollen to other flowers. Our work suggests that the interaction between plants and pollen-consuming pollinators has driven the evolution of floral morphology, resulting in a dramatic example of within flower dimorphism in sexual organs.

28-4 Oral

CORRELATIONAL SELECTION AND THE EVOLUTION OF THE HUMMINGBIRD POLLINATION SYNDROME IN *SILENE VIRGINICA* (CARYOPHYLLACEAE)

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Pollination syndromes are a multivariate collection of traits that reflect selection by specific pollinators for attraction and reward of those pollinators while optimizing pollen transfer efficiency. We expect that the non random combinations of floral traits that comprise specific pollination syndromes reflect selection favoring these specific combinations. In other words the underlying mode of selection is correlational or non additive, favoring some trait combinations over others. Unfortunately, there is little direct evidence that pollinators mediate correlational selection on floral traits. To document the role of correlational selection on floral trait evolution, we measured individual variation in six floral traits and yearly and lifetime total plant seed and fruit production of 758 plants across nine years of study in natural populations of the perennial, iteroparous Ruby Throated Hummingbird-pollinated *Silene virginica*. We also conducted an experimental manipulation of traits to quantify the contribution of non additive selection. Canonical analysis of the gamma matrix indicated that correlational selection was common. Our experiments indicate that hummingbirds prefer to visit certain trait combinations over others. In total, our analyses and experiments demonstrate that hummingbird mediated selection favors trait combinations and the integration of floral features of attraction and pollen transfer efficiency that are consistent with the hummingbird pollination syndrome.

28-5 Oral

ECOLOGICAL AND GENETIC CONSTRAINTS ON FLOWER EVOLUTION IN THE ANDEAN MONKEYFLOWER *MIMULUS LUTEUS*

Rodrigo Medel [1], Paulina Salas [1]

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Although pollinator-mediated natural selection has been measured on many floral traits and in many species, results often reflect the net selective impact of the pollinator assemblage as a whole, assuming additive selective effects of pollinators upon the flower phenotype. In consequence, the potential of individual pollinator species to constrain the expected strength and direction of evolutionary change is largely unknown. To determine the potential for ecological and genetic constraints on adaptive floral evolution, we set a factorial 2 x 2 experimental design to estimate the separate and joint selection effects of bees and hummingbirds on the flower phenotype of the Andean monkeyflower *Mimulus luteus*. In addition, we estimated the quantitative genetic basis of floral trait variation. Restricted maximum likelihood (REML) analyses of greenhouse-grown half-sib families were used to estimate genetic variances and covariances for corolla size, nectar guide size, and floral tube length, three traits involved in pollinator preference. When the genetic variance-covariance matrix was combined with experimental estimates of pollinator-mediated selection coefficients, the predicted multivariate evolutionary response differed from selection gradients in some but not all situations, depending of the treatment involved. This result suggests that the importance of genetic constraints on the evolution of floral characters is contingent to the ecological scenario where interactions occur and more specifically to the presence or absence of particular pollinator species responsible of phenotypic selection.

28-6 Oral

CAN POLLINATOR FORAGING BEHAVIOUR MAINTAIN DIVERGENT FLORAL MORPHS IN SYMPATRIC POPULATIONS OF *GLADIOLUS LONGICOLLIS* (IRIDACEAE)? INSIGHTS FROM A PATERNITY ANALYSIS IN A NATURAL HYBRID ZONE

Paul D. Rymer [1,2], Steven D. Johnson [3], Vincent Savolainen [1,2]

[1]*Imperial College London, Division of Biology, Ecology and Evolution section, Ascot, United Kingdom*
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Ecological speciation is a two step process with divergent selection followed by reinforcement leading to reproductive isolation. Pollinator mediated selection has long been suggested as a mechanism for the rapid diversification of angiosperms. While there is growing evidence for divergent selection in allopatric populations, few studies have quantified the role of pollinators in maintaining floral diversity in sympatry. Here we determine the mating patterns in a hybrid zone of *Gladiolus longicollis* containing extreme floral tube length variation (3-12cm) using a paternity analysis based on microsatellite markers. In particular, we address the fundamental question of whether hawkmoth pollinator foraging maintains short and long floral morphs in sympatry through assortative mating.

28-7 Oral

EVOLUTIONARY BREAKDOWN OF SPECIALIZATION: GENERALIZED AND AUTOGAMOUS POLLINATION SYSTEMS PROVIDE REPRODUCTIVE ASSURANCE IN ANTILLEAN GESNERIACEAE

Silvana Marten-Rodriguez [1,2], Abel Almarales-Castro [3], Charles B. Fenster [4], Elizabeth A. Zimmer [5]

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Specialized pollination mutualisms in oceanic islands may increase the risk of plant reproductive failure if pollinators are absent or scarce. Thus, pollinator-poor island faunas may promote the evolution of alternative modes of plant reproduction. We combined comparative methods and field experiments to evaluate the following hypotheses: 1) floral phenotypes in the Antillean tribe Gesnerieae (family Gesneriaceae) evolved in response to pollinator-mediated selection, 2) low pollinator service and pollen limitation favored the evolution of generalized flowers and autonomous self-pollination mechanisms. Mapping of pollination systems onto a combined two gene+ morphology phylogeny indicates that hummingbird pollination and outcrossing breeding systems are ancestral, with at least three independent origins of generalized pollination, and two origins of bat pollination associated with changes in the floral phenotype. Autonomous self-pollination evolved at least twice in ornithophilous lineages only. Field experiments revealed that specialists have lower pollinator visitation rates and higher pollen limitation levels than generalists; however, only hummingbird specialists use autonomous selfing as a reproductive assurance mechanism.

The evolution of generalized pollination systems may be related to the low frequency of hummingbird visitation to Gesnerieae flowers in the Antillean islands. However, since bat pollinated species are also pollen-limited, transitions to bat pollination may reflect selection via the male component of plant fitness. The maintenance and diversification of ornithophilous lineages may be facilitated by the evolution of autonomous selfing mechanisms. Our results support the notion that pollinator depauperate faunas on islands create selective environments that favor the evolution of generalization and autonomous selfing as reproductive assurance mechanisms.

28-1 Poster **Pollinator-driven speciation in Australian sexually deceptive orchids**

ROD PEAKALL[1], MICHAEL WHITEHEAD[1], JACQUI POLDY[2], RUSSELL BARROW[2], FLORIAN P. SCHIESTL[3], WITTKO FRANCKE[4]
[1]*The Australian National University, Department of Botany and Zoology, School of Biology, Canberra, Australia*
[2]*The Australian National University, Research School of Chemistry, Canberra, Australia*
[3]*University of Zurich, Institute of Systematic Botany, Zurich, Switzerland*
[4]*University of Hamburg, Department of Chemistry, Hamburg, Germany*

28-2 Poster **Genetic basis of reproductive isolation in a sexually deceptive orchid *(Ophrys):* implications from cDNA representational difference analysis (RDA)**

SHUQING XU[1,3], PHILIPP M. SCHLÜTER[1,2], UELI GROSSNIKLAUS[2], FLORIAN P. SCHIESTL[1]
[1]*University of Zurich, Institute of Systematic Botany, Zurich, Switzerland*
[2]*University of Zurich, Institute of Plant Biology, Zurich, Switzerland*
[3]*ETH Zurich, Institute of Integrative Biology, Zurich, Switzerland*

28-3 Poster **Does sexual organ placement contribute to reproductive isolation between distylous species?**

BARBARA KELLER, ELENA CONTI
University of Zurich, Institute of Systematic Botany, Zurich, Switzerland

28-4 Poster **How important are pollinators in shaping the patterns of genetic variation in mixed populations of *Rhinanthus minor* and *R. angustifolius*?**

RENATE A. WESSELINGH, LAURENT NATALIS, VÉRONIQUE DUCARME
Université Catholique de Louvain, Biodiversity Research Centre, Louvain-la-Neuve, Belgium

28-5 Poster **Pollen flow within a large population of *Arabidopsis lyrata***

SVERRE LUNDEMO[1], HANS K. STENØIEN[2,3], MOHSEN FALAHATI-ANBARAN[1], OUTI SAVOLAINEN[3]
[1]*Norwegian University of Science and Technology, Department of Biology, Trondheim, Norway*
[2]*Norwegian University of Science and Technology, Museum of Natural History and Technology, Systematics and Evolution Group, Section of Natural History, Trondheim, Norway*
[3]*University of Oulu, Department of Biology, Oulu, Finland*

28-6 Poster **Evolutionary potential of honesty-related traits in a plant-pollinator system**

PAULINA SALAS, RODRIGO MEDEL
Universidad de Chile, Departamento de Ciencias Ecológicas, Santiago, Chile

28-7 Poster **Honest signalling in *Dalechampia***

ROCIO PEREZ-BARRALES, W. SCOTT ARMBRUSTER
University of Portsmouth, School of Biological Sciences, Portsmouth, United Kingdom

28-8 Poster **The signaling function of an extra-floral display: what selects for signal development?**

TAMAR KEASAR[1], AVI SHMIDA[2], ADI SADEH[3]
[1]*University of Haifa, Department of Science Education - Biology, Tivon, Israel*
[2]*The Hebrew University, Department of Evolution Systematics and Ecology, Jerusalem, Israel*
[3]*Ben Gurion University, Department of Life Sciences, Beer Sheva, Israel*

28-9 Poster **Pollinator-mediated evolution of mutualistic and antagonistic traits in *Trollius europaeus***

SÉBASTIEN IBANEZ[1,2], CHRISTIANE GALLET[1,2], LAURENCE DESPRÉS[1,2]

[1]Laboratoire d'Ecologie Alpine, UMR 5553, Grenoble, France

[2]Station Alpine Joseph Fournier, UMS 2925, Col du Lautaret, France

28-10 Poster **Florivores decrease flowering duration and pollinator visitation**

VIRVE SÕBER, MARI MOORA, TIIT TEDER

University of Tartu, Institute of Ecology and Earth Sciences, Tartu, Estonia

28-11 Poster **Benefits and costs to pollinating, seed-eating insects: the effect of flower size and fruit abortion on larval performance**

ANNE BURKHARDT[1,2], LYNDA F. DELPH[3], GIORGINA BERNASCONI[1]

[1]University of Neuchatel, Laboratory of Evolutionary Botany, Neuchatel, Switzerland

[2]University of Lousanne, Lousanne, Switzerland

[3]Indiana University, Department of Biology, Bloomington, United States

28-12 Poster **Does pollen transfer efficiency drive the evolution of specialized deceptive pollination systems?**

GIOVANNI SCOPECE[1], SALVATORE COZZOLINO[1], STEVE D. JOHNSON[2], FLORIAN P. SCHIESTL[3]

[1]University of Naples Federico II, Department of Structural and Functional Biology, Naples, Italy

[2]University of KwaZulu-Natal, School of Biological and Conservation Sciences, Scottsville, South Africa

[3]University of Zürich, Institute of Systematic Botany, Zürich, Switzerland

28-13 Poster **Pollinator-mediated selection on floral traits in the orchid *Gymnadenia conopsea***

NINA SLETVOLD[1,2], JON ÅGREN[2]

[1]Norwegian University of Science and Technology, Museum of Natural History, Trondheim, Norway

[2]Uppsala University, Evolutionary Biology Centre, Department of Plant Ecology, Uppsala, Sweden

28-14 Poster **Effects of floral traits and plant genetic composition on pollinator behavior**

YUVAL SAPIR

Tel Aviv University, Department of Plant Sciences, Tel Aviv, Israel

28-15 Poster **Reproductive assurance and autofertility in the flora of Coastal Atacama Desert**

ALEJANDRA GONZALEZ[1], FERNANDA PEREZ[1,2]

[1]Universidad Católica de Chile, Center for Advanced Studies in Ecology and Biodiversity (CASEB) and Departamento de Ecología, Facultad de Ciencias Biológicas, Chile

[2]Universidad de Chile, Instituto de Ecología y Biodiversidad (IEB), Facultad de Sciencias, Chile

Evolution of shape: linking micro- and macroevolution

eseb
12th Congress
Turin 2009

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Program

Saturday August 29 - **Symposium 29**

Location: Room 3

Evolution of shape: linking micro- and macroevolution

Organizers: *Andrea Cardini, Università di Modena e Reggio Emilia, Italy*
Christian Peter Klingenberg, University of Manchester, United Kingdom

13.55 - 14.25	**LEANDRO MONTEIRO** (invited) Adaptive radiations in shape space: linking evolutionary processes to macroevolutionary patterns
14.25 - 14.55	**ANJALI GOSWAMI** (invited) Does the marsupial reproductive strategy constrain facial evolution?
14.55 - 15.15	**DEAN C. ADAMS** From microevolution to macroevolution: the evolution of phenotypic diversity in *Plethodon* salamanders
15.15 - 15.45	*Coffee break*
15.45 - 16.05	**IAN DWORKIN** Can we have it all? Measuring natural selection for a model genetic trait- wing shape in *Drosophila*
16.05 - 16.25	**STEPHEN H. MONTGOMERY** Microcephaly genes and the evolution of primate brain size
16.25 - 16.45	**THOMAS H.G. EZARD** How should evolutionary biologists differentiate species in multi-dimensional morphospace?
16.45 - 17.05	**EMMA SHERRATT** Convergent evolution in highly specialised burrowing vertebrates

29-1 Oral

ADAPTIVE RADIATIONS IN SHAPE SPACE: LINKING EVOLUTIONARY PROCESSES TO MACROEVOLUTIONARY PATTERNS

Leandro Monteiro [1], *Marcelo R. Nogueira* [2]

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The study of adaptive radiations is largely based on the correlation between phenotype and ecology. Interspecific data sets within a phylogenetic framework play a crucial role in these studies, and a number of methods that incorporate the structure of phylogenetic covariance among species have been available for a while. Recent comparative approaches evaluate the performance of alternative statistical models based on evolutionary processes and hypotheses, allowing for insights into the nature of evolutionary mechanisms and scenarios behind adaptive radiations. The phyllostomid bats present the most extensive ecological and phenotypic radiation among mammal families. This group is considered an important model system for studies of cranial ecomorphology and functional optimisation because of the constraints imposed by the requirements of flight. The mandible shape of 49 phyllostomid species was associated with relative diet composition (Insectivory, Carnivory, Nectarivory, Frugivory, Sanguivory) , and the performance of statistical models representing alternative evolutionary processes (Brownian motion, Stabilising selection with varying numbers of adaptive peaks) was evaluated. The results clearly indicate a process of directional selection in the deeper branches of the phylogenetic tree, when the main dietary divergence occurred. After this initial divergence, stabilising selection (niche conservatism) maintained the phenotypic divergence stable. Modern comparative methods and the model-based approach provide important insights into the evolutionary processes behind the macroevolutionary patterns in adaptive radiations.

29-2 Oral

DOES THE MARSUPIAL REPRODUCTIVE STRATEGY CONSTRAIN FACIAL EVOLUTION?

Anjali Goswami [1], Marcelo R. Sánchez-Villagra [2], P. David Polly [3]

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[2]Universitat Zurich, Palaeontologisches Institut und Museum, Zurich, Switzerland
[3]Indiana University, Department of Geological Sciences, Bloomington, Indiana

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Marsupial and placental mammals have disparate evolutionary histories. Marsupials represent only 5% of current mammalian taxonomic diversity and occupy a much smaller range of morphological and ecological diversity than placentals. Investigations of ontogenetic and morphological diversity have suggested that forelimb evolution is constrained in marsupials by their short gestation and requisite crawl to the pouch, where most development occurs. Our analyses of adult limb covariance, sequence heterochrony, and developmental modularity show correspondence among these factors and forelimb morphological evolution in marsupials.
Marsupials also quickly develop their oral apparatus to suckle immediately after birth. We conducted 3-D morphometric analyses of variation in cranial bone shape in embryonic, adult, and fossil marsupial and placentals to test the hypothesis that the marsupial form of reproduction also constrains the morphological evolution of the marsupial face. Analyses of landmark variance from embryological specimens do not support differences between marsupials and placentals in the oral apparatus, but placentals display greater variance in orbital and neurocranial landmarks. Analyses of adult and fossil taxa demonstrate that marsupials show significantly lower cranial disparity than placentals, but disparity in the oral apparatus is not significantly different between these two clades when rarefaction analyses are used to account for differences in taxonomic diversity or when ecologically-similar clades are compared. Cranial sequence heterochrony and developmental modularity also fail to show the correspondence with adult modularity and disparity observed in the postcranium, suggesting that cranial and postcranial evolution are influenced by different factors.

29-3 Oral

FROM MICROEVOLUTION TO MACROEVOLUTION: THE EVOLUTION OF PHENOTYPIC DIVERSITY IN *PLETHODON* SALAMANDERS

Dean C. Adams [1]

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A major goal in evolutionary biology is to determine how small-scale contemporary changes (microevolution) translate into large-scale patterns of biological diversity (macroevolution). Many studies of contemporary evolution examine phenotypic evolution along ecological gradients, often revealing that selection results in divergent phenotypic evolution across localities. If such processes contribute to macroevolutionary diversification, one predicts that adaptive differences across populations would be found in clades that exhibit greater phenotypic diversity than expected. However, making an explicit, quantitative link between microevolutionary patterns and macroevolutionary trends remains a challenge. One way to bridge the microevolutionary-macroevolutionary divide is to view microevolutionary patterns in a phylogenetic context. In this talk, I utilize this approach to quantify microevolutionary and macroevolutionary patterns of head shape evolution in *Plethodon* salamanders. I describe the contemporary morphological responses to proximate ecological interactions and interspecific competition, and show that while phenotypic responses in certain lineages are location-specific, similarities in diversification patterns do exist. When viewed in a phylogenetic context however, population-level diversification appears to generate homoplasious patterns, with similar morphologies evolving recurrently across taxa through evolutionary time. Thus, while diversification via competitive interactions represents a prominent feature of microevolutionary patterns in this group, it has not resulted in the expected macroevolutionary signature of adaptive diversification among lineages.

29-4 Oral

CAN WE HAVE IT ALL? MEASURING NATURAL SELECTION FOR A MODEL GENETIC TRAIT- WING SHAPE IN *DROSOPHILA*

Ian Dworkin [1]

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Over the past decade, wing shape in *Drosophila* has become a widely used system to study the genetics of complex multivariate phenotypes, phenotypic integration, fluctuating asymmetry among other evolutionary questions. However, little is known about how natural selection shapes variation for wing shape. I will summarize some of our recent work that suggests that natural selection acts upon variation for wing shape in natural populations, and provide evidence for stabilizing selection for wing size. In addition I will integrate these studies with our ongoing work mapping genetic polymorphisms that contribute to intra and inter-specific variation for wing shape in *Drosophila*. In particular I will discuss the role of natural variation in functionally verified cis-regulatory regions that function during wing development, and how these variants contribute to phenotypic variation.

29-5 Oral

MICROCEPHALY GENES AND THE EVOLUTION OF PRIMATE BRAIN SIZE

Stephen H. Montgomery [1], Isabella Capellini [2], Chris Venditti [3], Robert A. Barton [2], Nicholas I. Mundy [1]

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One fundamental issue in evolutionary genetics is whether the convergent evolution of complex traits is due to convergence at the molecular level. Microcephaly is a congenital disorder characterised by reduced growth of the cerebral cortex. Genes associated with microcephaly (ASPM, CDK5RAP2, CENPJ & MCPH1) are key candidates for involvement in the evolutionary expansion of hominoid brains, but their role in other primate lineages is poorly understood. Here we test the hypothesis that these loci were involved in brain size evolution across primates. For each gene we sequenced key exons in at least 20 primate genera representing a range of absolute and relative brain sizes. Through a thorough analysis of ancestral state reconstruction methods we identify the most reliable estimates of ancestral brain and body sizes. We confirm that the ancestral primate was likely to have been small (<50g), with a relative brain size below that observed in extant primates. Overall there was a directional increase in brain size during primate evolution; however, decreases in absolute brain size account for 6% of evolutionary time. We use these reconstructions to test for associations between absolute and relative adult brain, neocortex and neonatal brain size, and the rates of evolution of microcephaly genes. All four loci have experienced positive selection across primates. We find significant, phylogenetically corrected, correlations between the rate of evolution (dN/dS) and absolute neonatal brain size for ASPM and CDK5RAP2, but not CENPJ and MCPH1. These results strongly suggest ASPM and CDK5RAP2 are involved in the evolution of neurogenesis across primates.

29-6 Oral

HOW SHOULD EVOLUTIONARY BIOLOGISTS DIFFERENTIATE SPECIES IN MULTI-DIMENSIONAL MORPHOSPACE?

Thomas H.G. Ezard [1], Andy Purvis [1], Paul N. Pearson [2]

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[2]*University of Cardiff, Department of Earth Sciences, Cardiff, United Kingdom*

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Since the 1950s, taxonomists have speculated on the development of the planktonic foraminiferan genus *Turborotalia*. *Turborotalia* originated around 47 million years ago with relatively globular forms, metamorphosed and ended keeled and compressed, with speciation and extinction events also postulated. Whilst DNA barcoding has provoked rapid development of genetic clustering techniques, algorithmic developments for morphological traits have been hampered by theoretical limitations. Here, we refine novel clustering techniques in a hypothesis-driven approach that generates statistics describing sample homogeneity and employ it to resolve the arguments on *Turborotalia*'s evolutionary history. Using 12 morphometric traits on 200 individuals at each of 51 time intervals over ~13 million years, each sample was delimited statistically. On a macro-evolutionary scale, inferred species were statistically well-separated in four intervals. On a micro-evolutionary scale, a homogeneous sample tends to become more disparate in the subsequent interval, and vice versa, but there appeared no gradual increase in heterogeneity prior to speciation. The unified methodology elucidates patterns in evolutionary change that might otherwise remain cryptic.

29-7 Oral

CONVERGENT EVOLUTION IN HIGHLY SPECIALISED BURROWING VERTEBRATES

Emma Sherratt [1,2]

[1]*The University of Manchester, Faculty of Life Sciences, Manchester, United Kingdom*
[2]*The Natural History Museum, Zoology Department, London, United Kingdom*

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Caecilians are the only completely limbless amphibians, and occur on all the continents with tropical zones, except Australasia. Some species live in soil where the head play an important role in burrowing, although the degree to which each species leads a dedicated soil-dwelling existence varies. Caecilian skulls are characteristically heavily ossified, and in some species the orbit is closed by variations on surrounding bone configurations. This apomorphic character, known as ‘eye-under-bone’, is shown to be homoplastic when mapped onto molecular phylogenies. Consequently we expect the skull to retain considerable information about ecological-niche separation, but less on phylogenetic relatedness. The aim is to determine whether the caecilian skull shape is constrained by function, so that independently acquired traits for burrowing adaptation converge along parallel lineages in a phylogenetic tree. The overall skull shape in dedicated ‘eye-under-bone’ burrowers is hypothesised to be more similar among ecological analogues than between dedicated burrowers and their closest cryptic ‘open-orbit’ relatives. To test this, cranionmandibular shape was examined of three pairs of genera of caecilians from the family Caecilidae from South America, Sub-Saharan Africa, India and the Seychelles. In addition, a selection of unpaired species from both categories was included to represent the variation in each group. The skulls were visualised using Micro-Computed Tomography, bone segmented with threshold algorithms and shape measured using geometric morphometric techniques, specifically 3D landmarks. Multivariate ordination analyses were used to examine relative shape similarity among species and between ecological groups, and the findings were interpreted within a functional and evolutionary framework.

29-1 Poster **On the Origin of Phenotypic Differences between Species: What's Selection got to do with it?**

MELANIE J. MONROE, FOLMER BOKMA

Umeå University, Department of Ecology and Environmental Science, Umeå, Sweden

29-2 Poster **Cryptic species in Western and Central Africa cichlids**

ANDRÉ GILLES[1], CHARLES F. BILONG BILONG[2], CAROLINE COSTEDOAT[1], KATHRYN ELMER[3], AXEL MEYER[3], SERGE MORAND[4], ARNOLD NYOM BITJA[2], ANTOINE PARISELLE[4,5], NICOLAS PECH[1]

[1]*UMR CNRS 6116 IMEP, Université de Provence, Département de Persistance et Evolution de la Biodiversité, Marseille, France*
[2]*Université de Yaoundé, Département de Biologie et Physiologie Animale, Yaoundé, Cameroun*
[3]*Lehrstuhl für Zoologie und Evolutions biologie, Department of Biology, Konstanz, Germany*
[4]*Université de Montpellier, Institut des Sciences de l'Evolution, Montpellier, France*
[5]*IRD, Laboratoire d'Écologie et de Systématique, Dakar, Sénégal*

29-3 Poster **Cryptic species in Western and Central Africa cichlids**

CAROLINE COSTEDOAT[1], CHARLES F. BILONG BILONG[2], KATHRYN ELMER[3], ANDRÉ GILLES[1], AXEL MEYER[3], SERGE MORAND[4], ARNOLD NYOM BITJA[2], ANTOINE PARISELLE[5,4], NICOLAS PECH[1]

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[5]*IRD, Laboratoire d'Écologie et de Systématique, Dakar, Sénégal*

29-4 Poster **Independent size and shape divergence in an *Onthophagus* species-complex (Coleoptera: Scarabaeidae)**

ANNA L. M. MACAGNO, ASTRID PIZZO, ANTONIO ROLANDO, CLAUDIA PALESTRINI

Università degli Studi di Torino, Dipartimento di Biologia Animale e dell'Uomo, Torino, Italy

29-5 Poster **External trait constancy vs. internal trait divergence in dung beetles: a case study in the genus *Amidorus* (Coleoptera, Aphodiidae, Aphodiinae)**

ANGELA ROGGERO, ANTONIO ROLANDO, CLAUDIA PALESTRINI, CLAUDIA TOCCO

Università degli Studi di Torino, Dipartimento di Biologia Animale e dell'Uomo, Torino, Italy

29-6 Poster **Detecting biological distinctiveness using geometric morphometrics: an example case from the Vancouver Island marmot**

ANDREA CARDINI[1], DAVID NAGORSEN[2], PAUL O'HIGGINS[3], P. DAVID POLLY[4], RICHARD W.JR. THORINGTON[5], PAOLO TONGIORGI[1]

[1]*University of Modena & Reggio, Departmrnt of Museums, Modena, Italia*
[2]*University of British Columbia, Vancouver and Mammalia Biological Consulting, Vertebrate Museum, Vancouver, Canada*
[3]*University of York, Hull York Medical School, York, United Kingdom*
[4]*Indiana University, Department of Geological Sciences, Bloomington, United States*
[5]*National Museum of Natural History, Smithsonian Institution, Department of Vertebrate Zoology, Washington, United States*

29-7 Poster **Satb2 as a modulator of craniofacial development and evolution**

JENNIFER L. FISH, MICHAEL J. DEPEW

King's College London, Department of Craniofacial Development, London, United Kingdom

29-8 Poster **Evolution of modularity by directional selection and epistasis**

MIHAELA PAVLICEV[1,3], GUNTER P. WAGNER[2], JAMES M. CHEVERUD[3]
[1]*University of Oslo, Department of Biology CEES, Oslo, Norway*
[2]*Washington University, Department of Anatomy and Neurobiology, St. Louis, United States*
[3]*Yale University, Department of Ecology and Evolutionary Biology, New Haven , United States*

29-9 Poster **A developmental perspective on the evolution of phenotypic covariance structures: studying the space of covariance matrices**

PHILIPP MITTEROECKER
University of Vienna, Department of Theoretical Biology, Vienna, Austria

29-10 Poster **Through the hourglass: integrating quantitative genetics and phylogenomics approaches to untangle the evolution of a modular developmental pattern**

AMIR YASSIN[1,2], LUCIANA O. ARARIPE[2,3], KURT E. LINNEAU[1], APURVA NARECHANIA[1], JEAN R. DAVID[2], ROB DESALLE[1]
[1]*American Museum of Natural History, Sackler Institute for Comparative Genomics, Division of Invertebrate Zoology, New York, United States*
[2]*Centre National de la Recherche Scientifique, Laboratoire d' Evolution, Genomes et Speciation, Gif-sur-Yvette, France*
[3]*Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, United States*

29-11 Poster **Evolution of sensory organ morphology in *Drosophila***

CORINNA HOPFEN, MARLIES DOLEZAL, PABLO OROZCO-TERWENGEL, CHRISTIAN SCHLÖTTERER, ALISTAIR P. McGREGOR
Veterinärmedizinische Universität Wien, Institut für Populationsgenetik, Vienna, Austria

29-12 Poster **The genetic architecture of the wing shape in *Drosophila*: insights from selection-response time-series**

ARNAUD LE ROUZIC[1], DAVID HOULE[2], THOMAS F. HANSEN[1]
[1]*University of Oslo, Center for Ecology and Evolutionary Synthesis, Oslo, Norway*
[2]*Florida State University, Department of Biological Science, Tallahassee, United States*

29-13 Poster **Sexual selection and the evolution of wing shape**

NELLY A. GIDASZEWSKI[1], LEONARDO D. BACIGALUPE[2], MIKE G. RITCHIE[3], ALLEN J. MOORE[4], RHONDA R. SNOOK[1]
[1]*University of Sheffield, Department of Animal and Plant Sciences, Sheffield, United Kingdom*
[2]*Universidad de Concepcion, Departamento de Zoologia, Concepcion, Chile*
[3]*University of St Andrews, School of Biology, St Andrews, United Kingdom*
[4]*University of Exeter, Centre for Ecology and Conservation, Penryn, United Kingdom*

29-14 Poster **No need for sexual selection - fluctuating asymmetry and fitness in parthenogenetic honeybee workers**

H. MICHAEL G. LATTORFF, ROBIN F.A. MORITZ
MLU Halle-Wittenberg, Institute of Biology, Mol. Ökol, Halle, Germany

29-15 Poster **The allometric pattern of sexually dimorphic feather ornaments and factors affecting allometry**

JOSE J. CUERVO[1], ANDERS P. MOLLER[2]
[1]*Consejo Superior de Investigaciones Cientificas, Estacion Experimental de Zonas Aridas, Almeria, Spain*
[2]*CNRS Universite Paris-Sud, Laboratoire d' Ecologie, Systematique et Evolution, Orsay, France*

Hybrid speciation

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Program

Saturday August 29 - **Symposium 30**

Location: Room 4

Hybrid speciation

Organizers: *Diethard Tautz, Max-Planck Institute for Evolutionary Biology, Ploen, Germany*
James Mallet, University College London, London, United Kingdom

13.55 - 14.25	**LOREN RIESEBERG** (invited) The role of hybridization in evolution
14.25 - 14.55	**CHRIS C. NICE** (invited) Hybrid Speciation on Mountain Tops: Replicated Cases of Hybridization in Blue Butterflies
14.55 - 15.15	**ADRIAN C. BRENNAN** Hybrid speciation in *Senecio* (Asteraceae): why *Senecio squalidus* is more than just a hybrid
15.15 - 15.45	*Coffee break*
15.45 - 16.05	**CHRIS D. JIGGINS** Genetic evidence for Hybrid Trait Speciation in *Heliconius* butterflies
16.05 - 16.25	**STEIN A. SÆTHER** Speciation and sex-linked genomic islands of divergence in a flycatcher radiation
16.25 - 16.45	**KATHRYN STEMSHORN** Invasive *Cottus* in the River Rhine system and the Ijsselsea: emerging hybrid lineages?
16.45 - 17.05	**NICK H. BARTON** The consequences of rare hybridisation between red and sika deer

30-1 Oral

THE ROLE OF HYBRIDIZATION IN EVOLUTION

Loren Rieseberg [1], Michael Barker [2]

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The role of hybridization in evolution has been subject of intense discussion and speculation for more than a century. At one extreme, hybridization is considered to be a potent evolutionary force that contributes to adaptive evolution and speciation. In this view, the new gene combinations generated by hybridization promote the development and acquisition of novel adaptations. Others, in contrast, accord little evolutionary significance to hybridization, viewing it as a primarily local phenomenon with only transient effects. Unfortunately, definitive support for either viewpoint is lacking.

We will describe a new method for identifying recent and ancient hybrids from the analysis of a single genome, as well as several surprising discoveries resulting from the application of this approach to a diverse array of plant and animal species. We will show that hybridization is more frequent than previously believed, particularly in invasive species, and that > 13% of speciation events in flowering plants involve hybridization and genome duplication (allopolyploidy). We will explore the roles of recent and ancient hybridization and polyploidy on diversification rates in plants. Lastly, we will review case studies from our lab and others, which illustrate how new hybrid gene combinations have facilitated adaptation and speciation in nature.

30-2 Oral

HYBRID SPECIATION ON MOUNTAIN TOPS: REPLICATED CASES OF HYBRIDIZATION IN BLUE BUTTERFLIES

Chris C. Nice [1], James A. Fordyce [2], Zachariah Gompert [3], Matthew L. Forister [4]

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[2]University of Tennessee at Knoxville, Department of Ecology and Evolutionary Biology, Knoxville, United States
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The role of hybridization as an important mechanism for generating evolutionary novelty and facilitating the emergence of ecologically and evolutionarily distinct lineages has a history of neglect, particularly among zoologists. Recent evidence, however, suggests that the importance of hybridization in animal evolution has been prematurely dismissed. Here, we examine replicated cases of hybridization in a butterfly model system where potentially new species of hybrid origin have arisen. We combine manipulative field experiments with genomic-level molecular genetic data to test the hypothesis of hybrid speciation and address fundamental questions about the process of speciation in replicated putative hybrid species in four western North American mountain ranges. Specifically, we pose these questions: 1) Do independent hybrid events between the same two species result in different outcomes under different ecological settings? 2) How do hybrid traits contribute to reproductive isolation? 3) Do novel, adaptive traits arise directly from hybridization? The answers to these questions will generate novel insights into the processes that create and maintain geographic variation within and between species and characterize the extent to which gene exchange via hybridization contributes to the creation of new species.

30-3 Oral

HYBRID SPECIATION IN *SENECIO* (ASTERACEAE): WHY *SENECIO SQUALIDUS* IS MORE THAN JUST A HYBRID

Adrian C. Brennan [1], Daniel Barker [1], Simon J. Hiscock [2], Richard J. Abbott [1]

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The number of confirmed homoploid hybrid species remains relatively small despite the growing perceived importance of hybridization as a force for speciation. Often, the taxonomic status of these hybrid species remains debatable unless convincing genetic or ecological differentiation from both parent species can be demonstrated. *Senecio squalidus*, an invasive species in the UK since its introduction about 300 years ago, has long been proposed to be a homoploid hybrid species between the high and low altitude species, *S. aethnensis* and *S. chrysanthemifolius* respectively, from Mt. Etna, Sicily based on historical records. The source of *S. squalidus* introduced into Oxford Botanic Garden was likely to have been wild hybrids that are still abundant on Mt. Etna today. Recent morphological and genetical studies supported the hypothesis that *S. squalidus* is of hybrid origin by demonstrating that *S. squalidus* exhibits intermediate traits between its proposed parent species and marker alleles diagnostic of both parent species on Mt. Etna. These studies confirm the parentage and hybrid origin status of *S. squalidus*. Here, we present a comprehensive investigation of additional phenotypic traits and newly developed genetic markers that demonstrate that *S. squalidus* is fundamentally distinct from both parent species and from hybrids on Mt. Etna. Thus, the hypothesis that *S. squalidus* is a true example of hybrid speciation and not just another hybrid is supported.

30-4 Oral

GENETIC EVIDENCE FOR HYBRID TRAIT SPECIATION IN *HELICONIUS* BUTTERFLIES

Camilo Salazar [1,2], Simon Baxter [2], Carolina Pardo-Diaz [1], Mauricio Linares [3], Eldredge Bermingham [1], Chris D. Jiggins [2]

[1]*Smithsonian Tropical Research Institute, Panama, Panama*
[2]*University of Cambridge, Department of Zoology, Cambridge, United Kingdom*
[3]*Universidad de Los Andes, Ciencias Bilologicas, Bogota, Colombia*

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Homoploid hybrid speciation generates species without a change in chromosome number via introgressive hybridization. Recently, two alternatively routes by which this might occur have been discussed. *Heliconius* butterflies exhibit aposematic colour patterns that also act as cues in assortative mating. In this genus, *Heliconius heurippa,* has been proposed as a hybrid species and its colour pattern can be recreated by introgression of the *H. melpomene* red band into an *H. cydno* genetic background. This hybrid colour pattern is also involved in mate choice and leads reproductive isolation between *H. heurippa* and its close relatives. Here, we provide striking molecular evidence for adaptive introgression. The 670 SNPs distributed among 29 random coding genes (25,847bp) show *H. heurippa* related with *H. cydno* or the three species intermixed. In contrast, among 344 SNPs distributed among 14 genes in the red band region (18,629bp), 42 show *H. heurippa* related with *H. cydno* but a block of around 6000 bp located in the 3' of a putative kinesin gene groups *H. heurippa* with *H. melpomene*. This lies outside the distribution of likelihood values for species relationships derived from unlinked genes. The genealogy shows *H. melpomene* and *H. cydno* forming different clades with *H. heurippa* monophyletic inside *H. melpomene*. The kinesin gene shows the predicted pattern for adaptive introgression and is therefore the first clear candidate for a *Heliconius* wing patterning locus. The data provide the first molecular support for our model of 'Hybrid Trait Speciation' whereby adaptive traits evolve through hybridisation and lead to speciation.

30-5 Oral

SPECIATION AND SEX-LINKED GENOMIC ISLANDS OF DIVERGENCE IN A FLYCATCHER RADIATION

Stein A. Sæther [1], Silje Hogner [1], Thomas Borge [1], Torbjørn Bruvik [1], Glenn-Peter Sætre [1]

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The sex chromosomes have been suggested to play a key role in speciation by contributing disproportionally to the build-up of reproductive isolation between populations. This is because they may often contain genes that are involved in behavioural premating barriers and/or intrinsic postmating barriers to gene flow. Here we show that four *Ficedula* flycatcher species that separated from their common ancestor about 1.5 mya have diverged genetically much more on the Z-chromosome than on the autosomes. In all species-pairs comparisons, Z-linked genes had fewer shared polymorphisms and more fixed substitutions than autosomal genes. This pattern was irrespective of differences in the effect of drift (effective population size z:autosomes = 0.75) and mutation rate (estimated from out-group comparisons) between the Z-chromosome and autosomes, pointing to a role for selection in causing the observed heterogenic divergence. Since the Z contains genes that cause reproductive isolation in these birds (species-assortative mating as well as postzygotic incompatibilities) these results suggests that only some parts of the genome have "speciated" due to selection and the rest of the genome has hitchhiked along. In addition, contemporary hybridization in one of the involved species-pairs leads to autosomal but not sex-linked gene flow which suggest that differential gene flow during speciation may have increased the observed heterogeneity in divergence. If so, past episodes of selection against hybridization may have contributed to divergence even among currently allopatric species.

30-6 Oral

INVASIVE *COTTUS* IN THE RIVER RHINE SYSTEM AND THE IJSSELSEA: EMERGING HYBRID LINEAGES?

Kathryn Stemshorn [1], Arn W. Nolte [1], Diethard Tautz [1], Floyd Reed [1]

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The formation of new species is a possible outcome of hybridization and models have been put forward to explain this. Yet, the early steps of such a process remain to be documented. In the case of *Cottus*, contact between *C. perifretum* found in the Schelde system and *C. rhenanus* found in the Lower River Rhine became possible about 200 years ago, when these river systems were connected by man-made channels. Today, hybrid populations referred to as invasive sculpins are expanding into habitats that were not colonized by the parental species before, leading to the hypothesis that hybridization was instrumental in the recent colonization and range expansion. We analyzed 16 hybrid populations for 81 ancestry-informative SNP markers to explore the population structure and genomic ancestry of invasive sculpins to detect if hybridism could have promoted fitness. The populations can be grouped into three main clusters. One of these contains geographically very distant populations indicating that cohesion exists among hybrid populations suggesting, that emerging hybrid clusters begin to differentiate. We have applied Kimura's diffusion equation to study the assembly of hybrid gene pools and find that the distribution of allele frequencies in the emerging hybrid lineages can be largely explained by a mixed model including drift and migration. Some loci with signs of selective fixation of alleles from both parental species could be detected in this first screen.

30-7 Oral

THE CONSEQUENCES OF RARE HYBRIDISATION BETWEEN RED AND SIKA DEER

Nick H. Barton [1], Helen Senn [2], Josephine Pemberton [2]

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Sika deer (*Cervus nippon*) were introduced into Scotland about a century ago, and have since spread widely, so that they overlap at least 40% of the range of the native red deer (*Cervus elaphus*). We have recently sampled and analysed a transect in Kintyre, W. Scotland, where the two species overlap, for the third time in 15 years. Microsatellite markers show that although hybridisation is rare, there has been a variable amount of introgression among sampling sites. Introgression also varies from locus to locus, but rather than reflecting selection, this variation is likely to be the random consequence of a small number of F1 hybrids. Red deer carry diverse alleles, and so the number of F1s that backcrossed into sika can be identified. The genetic contribution of any one F1 hybrid has a highly variable distribution, which depends primarily on the number of its descendants in the first few generations (i.e., its reproductive value). This inherent randomness of backcross events reduces the effectiveness of selection, and makes the outcome of hybridisation highly uncertain.

30-1 Poster **Divergence in the face of gene flow: the case of two newts (Amphibia: Salamandridae)**

KRYSTYNA NADACHOWSKA[1], WIESLAW BABIK[2,3]
[1]*Jagiellonian University, Institute of Environmental Sciences, Krakow, Poland*
[2]*Polish Academy of Sciences, Institute of Systematics and Evolution of Animals, Krakow, Poland*
[3]*Helmholtz Centre for Environmental Research, UFZ - Halle, Germany*

30-2 Poster **Local adaptation and adaptive divergence in the recent homoploid hybrid *Senecio squalidus* L. following introduction and range expansion**

REBECCA I.C. ROSS
Oxford University, Department of Plant Sciences, Oxford, United Kingdom

30-3 Poster **Unexpected relics of goat *(Capra hircus)* mitochondrial DNA in the sheep *(Ovis aries)* genome**

MARCO PELLECCHIA[1], MARCIN RZEPUS[2], FRANCESCA SIBELLA[1], FABRIZIO GHISELLI[3], MARCO PASSAMONTI[3], HOVIRAG LANCIONI[4], ALESSANDRO ACHILLI[4], RICCARDO NEGRINI[1], PAOLO AJMONE-MARSAN[1]
[1]*Università Cattolica del Sacro Cuore, Istituto di Zootecnica, Piacenza, Italia*
[2]*University of Silesia, Department of Biology and Environmental Protection, Katowice, Poland*
[3]*Università di Bologna, Dipartimento di Biologia Evoluzionistica Sperimentale, Bologna, Italia*
[4]*Università di Perugina, Dipartimento di Biologia Cellulare e Ambientale, Perugia, Italia*

30-4 Poster **Introgression of the X chromosome across a mouse hybrid zone: a comparison of two distinct transects**

PETRA DUFKOVA[1,3], JAROSLAV PIALEK[1], MILOS MACHOLAN[2],
[1]*Institute of Vertebrate Biology ASCR, Department of Population Biology, Studenec, Czech Republic*
[2]*Institute of Animal Physiology and Genetics, Laboratory of Mammalian Evolutionary Genetics, Brno, Czech Republic*
[2]*University of South Bohemia, Ceske Budejovice, Czech Republic*

30-5 Poster **Karyotypes and genotypes of backcrossed offspring indicated possibility of hemiclonal reproduction called hybridogenesis in the three species of *Hexagrammos* greenlings**

MOTOKO R. KIMURA[1], HIROYUKI MUNEHARA[2], ARAI KATSUTOSHI[1], MASAKADO KAWATA[3], SYUITI ABE[4]
[1]*Hokkaido University, Graduate School of Environmental Science, Hakodate, Japan*
[2]*Hokkaido University, Field Science Center for Northern Biosphere, Hakodate, Japan*
[3]*Tohoku University, Graduate School of Life Sciences, Sendai, Japan*
[4]*Hokkaido University, Graduate School of Fisheries Sciences, Hakodate, Japan*

30-6 Poster **Microsatellite and single nucleotide polymorphism markers for quantitative trait loci mapping of wild house mice**

AGATA KAWALKO[1], JAN M. WOJCIK[1], JAROSLAV PIALEK[2], PETRA DUFKOVA[2]
[1]*Polish Academy of Science, Mammal Research Institute, Bialowieza, Poland*
[2]*Academy of Sciences of the Czech Republic, Department of Population Biology, Institute of Vertebrate Biology, Studenec, Czech Republic*

30-7 Poster **Recent speciation in the locally endemic allopolyploid peat moss *Sphagnum troendelagicum***

HANS K. STENOIEN[1], A. JONATHAN SHAW[2], KIRSTI STENGRUNDET[1], KJELL I. FLATBERG[1]
[1]*Norwegian University of Science and Technology, Museum of Natural History and Archaeology, Section of Natural History, Trondheim, Norway*
[2]*Duke University, Biology Department, Durham, United States*

30-8 Poster **Hybridization and sympatric speciation between two oak species**

PIERRE ABADIE, GUY ROUSSEL, ANTOINE KREMER, PAULINE GARNIER-GÉRÉ
INRA Bordeaux, UMR 1202 BIOGECO, Cestas, France

30-9 Poster **Autotetraploidy associated with reproductive isolation in domesticated *Saccharomyces cerevisiae***

WARREN ALBERTIN[1,4], AURÉLIE BOURGAIS[1], CHRISTINE DILLMANN[1], DELPHINE SICARD[1], DOMINIQUE DE VIENNE[1], MARINA BELY[2], MICHEL AIGLE[3], PHILLIPE MARULLO[4]
[1]Université Paris Sud, UMR 0320 / UMR 8120, Gif-sur-Yvette, France
[2]Université de Bordeaux, UMR 1219 - ISW, Villenave, France
[3]Université Lyon 1, UMR 5240 Microbiologie Adaptation et Pathogénie, Villeurbanne, France
[4]Faculté d'oenologi, UMR 1219 - ISW, Villenave d'Ornon, France

30-10 Poster **Low rate of hybridization between *Lissotriton helveticus* and *Lissotriton vulgaris* despite semi-permeable pre-zygotic barriers**

AURÉLIE JOHANET[1], CHRISTOPHE LEMAIRE[2], JEAN SECONDI[1]
[1]University of Angers, Laboratory Landscape and Biodiversity, Angers, France
[2]INRA, UMR Pavé, Angers, France

30-11 Poster **Differential response to stress in reciprocal hybrids and within-species crosses of *Silene dioica* and S. *latifolia***

ADRIEN FAVRE, MARIANNE DIEBOLD, SOPHIE KARRENBERG
ETH Zurich, Institute of Integrative Biology, Zurich, Switzerland

30-12 Poster **Chromosomal rearrangements and genetic differentiation among dioecious *Silene* species**

MASSIMILIANO GNESOTTO, NICOLAS BLAVET, MARIA-DOMENICA MOCCIA, ALEX WIDMER
ETH Zurich, Institute of Integrative Biology, Zurich, Switzerland

30-13 Poster **Some regular cytogenetical and genetical trends in evolution of unisexual lizards and some clonal vertebrate animals**

LARISSA KUPRIYANOVA
Zoological Institute of Russian Academy of Sciences, Department of Herpetology, St.Petersburg, Russia

30-14 Poster **The multiple reproductive strategies and speciation mechanisms of the unusual stick insect genus *Clonopsis* (Insecta Phasmida)**

LILIANA MILANI[1], FABRIZIO GHISELLI[1], MARCO PELLECCHIA[2], VALERIO SCALI[1], MARCO PASSAMONTI[1]
[1]Università di Bologna, Dipartimento di Biologia Evoluzionistica Sperimentale, Bologna, Italy
[2]Università Cattolica del Sacro Cuore, Laboratorio di Genetica Animale, Piacenza, Italy

30-15 Poster **Hybridization causes stable differences between male and female genomes in an ant**

JONNA KULMUNI[1],BERNHARD SEIFERT[2], PEKKA PAMILO[3]
[1]University of Oulu, Oulu, Finland
[2]State Museum of Natural History, Germany
[3]University of Helsinki, Helsinki, Finland

30-16 Poster **Molecular genetics of four morphological species of *Anacronueria* genues (Plecoptera: Perlidae) in sympatric speciation. Its implications taxonomical, phylogenetical, speciation**

MARIBET GAMBOA, JAZZMIN C. ARRIVILLAGA
Universidad Simon Bolivar, Estudios Ambientales, Caracas, Venezuela

30-17 Poster **Genetic distance between species predicts phenotypic novelty in their hybrids**

RIKE B. STELKENS[1,2,3], OLE SEEHAUSEN[2,3], CORINNE SCHMID[2,3]
[1]University of Lausanne, Department of Ecology and Evolution, Lausanne, Switzerland
[2]University of Bern, Institute of Ecology and Evolution, Bern, Switzerland
[3]Eawag Swiss Federal Institute of Aquatic Science and Technology, Departement of Fish Ecology and Evolution, Kastanienbaum, Switzerland

30-18 Poster **Potential exchange of adaptive traits between tetraploid species adapted to different flooding microhabitats**

MARC STIFT[1], CAMILLO BERENOS[2], PETER KUPERUS[3], PETER H. VAN TIENDEREN[3], PIETERNELLA C. LUTTIKHUIZEN[4]
[1]University of Glasgow, Division of Ecology and Evolutionary Biology, Glasgow, United Kingdom
[2]ETH Institutet for Integrative Biology, Zürich, Switzerland
[3]University of Amsterdam, Institute for Biodiversity and Ecosystem Dynamics, Amsterdam, Netherlands
[4]Royal Netherlands Institute for Sea Research Marine Ecology, Den Burg, Netherlands

30-19 Poster **Why to avoid producing hybrid daughters: Haldane's rule and fitness consequences of hybridization between two large gull species**

GRZEGORZ NEUBAUER[1], M. MAGDALENA ZAGALSKA-NEUBAUER[1,2], PIOTR NOWICKI[2]
[1]Polish Academy of Sciences, Ornithological Station, Museum and Institute of Zoology, Warszawa, Poland
[2]Jagiellonian University, Institute of Environmental Sciences, Kraków, Poland

30-20 Poster **Adaptation to Anthropogenic Change in Hybridizing *Daphnia*: Evidence from Resting Egg Banks**

PIET SPAAK[1,3], NORA BREDE[2], CHRISTIAN RELLSTAB[1]
[1]Eawag, Department of Aquatic Ecology, Duebendorf, Switzerland
[2]Goethe-University, Department of Ecology and Evolution, Frankfurt am Main, Germany
[3]ETH Zurich, Institute of Integrative Biology, Zurich, Switzerland

30-21 Poster **Hybrid speciation in a fungal pathogen: ecological and evolutionary determinants of hybrid formation and persistence**

AMANDA K. GIBSON[1,2], TATIANA GIRAUD[1], MICHAEL E. HOOD[2]
[1]Université de Paris-Sud XI, Laboratoire Ecologie, Systématique et Evolution, Orsay, France
[2]Amherst College, Department of Biology, Amherst, United States

30-22 Poster **Phylogeny of baboons in Southern Africa**

CHRISTINA KELLER, CHRISTIAN ROOS, JULIA FISCHER, DIETMAR ZINNER
German Primate Center, Department of Cognitive Ethology, Goettingen, Germany

30-23 Poster **Is the Italian Sparrow a result of hybrid speciation?**

JO S. HERMANSEN, STEIN A. SÆTHER, THOMAS BORGE, ELIN HJELLE, TORE O. ELGVIN, GLENN-PETER SÆTRE
University of Oslo, Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Oslo, Norway

30-24 Poster **Assortative mating and spatial structure in hybrid zones**

LEITHEN K. M'GONIGLE, RICHARD G. FITZJOHN
University of British Columbia, Department of Zoology, Vancouver, Canada

30-25 Poster **Collapse of ecological speciation through hybridization: the breakdown of sexual isolation in a threespine stickleback species pair (*Gasterosteus* spp.)**

ALYCIA R. LACKEY[1], JANETTE W. BOUGHMAN[2]
[1]University of Wisconsin at Madison, Department of Zoology, Madison, United States
[2]Center for Rapid Evolution, Madison, United States

30-26 Poster **Gain and loss of the "sword", a sexually selected trait in swordtail fishes (genus *Xiphophorus*)**

JI HYOUN KANG[1], MANFRED SCHARTL[2], AXEL MEYER[1]
[1]University of Konstanz, Department of Evolutionary Biology, Konstanz Research School of Chemical Biology, Konstanz, Germany
[2]University of Würzburg, Physiological Chemistry I, Biozentrum, Würzburg, Germany

30-27 Poster **Genomic processes underlying adaptive evolution of *Microbotryum* hybrid parasites to novel hosts**

ELSA PETIT, DANIEL PETERSON, MICHAEL E. HOOD
Amherst College, Biology Department, Amherst, United States

30-28 Poster **Spatial genetic structure in the hybrid zone between chromosomally distinct races of the common shrew *Sorex araneus* in Poland**

MIROSLAW RATKIEWICZ[1,3], AGATA BANASZEK[2], KATARZYNA JADWISZCZAK[2], WLODZIMIERZ CHETNICKI[2], STANISLAW FEDYK[2]
[1]University of Bialystok, Department of Vertebrate Zoology, Institute of Biology, Bialystok, Poland
[2]University of Bialystok, Institute of Biology, Bialystok, Poland
[3]Università degli Studi di Torino, Torino, Italy

30-29 Poster **Diversification of Eurasian shads: how much introgression?**

RUI FARIA[1,6], CEMAL TURAN[2], EKATERINA VASIL´EVA[3], GRACIELA SOTELO[4,7], LEONID FEDORENKO[5], PAULO ALEXANDRINO[1,8], SERGEY MEZHZHERIN[5]
[1]CIBIO University of Porto, Research Center in Biodiversity and Genetic Resources, Vairao, Portugal
[2]Mustafa Kemal University, Faculty of Fisheries, Hatay, Turkey
[3]Moscow State University, Department of Biology, Moscow, Russia
[4]Facultade de Bioloxía de Vigo, Departamento de Bioquímica, Xenética e Inmunoloxía, Vigo, Spain
[5]National Academy of Sciences, Schmalhausen Institute of Zoolog, Kiev, Ukraine
[6]University Pompeu Fabra, IBE, Institute of Evolutionary Biology, (UPF-CSIC), Barcelona, Spain
[7]University Pompeu Fabra, Bioevo, Barcelona, Spain
[8]Universidade do Porto, Facultade de Ciencias, Porto, Portugal

30-30 Poster **Alternative mating tactics and conspecific sperm precedence in unidirectionally hybridising sunfish**

SIMONE IMMLER[1], MATTHEW B. HAMILTON[2], NATHAN J. POSLUSNY[2], JOHN M. EPIFANIO[3]
[1]University of Uppsala, Department of Animal Ecology, Uppsala, Sweden
[2]Georgetown University, Washington DC, United States
[3]University of Illinois, Champaign, United States

The evolution of development across the species boundary

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12th Congress
Turin 2009

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Program

Saturday August 29 - **Symposium 31**

Location: Room 5

The evolution of development across the species boundary

Organizers: *Giuseppe Fusco, Università di Padova, Italy*
Alessandro Minelli, Università di Padova, Italy

13.55 - 14.25	**ARTYOM KOPP** (invited) Origin and evolution of a novel trait: from evo-devo to quantitative developmental genomics
14.25 - 14.55	**BARBARA GRAVENDEEL** (invited) The Role of Gene Duplication and Subfunctionalization in Orchid Evolution
14.55 - 15.15	**ALEKSANDAR POPADIC** Molecular mechanisms governing the establishment of species-specific morphologies – emerging views
15.15 - 15.45	*Coffee break*
15.45 - 16.05	**SIMONE KIENLE** Natural variation of vulva induction among wild *Pristionchus pacificus* isolates
16.05 - 16.25	**RUSSELL BONDURIANSKY** The evolutionary ecology of reaction norms: inter-specific variation in developmental plasticity in the Australian stilt-legged flies (Neriidae: *Telostylinus*)
16.25 - 16.45	**SABRINA RENAUD** Mandible shape in hybrid mice
16.45 - 17.05	**ALESSANDRO MINELLI** Segmentation and speciation

31-1 Oral

ORIGIN AND EVOLUTION OF A NOVEL TRAIT: FROM EVO-DEVO TO QUANTITATIVE DEVELOPMENTAL GENOMICS

Artyom Kopp [1], Kohtaro Tanaka [1], Olga Barmina [1], Chen-Siang Ng [1]

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The sex comb of *Drosophila* is an excellent model for reconstructing the genetic and molecular mechanisms responsible for the origin and diversification of new morphological traits. This male-specific array of modified bristles evolved recently in one *Drosophila* lineage, and shows dramatic diversity within that lineage. Sex comb evolution is associated with the origin of novel and previously undocumented interactions between HOX and sex determination genes. Activity of the sex determination pathway was brought under the control of the HOX code to become segment-specific, while HOX gene expression became sexually dimorphic. At the same time, both HOX and sex determination genes were integrated into the intrasegmental spatial patterning network, and acquired new joint downstream targets. Together, these changes reflect the assembly of a novel sex-specific developmental pathway under sexual selection. Similar sex comb morphologies evolved independently in multiple *Drosophila* species. Convergent evolution at the phenotypic level reflects convergent changes in the expression of HOX and sex determination genes, involving both independent gains and losses of regulatory interactions. However, the downstream cell differentiation programs have diverged between species, and in some evolutionary lineages similar adult morphologies are produced by completely different morphogenetic mechanisms. Sex combs often change on microevolutionary timescales, and can differ spectacularly between sibling species and show large quantitative variation within species. To understand the genetic and cell-biological basis of these microevolutionary changes, we have combined quantitative-genetic analysis with microarray profiling of sex- and segment-specific gene expression. Our results suggest that quantitative changes in the expression of multiple genes can produce qualitatively novel morphological phenotypes.

31-2 Oral

THE ROLE OF GENE DUPLICATION AND SUBFUNCTIONALIZATION IN ORCHID EVOLUTION

Barbara Gravendeel [1]

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How fundamental novel body plans originate during evolution is still controversial. The Modern Synthesis theory explains how gradual processes by natural selection can be responsible for evolution. Homeotic mutants, however, that are able to establish stable populations in a natural environment, so-called “hopeful monsters”, prove that a saltational mode of character change is a potential alternative mechanism for speciation. Homeosis is a result of changes in developmental genes. Homeotic orchid mutants were investigated in which different perianth whorls changed organ identity compared to the wildtype: petals became sepals, lips became petals, petals became lips and staminodes became stamens. These morphological changes seem to be caused by a different expression of MADS-box B class involved in floral development. Implications of gene duplication and subfunctionalization for the origin of major key innovations during orchid evolution are discussed.

31-3 Oral

MOLECULAR MECHANISMS GOVERNING THE ESTABLISHMENT OF SPECIES-SPECIFIC MORPHOLOGIES – EMERGING VIEWS

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The origin of macro- and microevolutionary differences is a long standing topic in evolutionary biology. In the past two decades, evolutionary developmental studies have been especially revealing in showing the importance of the hox genes in the large scale diversification of animal body plans. What is still unknown is to what degree do homeotic genes play a role in the establishment of the species-specific morphologies. To address this question, I focus on hemimetabolous insects and discuss how their mode of development may be particularly suitable for generating phenotypic variation. More specifically, two genes, *Ultrabithorax* and *Sex combs reduced*, are used to illustrate how the differences in their functions during embryonic and post-embryonic development may have a significant impact on morphological evolution. By using insect hind legs as a model, it is possible to visualize and understand how small, population-level differences in the expression of *Ubx* could over time lead to the large morphological differences. In the same way, a common *Scr*-triggered mechanism may account for some of the diversity found in the insect prothorax. These model studies indicate that in addition to their early embryonic function in establishment of segmental identity, hox genes may also play a large role in generating species-specific morphologies.

31-4 Oral

NATURAL VARIATION OF VULVA INDUCTION AMONG WILD *PRISTIONCHUS PACIFICUS* ISOLATES

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The nematode *Pristionchus pacificus* has been established as a model system in evolutionary developmental biology. Previous studies focused on macroevolutionary differences between the reference strains of *P. pacificus* (PS312) and *Caenorhabditis elegans* (N2). To add a microevolutionary perspective to the evo-devo studies in *P. pacificus*, we isolated more than 100 different strains of the species from around the world and examined natural variation. These strains showed high diversity, both at the molecular and the phenotypic level. One of the observed variations involves development of the vulva specifically due to induction by the gonad. The vulva (the egg laying organ of nematodes) develops from three vulva precursor cells (VPCs). In PS312 differentiation of the VPCs depends on a continuous inductive Wnt signal from the somatic gonad. However in some of the obtained strains, VPCs were still able to differentiate after ablation of the somatic gonad. To identify the involved loci we carried out QTL analysis using two isolates that showed the most extreme phenotypes. We crossed these strains and obtained recombinant inbred lines (RILs) by selfing individual F2 progeny. Gonad ablation experiments and genotyping of more than 200 RILs revealed a 30cM region on Chromosome I associated with the vulva induction trait. Currently we are testing candidate genes in this interval that are known to be involved in vulva signaling in PS312. Together, the microevolutionary perspective of *P. pacificus* vulva induction is an effort to integrate evo-devo studies in evolutionary theory.

31-5 Oral

THE EVOLUTIONARY ECOLOGY OF REACTION NORMS: INTER-SPECIFIC VARIATION IN DEVELOPMENTAL PLASTICITY IN THE AUSTRALIAN STILT-LEGGED FLIES (NERIIDAE: *TELOSTYLINUS*)

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Comparative studies of development have largely focused on characterizing 'typical' patterns, but many aspects of development are highly plastic. Taking such plasticity (i.e., developmental reaction norms) into account may lead to new microevolutionary insights. The Australian species of *Telostylinus* differ in average body size and shape, with the temperate-zone *T. angusticollis* being much larger and more sexually dimorphic than the tropical-zone *T. lineolatus*. Experimental manipulation of a key environmental parameter — larval diet — has revealed a striking contrast in developmental reaction norms between these species. In *T. angusticollis*, larval diet quality has a strong positive effect on adult body size, as well as sexual dimorphism in both size and shape. These effects are driven primarily by heightened expression of secondary sexual traits in adult males reared on rich larval diet. *T. lineolatus* exhibits much weaker developmental plasticity, and its reaction norm is negative over part of the diet quality gradient. As a result, *T. angusticollis* adults reared on poor larval diet are virtually indistinguishable in body size and shape from wild-collected adults of *T. lineolatus*. Moreover, an analysis of developmental noise in a discrete morphological character that differentiates the two species shows that *T. angusticollis* individuals reared on a poor larval diet often tend towards the typical character state of *T. lineolatus*. This inter-specific variation in reaction norms may reflect adaptive responses to an ecological parameter — the temporal stability of the food resources exploited by these species in their natural habitats. An evolutionary divergence in reaction norms, perhaps in response to an ecological parameter, thus appears to have produced a cascade of phenotypic differences, and may have played an important role in speciation.

31-6 Oral

MANDIBLE SHAPE IN HYBRID MICE

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Hybridization between closely related species is frequently seen as retarding evolutionary divergence but can also promote it by creating novel phenotypes due to new genetic combinations and developmental interactions. We therefore investigated how hybridization affects the phenotype of the mouse mandible, a feature that numerous evo-devo studies have shown to be composed of several developmental modules underlain by complex, pleiotropic interactions.

Hybrids were bred in controlled conditions, as well as their parents from two strains documenting two mouse sub-species. The mandible shape was quantified using geometric morphometrics. Its shape was considered as a whole or partitioned according developmental modules. Results show that the mandibles of hybrids are intermediate between parental phenotypes as expected for a complex multigenic character; a slight transgressive effect seems nevertheless to occur.

Hybrids also appear to be characterized by a larger size than the parental groups because of a heterotic effect. Hence, the relationship between size and shape was investigated, because size difference may lead to shape divergence through allometric processes. Allometry as a source of the hybrid divergence was however poorly supported, because no consistent direction of allometric variation emerged across the groups.

More strikingly, focusing on each module of the mandible provided discrepant patterns of divergence between the hybrids and the parental groups. The modular development of the mouse mandible may contribute to its potential of differentiation by allowing new combinations of shape among modules.

31-7 Oral

SEGMENTATION AND SPECIATION

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Arthropods include major clades with a fixed or almost fixed number of trunk segments, e.g. the insects and the malacostracan crustaceans, alongside clades, as the myriapods, where variation is conspicuous both within species and among closely related species. The evolvability of this trait is thus quite unevenly distributed within the clade. In centipedes, there is evidence that some recent speciation events were associated to an approximate doubling of the original segment number. A newly discovered species of scolopender has either 39 or 43 leg-bearing segments, while its sister species has either 21 or 23, these two values being the only numbers found in all the remaining 700+ species of Scolopendromorpha known to date. A few species of mecistocephalid centipedes have segment numbers about twice the putative primitive condition found in their closest relatives, and this higher segment number is associated with intraspecific variation for the same trait, at variance with the numerical invariance found in most of the remaining 100+ species in the clade. These examples point to a complex genotype-phenotype mapping: nearest neighbors in the morphospace of segment numbers are not necessarily nearest neighbors in the space of the developmental pathways that determine the final number of body segments, and vice-versa. When the genotype-phenotype mapping is complex, as it seems to be in the case of centipede segmentation, a sound knowledge of the relevant developmental pathways is essential to understand phenotypic evolution, as this involves complex relationship among character variation, evolvability, and canalization.

31-1 Poster **A novel role for Ubx in the evolution of the appendage ground plan in water striders**

ABDERRAHMAN KHILA[1,2], EHAB ABOUHEIF[2], LOCKE ROWE[1]
[1]University of Toronto, Department of Ecology and Evolutionary Biology, Toronto, Canada
[2]McGill University, Department of Biology, Montreal, Canada

31-2 Poster **Developmental mode transitions and population connectivity in the polychaete *Pygospio elegans***

JENNI KESÄNIEMI, EMILY KNOTT
University of Jyväskylä, Department of Biological and Environmental Science, Jyväskylä, Finland

31-3 Poster **The genetic and molecular basis of parallel evolution in egg-spots of cichlid fishes**

EMILIA SANTOS, WALTER SALZBURGER
University of Basel, Zoological Institute, Basel, Switzerland

31-4 Poster **The genetic basis of wing pattern evolution in *Heliconius* butterflies**

CHRIS D. JIGGINS
University of Cambridge, Department of Zoology, Cambridge, United Kingdom

31-5 Poster **Genetic speciation: asymmetric reproductive isolation between *Lutzomyia pseudolongipalpis* and *Lutzomyia longipalpis* (species C2), implications within “longipalpis complex”**

JAZZMIN C. ARRIVILLAGA
Universidad Simon Bolivar, Lab. de Genetica de Poblaciones, Seccion Invertebrados, Estudios Ambientales, Caracas, Venezuela

31-6 Poster **Diverging functions of Scr between embryonic and post-embryonic development in a hemimetabolous insect, *Oncopeltus fasciatus***

STEVEN HRYCAJ, JOHN CHESEBRO, ALEKSANDAR POPADIC
Wayne State University, Department of Biological Sciences, Detroit, United States

31-7 Poster **Transcriptional regulation of human brain development and aging**

PHILIPP KHAITOVICH[1,3], MEHMET SOMEL[1,3], SONG GUO[1], WEI CHEN[2], YUAN YUAN[1]
[1]CAS-MPG Partner Institute for Computational Biology, Department of Comparative Biology, Shanghai, China
[2]Max Delbrück Center for Molecular Medicine, Berlin, Germany
[3]Max Plank Institute for Evolutionary Anthropology, Leipzig, Germany

31-8 Poster **Hox gene expression in the dogfish and the evolution of vertebrate appendages**

SILVAN OULION[1,2], VÉRONIQUE BORDAY-BIRRAUX[1,3], PATRICK LAURENTI[1,3], DIDIER CASANE[1,3]
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[2]Université Paris 11, Orsay, France
[3]Université Paris 7, Paris, France

31-9 Poster **Evolution and development of simple and trifid tendrils in *Bignonieae* (Bignoniaceae)**

MARIANE S. SOUSA-BAENA, LUCIA G. LOHMANN
Universidade de São Paulo, Department of Botany, São Paulo, Brazil

31-10 Poster **Expression and function of nubbin in embryonic development of *Acheta domesticus***

NATALIYA TURCHYN, ALEKSANDAR POPADIC, JOHN CHESEBRO, STEVE HRYCAJ

Wayne State University, Department of Biological Sciences, Detroit, United States

31-11 Poster **RNAi in the beetle *Tribolium* elucidates the transition to long germ development in Diptera**

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