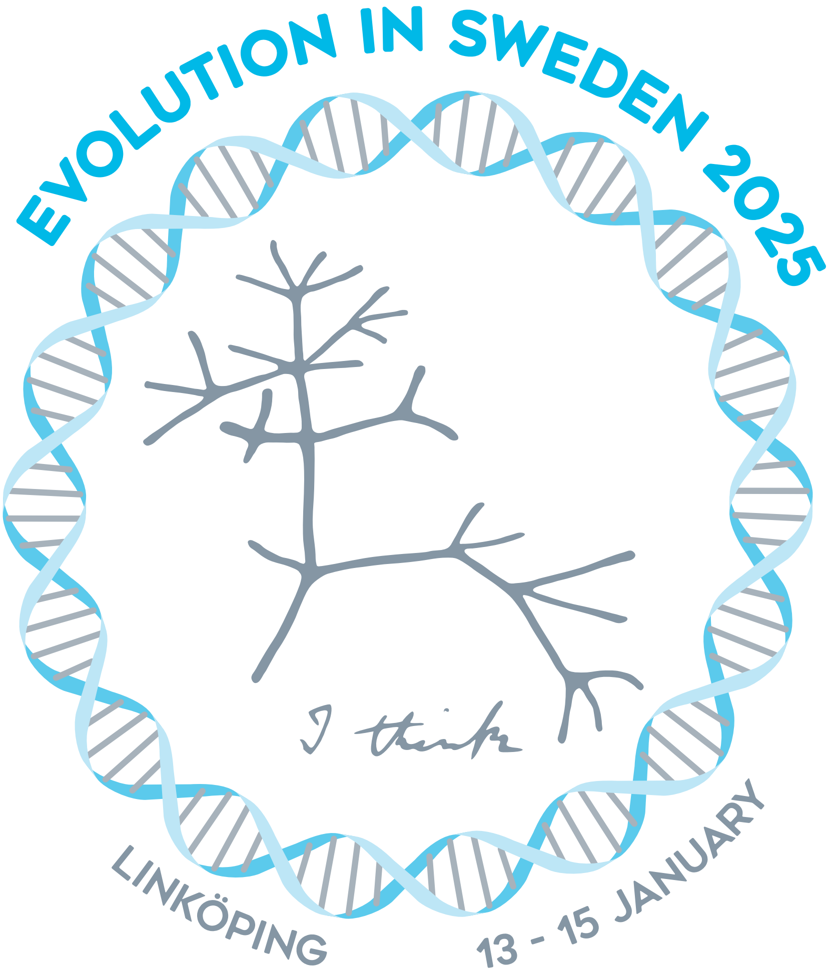
Evolution in Sweden 2025

January 13 – 15, 2025, Linköping



LINKÖPINGS UNIVERSITET

SciLifeLab

QIAGEN

Dear conference participant,

We look forward to welcoming you to the Evolution in Sweden conference in Linköping, 13th-15th January, 2025! This pdf contains the abstracts (oral and poster) for the conference, a preliminary (hopefully final, but any changes will be updated on a google docs excel file and sent to everyone) program.

The conference will be held in the C-building at the Valla (main) campus of Linköping University. The conference will be held in the lecture theatre C4, with the posters set-up in the foyer-area outside C4. Registration is from 9.30 until 13.00 outside the lecture hall on the 13th January.

There is a lunch venue booked at the University restaurant Kårallen (see map on the next page), which is situated in the next building down from the C-building (two minutes walk from the lecture hall). We have booked a reservation for all those who indicated that they would like a reservation (and can most likely accommodate any who had forgotten to book or changed their minds). The cost of lunch is at everyone's own expense. In addition, we will provide tea, coffee and biscuits at the fika breaks, with this generously provided by Qiagen (stop by their booth at the conference and say hello!). We would also like to thank the SciLifeLab for generously hosting the plenary speakers and for hosting a DDLS speaker session on the 14th!

We have a poster session on the 13th and 14th outside the lecture theatre, and have also highlighted a conference pub in town (O'Leary's). This was picked because of its size, but we don't have any actual reservations (but it is pretty huge on the inside). It is located in the main square (Storatorget), and several other pubs are also located on the main square or on the next street (Ågatan) for those who wise to meet for a drink in the evenings.

We hope you all have a lovely Christmas and New Year, and look forward to all the exciting talks and seeing everyone in the new year.

Best

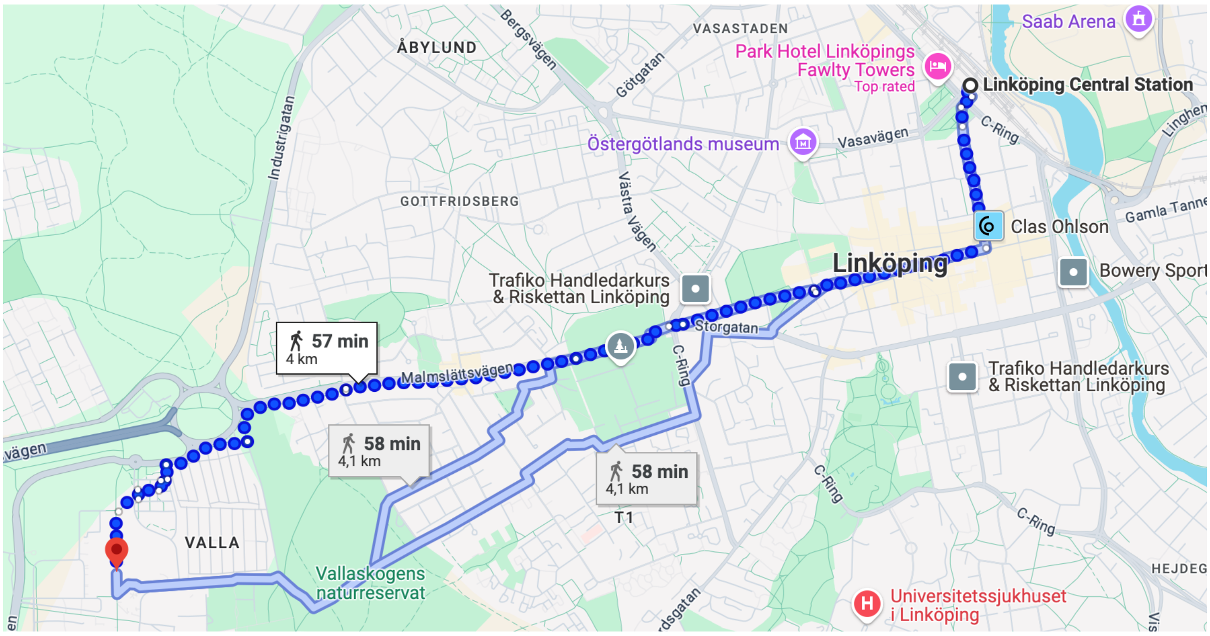
The Evolution in Sweden Linköping organizing committee

Dominic Wright (chair), Rie Henriksen, Per Jensen, Urban Friberg and Krzysztof Bartoszek

Getting to the venue:

From the bus station (next to the train station), you can take the bus numbers 4, 540, 39, otherwise it is around a one hour walk. The geolocation of the building is

58°24'05.9"N 15°34'41.1"E



Maps showing the conference location (C building), venue location (C4 lecture hall), nearest bus stop, and lunch venue

Conference venue (C-building, lecture Hall C4)

Bus stop

Conference venue (C-building, lecture Hall C4)

Lunch location (Kårallen restaurant)

EVOLUTION IN SWEDEN LINKÖPING 2025 FULL PROGRAM

January 13th

09:30	**On-site registration outside C4**	
12:00	**Lunch**	
12:45	Welcome	
13:00	**PLENARY - Tom Gilbert**	
14:00	Jessica Abbott	Change in the G-matrix as a result of female-limited X chromosome evolution
14:15	Ted Morrow	The adaptive value of recombination in resolving intralocus sexual conflict by gene duplication
14:30	Ingo Müller	Hybridisation patterns in the birds-of-paradise genus Paradisaea
14:45	Mafalda Sousa Ferreira	The role of introgression for adaptation of Atlantic herring to the Baltic sea
15:00	**FIKA**	**Sponsored by Qiagen**
15:30	Krzysztof Bartoszek	Fast inference for multivariate phylogenetic comparative methods
15:45	Ivan Prates	Unraveling the genomic underpinnings of parallel evolution in Mediterranean wall lizards
16:00	Anna Qvarnström	Inheritance of material wealth in a natural population
16:15	Enya Van Poucke	Domestication and Early Stress Resilience: Insights from White Leghorns and Red Junglefowl.
16:30	Alexandre Rego	Selective hearts, selected genes: genomic consequences of different mating regimes
16:45	Anna Runemark	The genomic basis of adaptation to a new host plant
17:00	Lars Rönnegård	Could selection for decreased variability in milk yield lead to asocial cows?
17:15	Pamela Santana	Evolution of flower shape in a coevolved system
17:30	Hanna Sigeman	A novel supergene explains alternative reproductive strategies in the ant M. ruginodis
17:45	**POSTER SESSION**	
20:00	**Conference Pub**	**O'Leary's Storatorget**

January 14th

09:00	**PLENARY - Kees Van Oers**	
10:00	**FIKA**	**Sponsored by Qiagen**
	DDLS Session	
10:30	Jacob Höglund	The SciLifeLab Planetary Biology Capability
10:45	Lisandro Milocco	Toward predictive evo-devo: a data-driven approach to modeling phenotypic variation
11:00	Nikolay Oskolkov	aMeta: a computational method for data-driven ancient metagenomic analysis
11:15	Masahito Tsuboi	Dialectical relationships between microevolution and macroevolution
11:30	José Cerca	Step by step, an adaptive radiation is made: Empirical evidence for the 'least action effect'
11:45	Lennart Winkler	How ecologically relevant resource distributions influence condition-dependent trade-offs

13:15	Staffan Bensch	Identifying the elusive migration genes
13:30	David Wheatcroft	TBC
13:45	David Berger	Strong Selection, but low repeatability: Temperature-specific effects on genomic predictions of adaptation
14:00	Folmer Bokma	Contrasting evolution in incipient versus established species
14:15	Diego Stingo Hirmas	Prenatal maternal stress underlies multi-hierarchical behavioural plasticity
14:30	Marianne Dehasque	From Wild to Tamed and Back: the evolutionary history of Sardinian sheep
14:45	Eran Elhaik	Why All PCAs in Evolutionary Biology are Likely Wrong

15:00	**FIKA**	**Sponsored by Qiagen**
15:30	Turid Everitt	Investigating the role of meiotic recombination in social insects - Termites adding an important piece to the puzzle
15:45	John Fitzpatrick	The evolution of conspicuous markings in skates and rays
16:00	Samyuktha Rajan	Mechanisms of mixed singing and species recognition in sympatric flycatchers
16:15	Ana Gomes	Experimental examination of the neural background to cognitive variation across species in Poeciliid fishes
16:30	Jake Goodall	Atlantic Herring - Population trends and perspectives from the Baltic Sea
16:45	Chloé Haberkorn	Adaptive benefits of hybridization in Saccharomyces yeast under thermal stress: genomic and fitness analyses
17:00	Christina Hansen Whea	The importance of standing ancestral variation in behavioural evolution
17:15	Joshua Hufton	Epigenetic regulation of immune response in the Swedish sand lizard (Lacerta agilis)

17:30	**POSTER SESSION**	
20:00	**Conference Pub**	**O'Leary's Storatorget**

January 15th

09:00	**PLENARY - Susan Johnston**	

10:00	**FIKA**	**Sponsored by Qiagen**
10:30	Zeeshan Syed	A study of the aging transcriptome from an adaptive perspective
10:45	Julia Höglund	Characterisation and quantification of deleterious genetic variants in non-model organisms: from present to extinct species
11:00	Martin Johnsson	Loss of genetic variation and establishment of damaging variants in effectively small populations
11:15	Cheng Ma	The adaptive evolution of herring to different salinities
11:30	R. Axel W. Wiberg	Testing genomic predictions of sexually antagonistic coevolution: Natural variation in the sex-peptide network in Drosophila melanogaster
11:45	Dick Moberg	Speciation and Temporal Dynamics of Female Sperm Management
12:00	**LUNCH**	

Abstract number: Plenary

Title: Domestication hologenomics – how did our ancestors tame the wolf?

Name: Prof. Tom Gilbert

University: University of Copenhagen

Comparisons of the genomes of contemporary domestic animals and plants with those of their wild relatives, have provided a wealth of insights into not only when and where our ancestors started the process, but also what specific genetic variants are key to modern phenotypes. Furthermore, once coupled to palaeogenomic data, such datasets can also even reveal the order in which such variants arose, shedding further insights into the process itself. However, while there is no doubt that we have learnt much about domestication in general, and indeed for most domestic species we can clearly document the genetic basis of why the end product differs from the start, I argue that there may be certain processes that were involved that have been largely overlooked, in particular related to the so-called hologenome.

Biography:
Tom Gilbert is Professor of Palaeogenomics at the University of Copenhagen, Professor II at NTNU University Museum, and Director of the DNRF Center for Evolutionary Hologenomics. He holds a PhD in the study of ancient DNA from the University of Oxford, and has been active in both trying to develop methods to both expand the potential of ancient DNA to our understanding of the past, as well as more recently leading research aimed at revisiting our understanding of ecological and evolutionary processes using hologenomic techniques – ie the integrative approach of combining host genomes with those of their microbiomes.

Abstract number: Plenary

Title: The epigenetics of Animal Personality

Name: Prof. Kees Van Oers

University: Netherlands Institute of Ecology/ Wageningen University

Abstract:

Epigenetic mechanisms are those molecular mechanisms that affect gene expression without changing the DNA sequence. The value of epigenetic mechanisms is increasingly recognized, also in relation to questions in ecology and evolution. However, epigenetic research related to behavioural variation in the natural habitat is still in its infancy. The flexible nature of epigenetic marks opens the possibility that such changes are adaptive, while at the same time may simply be the consequence of environmental variation. Hence, changes in epigenetic marks can function as switches in order to help an organism develop, as signals of aging via accumulation of methylation over time, but they also may aid organisms to cope with changing circumstances throughout their lifetime. In this presentation, I use data of our great tit system to show examples of how tissue and cell-specific epigenetic patterns, mainly focusing on DNA methylation, may affect behavioral phenotypes such as exploratory behavior and reversal learning performance. I discuss what the role is of epigenetic mechanisms for behavioral adaptation to changing environments.

Biography:

Kees van Oers is an evolutionary behavioural ecologist. He currently holds a chair in Animal Personality at Wageningen University and is senior scientist at the Netherlands Institute of Ecology (NIOO-KNAW). His research focuses on explaining the causes and consequences of individual variation in animal behaviour, mainly cognitive and animal personality traits. He does this from an ecological and evolutionary point of view, at the crossroads between behavioural ecology and behaviour genetics. His goal is to find answers to fundamental and strategic questions related to individual responses to changing environments. This is relevant since the world and therefore the environment is constantly changing partly due to human influences affecting biodiversity at all functional levels.

Abstract number: Plenary

Title: The causes and consequences of sex differences in recombination rates.

Name: Dr. Susan Johnston

University: Edinburgh University

Abstract:

The rate of meiotic recombination often shows large differences between the sexes. It can be strongly female-biased (humans), strongly male-biased (macaques/sheep) or somewhere in between. Understanding why this happens is key to understanding the evolution of recombination rates, yet the causes and consequences of this phenomenon remain unknown. This talk will focus on our most recent work in house sparrows (*Passer domesticus*), with broader context from work in mammals and fish. We use genomic data in large pedigrees to characterise individual recombination rates and landscapes to: (a) investigate the heritability and genomic basis of variation in recombination rates; (b) identify genomic correlates with fine-scale sex-differences in recombination landscapes; and (c) use genomic prediction approaches to understand the relationship between recombination and fitness within each sex. Our work provides a foundation for broader understanding of the vast diversity of recombination rates in eukaryotic genomes.

Biography:

Susan Johnston is an evolutionary quantitative geneticist based at the University of Edinburgh, Scotland, where she is a Senior Lecturer and Royal Society University Research Fellow. Her research centres on using genomic information to understand selection and evolution in both wild and domesticated populations. At the moment, her group focusses on questions related to genomic signatures of sexual conflict, the maintenance of genetic variation in immunity, and the causes and consequence of recombination landscape variation. She does this by taking advantage of long-term ecological datasets and deep pedigrees with genomic data in mammals, birds and fish.

Abstract number: O1

Title: Change in the G-matrix as a result of female-limited X chromosome evolution

Name: Jessica Abbott

University: Lund University

Abstract:

Genetic variation on the X chromosome is likely to be subject to unequal sex-specific selection pressures. This is due to its unequal transmission pattern between the sexes, combined with the potential for stronger sexual selection in one sex. Nevertheless, the evolution of sexual dimorphism may be constrained by the shared genetic basis of homologous traits. After more than 147 generations of female-limited X chromosome (FLX) experimental evolution we estimated the phenotypic response to selection and quantitative genetic parameters for three homologous traits in Drosophila melanogaster (wing length, desiccation resistance, and locomotory activity). We expected that changes in allele frequencies associated with phenotypic feminization as a result of FLX evolution might modify the underlying genetic basis of these traits. We found evidence of a significant phenotypic change in desiccation resistance in the FLX selection regime, but contrary to our expectations, this change was not consistent with feminization. We also found some evidence of consistent changes in the genetic architecture of locomotory activity in the FLX selection regime, which was surprising given that this trait did not show any evidence of a phenotypic change. We outline a number of possible explanations for this result.

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Key words: quantitative genetics, sexual conflict, experimental evolution, sex chromosomes

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Abstract number: O2

Title: The adaptive value of recombination in resolving intralocus sexual conflict by gene duplication

Name: Ted Morrow

University: Karlstad University

Abstract:

We investigate whether recombination can play a role in resolving intralocus sexual conflict. Errors during recombination resulting in gene duplications may provide a long-term evolutionary advantage if those loci also experience sexually antagonistic (SA) selection since, after duplication, sex-specific expression profiles will be free to evolve, thereby reducing the load on population fitness. Using data on candidate SA loci from Drosophila melanogaster and humans we found single-nucleotide polymorphisms (SNPs) with net-positive effects across the two sexes occurred at higher frequencies than SNPs with net-negative effects. In flies, higher recombination rates were associated with more intense levels of sexual conflict and genes with paralogs occur in regions with higher recombination rates. Genes experiencing higher levels of conflict also showed both a higher proportion and higher numbers of paralogs. Our results support a possible route towards resolution of an adaptive conflict via gene duplication that is facilitated by higher recombination rates.

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Key words: Sexual conflict, recombination, resolution, gene duplication

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Abstract number: O3

Title: Hybridisation patterns in the birds-of-paradise genus Paradisaea

Name: Ingo Müller

University: Swedish Museum of Natural History / Stockholm University

Abstract:

Hybridisation offers a great opportunity to study speciation, by allowing us to investigate mechanisms driving reproductive isolation between populations. Sexual selection is one mechanism that could ultimately reduce the prevalence of hybridization and promote speciation. However, interestingly, our previous research has shown that hybridization may be surprisingly common in taxa with extreme forms of sexual selection, such as lekking Birds-of-Paradise. In this study, we investigated hybridisation patterns within the genus Paradisaea using a whole-genome dataset of more than 100 samples, primarily obtained from historical samples (hDNA). Through comprehensive population genetic and phylogenetic analyses, we assessed the prevalence of hybridisation within the genus and found significant mixing between species with sympatric distributions on New Guinea's mainland. We also identified patterns of introgression driven by backcrossing deep into the parental species' distributions. Finally, our study further highlights the importance of museum collections to study genomic change in species that are difficult to sample in the wild.

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Key words: Museomics, Hybridisation, Population Genomics, Phylogenetics, Bioinformatics

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Abstract number: O4

Title: aMeta: a computational method for data-driven ancient metagenomic analysis

Name: Nikolay Oskolkov

University: Lund University

Abstract:

Analysis of microbial data from archaeological samples is a growing field with great potential for understanding ancient environments, lifestyles, and diseases. However, high error rates have been a challenge in ancient metagenomics, and the availability of computational frameworks that meet the demands of the field is limited. Here, we propose aMeta [1], an accurate metagenomic profiling workflow for ancient DNA which is designed to minimize the amount of false discoveries and computer memory requirements. Using simulated data, we benchmark aMeta against a current state-of-the-art workflow and demonstrate its superiority in microbial detection and authentication, as well as substantially lower usage of computer memory.

[1] Zoé Pochon, Nora Bergfeldt, Emrah Kırdök, Mário Vicente, Thijessen Naidoo, Tom van der Valk, N. Ezgi Altınışık, Maja Krzewińska, Love Dalen, Anders Götherström, Claudio Mirabello, Per Unneberg and Nikolay Oskolkov, aMeta: an accurate and memory-efficient ancient Metagenomic profiling workflow, Genome Biology 2023, 24 (242), https://doi.org/10.1186/s13059-023-03083-9

Authors: Nikolay Oskolkov, Biology Department, Science for Life Laboratory, National Bioinformatics Infrastructure Sweden, Lund University, Lund, Sweden

Key words: ancient DNA, metagenomics, microbiome, ancient metagenomics, microbial pathogens

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Abstract number: O5

Title: Fast inference for multivariate phylogenetic comparative methods

Name: Krzysztof Bartoszek

University: Linköping University

Abstract:

Co-adaptation is key to understanding species evolution. Different traits have to function together so that the organism can work as a whole. Hence, all changes to environmental pressures have to be coordinated. Since 2019, we have been developing R packages that are able to very efficiently do estimation for general, multivariate Gaussian processes realized over a phylogenetic tree. Using the likelihood computational engine PCMBase (on CRAN) mvSLOUCH (on CRAN) now is able to efficiently work with multivariate phylogenetic Ornstein-Uhlenbeck models. The user is able to propose specific model parameterizations that correspond to particular hypotheses about relationships between traits. In the talk I will discuss how one can setup different hypotheses concerning relationships between the traits in terms of model parameters and discuss particular aspects of the estimation procedures, based on our recent wide simulation studies. The software's possibilities will be illustrated by considering the evolution of functional traits in a dataset of 1252 angiosperms.

Authors: Krzysztof Bartoszek

Key words: phylogenetic comparative methods, R, maximum likelihood inference, pruning algorithm, angiosperms

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Abstract number: O6

Title: Unraveling the genomic underpinnings of parallel evolution in Mediterranean wall lizards

Name: Ivan Prates

University: Lund University

Abstract:

Shared phenotypes among distantly related species provide compelling evidence of parallel evolution in response to common ecological pressures or developmental biases. Nevertheless, the genetic mechanisms underlying parallel evolution remain poorly known. Here, we perform a comparative phenomic and genomic study of Mediterranean wall lizards (genus Podarcis). We show that several Podarcis species independently evolved a similar suite of consistently correlated characters, including coloration, morphology, and behavior. In each species, this 'syndrome' is present in only some populations, which enabled us to investigate the genomic basis of the repeated evolution of complex phenotypes. To this end, we employed whole-genome re-sequencing and genome scans to identify and compare loci associated with the syndrome across species, finding both shared and unique outlier loci. This combined approach provides insights into the factors underpinning repeated evolutionary outcomes – a pervasive feature of life on Earth.

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Key words: Parallel evolution, phenotype, coloration, genomics, adaptation

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Abstract number: O7

Title: Inheritance of material wealth in a natural population

Name: Anna Qvarnström

University: Uppsala University

Abstract:

Evolutionary adaptation occurs when individuals vary in access to fitness-relevant resources and these differences in “material wealth” are heritable. It is typically assumed that the evolutionary outcomes only depend on heritable variation in the phenotypic abilities needed to acquire material wealth. Here, we scrutinize this assumption by investigating additional mechanism underlying inheritance of material wealth in collared flycatchers. A genome-wide-association analyses reveals a high genomic heritability (h2=0.405+/-0.08) of access to caterpillar larvae, a fitness-relevant resource, in the birds’ breeding territories. Analyses of the top 100 SNPs associated with this material wealth reveal little evidence for corresponding associations with causal phenotypic acquisition abilities. Simulations, experimental and long-term monitoring data instead imply that heritability of material wealth is largely explained by philopatry that causes within-population genetic structure across a heterogeneous landscape. Therefore, allelic variants associated with high wealth may spread in the population without having causal connections to traits promoting local adaptation.

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Key words: site fidelity, social inheritance, landscape genomics, heritability, GWAS, animal breeding model,

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Abstract number: O8

Title: Mechanisms of mixed singing and species recognition in sympatric flycatchers

Name: Samyuktha Rajan

University: Stockholm University

Abstract:

Assortative mating relies heavily on recognizing conspecifics, a process often mediated by acoustic signals in birds. On the island of Öland, where pied and collared flycatchers occur in sympatry, pied flycatchers deviate from their species-specific songs by producing a converged 'mixed' song that partly resembles collared flycatcher song. This asymmetric song convergence has previously been shown to increase interspecies mating errors. However, it remains unclear whether pied flycatchers incorporate collared flycatcher syllables into their songs (true mixed singing) or simply modify their own songs to approximate collared flycatchers' due to broad learning predispositions. To disentangle these hypotheses, we conducted an in-depth acoustic analysis to trace the origins of syllables within mixed songs. This study provides insights into the mechanisms underlying asymmetric song learning in natural populations, which can ultimately help us predict how song learning may impact reproductive isolation and the evolutionary trajectory of these species.

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Key words: Speciation, cultural evolution, song learning, Ficedula

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Abstract number: O9

Title: Selective hearts, selected genes: genomic consequences of different mating regimes

Name: Alexandre Rego

University: Uppsala University

Abstract:

Sexual selection is theorized to play a pivotal role in shaping genomic variation and architecture, either by purging deleterious alleles or by maintaining genetic diversity through balancing selection across the sexes. Despite its theoretical importance, empirical tests of this hypothesis remain limited. Here, we conducted experimental evolution spanning 90 generations in seed beetles maintained under three alternative mating regimes: polygamy (intense sexual selection), monogamy (eliminating sexual selection), and male-limited selection (restricting selection to males). By comparing these regimes, we investigated how sexual selection interacts with natural selection to shape genomic variation, focusing on estimating the relative importance of purging of deleterious alleles and the maintenance of genetic variation through sexually antagonistic selection. By integrating transcriptomic and genomic analyses, we provide a comprehensive view of how mating systems influence genomic variation and pinpoint genetic mechanisms underpinning sex-specific adaptation and conflict.

Authors: Alexandre Rego, Uppsala University, Sweden Mareike Koppik, Martin-Luther University Halle-Wittenberg, Germany Julian Baur, Uppsala University, Sweden David Berger, Uppsala University, Sweden

Key words: sexual selection, experimental evolution, genetic variation, genomic architecture, Callosobruchus maculatus

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Abstract number: O10

Title: The genomic basis of adaptation to a new host plant

Name: Anna Runemark

University: Lund University

Abstract:

While populations are known to rapidly adapt to new ecological niches, how divergent ecological adaptation translates into reproductive isolation and ultimately speciation is a topic of current debate. Here, we use Tephritis conura peacock flies adapted to different thistle host plants to uncover the genomic basis enabling the use of different thistle host plants, also in sympatry. We document a large inversion on chromosome 3 which consistently differs between host plant races of T. conura. This inversion is enriched for both metabolic processes and reproductive processes, providing a potential mechanism for coupling divergent ecological adaptation to reproductive isolation. We uncover that genes that are differentially expressed between feeding larvae of the different host races, the life stage under strongest viability selection, are enriched in the inversion. Finally, we document strong both pre- and postzygotic reproductive barriers, contributing to the potential for these host races to eventually form different species.

Authors: Runemark, Anna1* Steward, Rachel1 Ortega, Jesús2 Nilsson, Kalle1 Nolen, Zachary1 Choudhary, Shruti3 Yajuan Huang4

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Key words: speciation, inversion, gene expression, host plant adaptation

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Abstract number: O11

Title: Could selection for decreased variability in milk yield lead to asocial cows?

Name: Lars Rönnegård

University: SLU

Abstract:

Competition and indirect genetic effects (IGEs) result in a measurable genetic variation in variability, which can be estimated using a DHGLM producing estimated breeding values for variability (vEBV). We investigate how selection on vEBVs may affect the number of contacts a cow has in a model including IGEs. For each scenario, 20 replicates with 100 farms with 100 cows each were simulated. Milk yield was simulated using three correlated genetic components: direct, indirect and number of contacts. The number of contacts per cow was simulated using a social network algorithm. The simulated heritabilities were around 0.3 for direct and indirect genetic effects and 0.5 for number of contacts. The correlation between the vEBVs and the simulated true breeding values (TBVs) for the number of contacts was calculated. The results show that selection for reduced vEBVs can reduce the number of contacts a cow has.

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Key words: phenotypic variability, social genetic effects, social network analysis, breeding value

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Abstract number: O12

Title: Evolution of flower shape in a coevolved system

Name: Pamela Santana

University: Lund University

Abstract:

Pollination interactions typically provide mutual fitness benefits to individuals of species interacting. Variation in the fitness benefits creates opportunities for natural selection to shape the traits mediating the interaction. Often, plant-pollinator interactions are mediated by multiple traits, and their combination ultimately determines the final interaction outcome. Plant-pollinator interactions face additional complexity, as change in one species may drive evolutionary change also in the interacting species, i.e. coevolution. The dynamic nature of coadaptation imposes a challenge for understanding how complex traits evolve in both species, and the reciprocity of evolution will depend also on the importance of the surrounding pollinator community. Here, we begin to address this topic from the plant perspective by investigating trait modularity and integration of L. bolanderi flowers, as flower modular organization is a key aspect to ensure evolvability. Our results indicate that coevolution is facilitated by trait modularity.

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Key words: Pollination, Fitness, Trait integration, Modularity, Evolvability

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Abstract number: O13

Title: A novel supergene explains alternative reproductive strategies in the ant M. ruginodis

Name: Hanna Sigeman

University: Uppsala University

Abstract:

Many ant species have two alternative reproductive strategies. Large queens disperse to form single-queen colonies while small queens remain in their natal colonies as part of multi-queen groups. Although the genetic basis of these strategies has been elucidated in five ant lineages, many species remain unstudied. We investigate the genetic basis of alternative reproductive strategies in a novel system: the queen-size dimorphic ant Myrmica ruginodis. We captured 95 queens from 31 colonies in southern Finland, and using whole-genome sequencing, we found a novel 9 Mb supergene linked to queen size and social organization. Queens homozygous for the ancestral haplotype ("AA") were larger and found only in single-queen colonies, while multi-queen colonies contained mixed haplotypes ("AB" and "BB"). This supergene is non-homologous to previously identified supergenes in ants, representing a novel evolutionary pathway to alternative reproductive strategies in ants.

Authors: Sigeman Hanna, University of Oulu (Finland) / Uppsala University (Sweden)

Key words: Supergene, genomics, ants, queen

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Abstract number: O14

Title: The role of introgression for adaptation of Atlantic herring to the Baltic sea

Name: Mafalda Sousa Ferreira

University: SciLifeLab Stockholm University

Abstract:

Introgressive hybridization can allow adaptation to new environments, but it can also impact fitness and compromise species survival. We study the role of genomic introgression for adaptation and divergence in two sister marine fish species, the Atlantic and Pacific herring, which are in contact in the Arctic Ocean. Using high-coverage whole genomes of 125 individuals representing the distribution of Atlantic and Pacific herring as well as the contact zone, we confirm previously described signatures of gene flow from Atlantic to Arctic Pacific herring, but find almost no introgression in the opposite direction. The remarkable exception is the spring-spawning Baltic herring ecotype, where we find Arctic Pacific introgression in high frequency in approximately 0.29% of the genome. Our analysis suggests that the introgressed genomic regions harbor genes involved in body growth and lipid metabolism and thus may have contributed to ecological adaptation in the Baltic Sea.

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Key words: Adaptation, Introgression, Atlantic Herring, Genomics

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Abstract number: O15

Title: Prenatal maternal stress underlies multi-hierarchical behavioural plasticity

Name: Diego Stingo Hirmas

University: Linköpings Universitet

Abstract:

Although prenatal stress (PS) has been observed to have long-term effects on the behaviour of many species, results vary significantly across studies. Recent research has shown that consistent differences in individual predictability exist when measured across a reaction norm. We aimed to assess whether PS could not only influence an animal's mean behavioural response but also its variability across multiple measurements. Hens of an advanced intercross of Red junglefowl and white leghorn chickens were implanted with either corticosterone to simulate maternal stress or placebo pellets subcutaneously. The offspring were repeatedly tested in an open-field test. We found that prenatal maternal corticosterone levels affected the offspring's mean anxiety-related response as well as how predictable they were in their behavioural responses. These results show that PS can cause heterogeneity of within-individual behavioural variability and highlight the role of reaction norms as a significant component when studying prenatal stressors' effect on animal behaviour.

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Key words: prenatal stress, behavioural plasticity, anxiety, predictability, residual intra-individual variation

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Abstract number: O16

Title: A study of the aging transcriptome from an adaptive perspective

Name: Zeeshan Syed

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Abstract:

Differential gene-expression (DE) with age is generally attributed to the organism's reduced ability to maintain optimal expression. An alternative possibility is that a significant portion of DE is an adaptive response to poor physiological condition. Here, we test this hypothesis by genetically manipulating condition (independent of age) in female Drosophila melanogaster. Transcriptomic comparison of DE in the head due to reduced condition showed substantial overlap with that due to age. Gene ontology (GO) analyses revealed adaptive responses to poor condition and cellular damage by down- and up-regulated genes respectively. Further, downregulated (by either or both age and condition) genes belonging to the enriched GO terms showed (a) negatively correlation between tissue-specificity and the extent of DE and (b) signatures of purifying selection. These results suggest that a substantial proportion of the aging transcriptome is consistent with condition-dependent adaptive expression aimed at mitigating rather than causing aging.

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Key words: aging, transcriptomics, condition-dependence, adaptation

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Abstract number: O17

Title: Testing genomic predictions of sexually antagonistic coevolution: Natural variation in the sex-peptide network in Drosophila melanogaster

Name: R. Axel W. Wiberg

University: Stockholm University

Abstract:

Sexually antagonistic coevolution (SAC) drives evolutionary dynamics, with males and females evolving traits that enhance their fitness but harming the opposite sex. While SAC is well-studied phenotypically, it's genomic basis remains poorly understood. In Drosophila melanogaster, conflicts over re-mating rates is likely mediated by the sex-peptide (SP) network, a set of interacting male and female proteins. Males benefit from reducing female remating rates to ensure paternity, while females may should prefer to remate when advantageous. However, the role of natural genetic variation in the SP-network in shaping these behaviors is understudied. Here, we test genomic predictions of SAC in D. melanogaster populations identified by natural patterns of genetic co-variation at SP-network loci. We compare populations where males, females, or neither sex has an inferred advantage. We hypothesize that populations with a female advantage will show higher remating rates and reduced fitness costs to females compared to populations favoring males.

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Key words: Sexual conflict, sexually antagonistic coevolution, sex-peptide network

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Abstract number: O18

Title: Dialectical relationships between microevolution and macroevolution

Name: Masahito Tsuboi

University: Lund Unviersity

Abstract:

Variation enables short-term evolution (microevolution), but its role in log-term evolution (macroevolution) remains debated. In my contribution, I will present analyses of extensive and multivariate Drosophila wing data spanning six levels of biological organization. Our results reveal consistent positive correlations between microevolutionary variation and macroevolutionary divergence, from variation within an individual to 40 million years of macroevolution. Surprisingly, the strongest relationship was observed between developmental noise and macroevolutionary divergence—levels thought to be the most distant—whereas the relationship between standing genetic variation and population divergence was modest, despite established theoretical predictions. Based on these results, I will propose pluralistic and dialectical relationships between microevolution and macroevolution, and discuss how data-driven approaches can integrate theory to advance 21st-century life sciences.

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Key words: evolutionary prediction, macroevolution, causation, data-and-theory-driven

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Abstract number: O19

Title: Domestication and Early Stress Resilience: Insights from White Leghorns and Red Junglefowl.

Name: Enya Van Poucke

University: Linköping University

Abstract:

Stress tolerance is a key factor in domestication, with studies showing that domestic species generally exhibit greater resilience than their wild ancestors. This study compares the stress responses of domestic White Leghorn (WL) laying hen chicks to those of their ancestral Red Junglefowl (RJF) when subjected to a pseudo-commercial hatchery procedure. Forty-four WL chicks and 40 RJF chicks underwent a series of stress-inducing treatments, including exposure to industrial noise and handling. Behavioral tests assessed their stress reactivity. Results indicated that RJF chicks emerged faster in a novel arena and vocalized more during social isolation, suggesting increased exploration and and a stronger tendency to re-establish social contact. Interestingly, both WL and RJF chicks from the hatchery treatment showed lower corticosterone (CORT) levels during restraint tests compared to controls, hinting at potential stress-priming. Overall, domestication may not significantly affect stress resilience in this context, with adaptability possibly linked to their precocial nature.

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Key words: Domestication, Early Stress, Commercial Hatchery

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Abstract number: O20

Title: Identifying the elusive migration genes

Name: Staffan Bensch

University: Lund University

Abstract:

It is amazing how tiny songbirds, weighing less than 10 grams, can fly with a strong determination in a specific direction, crossing huge geographical barriers to reach their winter grounds on another continent, all guided by their genes. Recently, we found a large and complex genomic region that directs willow warblers of two subspecies, trochilus and acredula, to different parts of Africa with great accuracy. We call this region MARB (Migration Associated Repeat Block). It seems to be passed down as a single unit without mixing, but we do not yet know if similar regions exist in other species or where exactly it is in the genome. In this talk, I will discuss the methods we have used to tackle these questions and share our progress in understanding how MARB influences songbird migration routes.

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Key words: Bird migration, genomics

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Abstract number: O21

Title: NA

Name: David Wheatcroft

University: Stockholms universitet

Abstract:

Population divergence in mating traits and preferences plays a critical role in speciation. Thus, uncovering how population divergence emerges and how it is maintained is a long-term goal in evolutionary biology. Songbird song is acquired through social learning, which has alternatively been hypothesized to facilitate or impede population and species differences. Here, I outline my group's recent work on song divergence across pied flycatcher (Ficedula hypoleuca) populations and exploring the implications for reproductive isolation with the closely related collared flycatcher (F albicollis) where they co-occur. Our approach combines field experiments, acoustic analyses, RNA sequencing, and captive rearing.

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Key words: Songbirds, mating traits, speciation

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Abstract number: O22

Title: Strong Selection, but low repeatability: Temperature-specific effects on genomic predictions of adaptation

Name: David Berger

University: Uppsala University

Abstract:

Climate warming is increasing temperatures beyond the optima of many ectotherms, which imposes strong selection on basal physiological and metabolic processes. This suggests that adaptation to climate warming should be relatively predictable. We tested this hypothesis from the level of genes to life-history traits by conducting an evolve-and-resequence experiment in a cosmopolitan insect pest. Indeed, phenotypic evolution was faster and more repeatable at hot temperature. However, at the genome-level, adaptation to heat was less repeatable than cold-adaptation. Moreover, while genomic predictions of phenotypic (mal)adaptation to hot temperature were accurate when applied to populations of the same geographic origin, they were highly inaccurate for populations of different geographic origin. These results seem best explained by an increased importance of epistasis during adaptation to heat and imply that genomic predictions of adaptation in key life-history traits, which mediate the agricultural impact of insect pests, may become increasingly difficult as climate warms.

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Key words: Repeatability of evolution, climate change, pest impact

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Abstract number: O23

Title: Contrasting evolution in incipient versus established species

Name: Folmer Bokma

University: Karlstad University

Abstract:

Are differences between species the long-term consequence of microevolution within species, or does speciation involve fundamentally different processes? I developed a phylogenetic method that decomposes interspecific trait covariance into two components: trait coevolution along phylogeny branches and at bifurcations. Applying this method shows, for example, that primate brain and body size evolve less correlatedly during speciation than between speciation events. With improved computational methods, we could apply this approach to large trait matrices, like gene expression data, to explore the molecular basis of the tempo and mode in phenotypic evolution. This opens new avenues for data-driven study of speciation, evolvability, and the relation between micro- and macroevolution.

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Key words: speciation, macroevolution, trait covariance, gene expression, coevolution

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Abstract number: O24

Title: How ecologically relevant resource distributions influence condition-dependent trade-offs

Name: Lennart Winkler

University: SLU Uppsala

Abstract:

Trade-offs are a central part of evolutionary biology. Individuals are assumed to trade investment in one energetically demanding trait against another, particularly when resources are limited. Most previous studies experimentally tested for trade-offs by manipulating resources quantity (e.g., high vs. restricted resources). However, this approach is unlikely to reflect the distribution of resources in natural populations. Here, we examine how a range of ecologically relevant distributions of resources influences trade-offs among pre-copulatory, post-copulatory and immune traits in male field crickets. Our results indicate that the emergence of trade-offs was sensitive to the underlying distribution of resources among males. Importantly, trade-offs were more likely when only high and low condition individuals were included – the least ecologically relevant resource distribution we considered. This cautions that experimental designs that do not reflect ecologically relevant conditions might identify trade-offs that are less relevant in natural populations.

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Key words: Trade-offs, Condition-dependence, Sexual Selection, Evolutionary Ecology

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Abstract number: O25

Title: From Wild to Tamed and Back: the evolutionary history of Sardinian sheep

Name: Marianne Dehasque

University: Uppsala University

Abstract:

Sardinia hosts three sympatric sheep lineages with distinct selective histories: the Sardinian mouflon, likely representing feral remnants of early domesticated sheep

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Key words: the Nera sheep, a local breed with ancestral traits

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Abstract number: O26

Title: Why All PCAs in Evolutionary Biology are Likely Wrong

Name: Eran Elhaik

University: Lund University

Abstract:

Irreproducibility in science hinders progress, wastes resources, and poses risks and biases. Addressing this issue requires examining commonly used methods, such as principal components analysis (PCA), a popular statistical tool in evolutionary biology and related fields. Despite its widespread use and citation, PCA's accuracy for genetic applications has never been conclusively proven. We argue that its results are often artifacts, and its popularity stems from the ease of manipulating outcomes, creating significant reproducibility issues. This is particularly problematic in ancient DNA studies, where bioinformatics methods are critical. To support our claims, we developed a model that compares true genetic distances to those produced by PCA, showing its bias and propensity to generate misleading results. Using real genetic data, we demonstrate how PCA leads to false conclusions and propose an alternative approach for measuring genetic distances. Our findings suggest PCA is unsuitable for genetic studies and call for reevaluation ~250,000 studies.

Authors: Eran Elhaik, Lund University, Sweden

Key words: PCA, evolutionary biology, paleogenomics, physical anthropology, reproducibility crisis

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Abstract number: O27

Title: Investigating the role of meiotic recombination in social insects - Termites adding an important piece to the puzzle

Name: Turid Everitt

University: Uppsala University

Abstract:

Meiotic recombination is an essential process in sexually reproducing organisms as it increases the efficiency of selection. There is however great variation in recombination rate across the tree of life, with eusocial insects from the order Hymenoptera in the topmost range. It has been hypothesized that eusociality leads to selection for high recombination rate as this would increase the genetic diversity in colonies and reduce kin conflict. The association between eusociality and high recombination rate has however not previously been studied outside of Hymenoptera. In this study we show that two termite species, which are eusocial insects from a different order, have substantially lower recombination rates than eusocial hymenopteran insects, contradicting aforementioned hypothesis. We present an alternative hypothesis, relating the high recombination rate in eusocial hymenopteran insects to their skewed sex-ratio of reproductive individuals, where the high number of haploid males present an efficient way to test different haplotypes.

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Key words: Recombination rate, eusociality, selection, genomics

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Abstract number: O28

Title: The evolution of conspicuous markings in skates and rays

Name: John Fitzpatrick

University: Stockholm University

Abstract:

Prey use a wide range of anti-predator defences to avoid predation. Yet few studies have examined the evolution of multiple anti-predator defences while simultaneously incorporating ecologically relevant factors at a macroevolutionary scale. Here was examine the evolution of anti-predator defences in 580 skates and rays (>90% of extant species), a diverse group of cartilaginous fishes. We demonstrate that skates and rays have evolved distinct anti-predator defences that are shaped by ecological factors. In particular, skates and rays lacking robust anti-predator defences and living at shallower depths were more likely to evolve conspicuous anti-predator markings than species with robust defences and species living at deeper depths. Together our findings suggest that the evolution of conspicuous markings is predominantly driven by trade-offs among alternative anti-predator defences and the visual environment in skates and rays. These findings have wider implications for our understanding of functional trade-offs in anti-predator defences.

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Key words: predation, visual signals, trade-offs, defence portfolio

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Abstract number: O29

Title: Step by step, an adaptive radiation is made: Empirical evidence for the ‘least action effect’

Name: José Cerca

University: Naturhistoriska

Abstract:

Abs: Adaptive radiations occur when a single lineage diversifies to exploit a broad range of ecological niches. However, the sequence of ecological occupation remains poorly understood. Two potential scenarios are herein proposed: random occupation, where species fill niches without a discernible pattern, and progressive occupation, where species track specific environmental gradients in a systematic manner. In this study, I examined four well-known adaptive radiations: Galápagos finches (Galápagos), Descurainia (Macaronesia), Aeonium (Macaronesia), and Anoles (West Indies). By analyzing phylogenetic and ecological distances between species, I found evidence supporting the hypothesis of progressive ecological occupation. This suggests that species diversify along a structured niche axis, implying that adaptive radiations may follow a more predictable, directional pattern. These findings are framed within the context of the ‘least action principle’ described by Gavrilets and Vose (2005).

Authors: None

Key words: Adaptive radiation

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Abstract number: O30

Title: Experimental examination of the neural background to cognitive variation across species in Poeciliid fishes

Name: Ana Gomes

University: Stockholm University

Abstract:

Cognitive performance is hypothesized to be linked to brain size. However, the few phylogenetically controlled studies that have tested this hypothesis focus primarily on mammals and birds, consider only distantly related species, and have not examined individual brain regions. Here, we overcome these limitations by experimentally quantifying cognitive performance and brain size in 173 individuals from 18 fish species from a single family of fishes - the Poeciliidae. For all individuals, we assessed performance on three cognitive tasks: reversal learning, detour-reaching, and object permanence. We then measured each individuals total brain volume, and the volume of different brain regions. This approach offers a robust assessment of the relation between relative brain volume and cognition. Indeed we find evidence that brain regions may be important in some cognition axis. Thus our results shed light on the evolution of cognitive performance and highlight the important of considering the scale of macroevolutionary studies.

Authors: Gomes, Ana Cristina R., De Meester, Gilles, Boussard, Annika , Shamsgovara, Arezo, Amcoff, Mirjam, Wheatcroft, David, Kolm, Niclas, Fitzpatrick, John L.

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Key words: cognition, brain size, brain regions, Poeciliidae, fish

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Abstract number: O31

Title: Atlantic Herring - Population trends and perspectives from the Baltic Sea

Name: Jake Goodall

University: Uppsala University

Abstract:

The Atlantic herring (Clupea harengus) is one of the most abundant vertebrates on earth, with an effective population size of one trillion. The species exhibits minute genetic differentiation at neutral loci and strong differentiation across selectively adaptive loci underlying ecological adaptation. Recently, a novel herring-specific SNP array was developed, increasing the accessibility of large-scale population genetic studies for the species. Here, we present ongoing research from the Baltic Sea, a region experiencing significant fishing pressure across the majority of stocks. Notably, we aim to discuss ecosystem-scale clines in genetic variation across the Baltic relative to factors such as latitude and salinity. Additionally, we discuss the discovery of novel Baltic ecotypes, such as the recently described Slåttersill, a large, piscivorous Baltic herring. Overall, we aim to highlight novel herring research and explore variable patterns of genetic diversity found in the Baltic Sea.

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Key words: Herring, Population Genetics, SNP, Ecotype

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Abstract number: O32

Title: Adaptive benefits of hybridization in Saccharomyces yeast under thermal stress: genomic and fitness analyses

Name: Chloé Haberkorn

University: Stockholm University

Abstract:

Accelerating climate change urges us to better understand and predict evolutionary responses to temperature shifts. Hybridization, by increasing genetic variation, can widen the range of adaptive responses and genetic mechanisms available to populations, which may allow them to survive fluctuating temperature conditions. Here, we explored the evolutionary consequences of hybridization between two species of Saccharomyces yeast, by evolving both hybrid and parental strains for 200 generations under hot, cold and fluctuating temperature regimes, and collecting whole genome sequencing data. Fitness was measured for each population, in all three temperature conditions, before and after experimental evolution. Overall, hybrids showed intermediate fitness to their parents, but a few hybrids evolved in hot conditions were clearly winning, with a higher fitness than that of their ancestors, in all three temperatures. Genomic exploration of mutations in hot-evolved hybrid populations revealed that hybridization can affect cellular stress-management pathways, leading to increased fitness in hot environments.

Authors: Chloé Haberkorn, Gerda Saxer, Noah Gettle, Jacob Elsen, Nahui Medina Chavez, Duncan Greig, Michael Travisano, Rike Stelkens

Key words: experimental evolution, climate change, yeasts, hybridization

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Abstract number: O33

Title: The importance of standing ancestral variation in behavioural evolution

Name: Christina Hansen Wheat

University: Stockholm University

Abstract:

Understanding how behaviours evolve is a long-standing goal in evolutionary biology. While novel mutations can be strong drivers of phenotypic change, a growing body of evidence now suggests that evolutionary change relies heavily upon standing genetic variation. However, the highly complex genetic basis of behavioural traits makes it challenging to establish the ancestral origins of behaviour through genomic studies. An alternative approach is to compare behaviours between groups of ancestral and derived species. In this context, I will use examples from separate behavioural tests conducted on European grey wolves and domestic dogs hand-raised under identical conditions. The results highlight two key points: 1) two behaviours (i.e. fetching and human-directed attachment) widely labelled as being unique to dogs are expressed in wolves, suggesting that selection acts on standing ancestral variation for these traits, and 2) identifying rare behavioural variation among ancestral populations could provide significant insights into how behaviours evolve.

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Key words: Behavioural evolution, standing variation

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Abstract number: O34

Title: Epigenetic regulation of immune response in the Swedish sand lizard (Lacerta agilis)

Name: Joshua Hufton

University: Uppsala universitet

Abstract:

Sand lizards (Lacerta agilis) are found across Europe, even stretching as far north to extremely cold environments such as in Sweden. Being highly adapted to such extreme temperatures makes them highly susceptible to climate change, and the knock-on effects this could have on disease dynamics. Using an experimentally isolated, outbreed, island population in southern Sweden we are investigating immunogenetics and epigenetics in these highly adaptable populations. Using immune challenge experiments, we are characterising the sand lizard immune response using RNA and bisulfite sequencing, and assessing the role of DNA methylation in reptilian immunity. This study will greatly improve our understanding of epigenetic regulation of immunity in reptiles in general but also give us key insights into specific genes underlying the Swedish sand lizard immune response. Our results are also important for the conservation of the species in Sweden, which are expected to face novel changes in disease dynamics as a result of climate change.

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Key words: Epigenetics, reptiles, immunity, gene expression, conservation

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Abstract number: O35

Title: The SciLifeLab Planetary Biology Capability

Name: Jacob Höglund

University: Uppsala

Abstract:

Planetary Biology Capability SciLifeLab's Planetary Biology capability sprung out of a need for trans-disciplinary and coordinated approaches to study life on Earth, with a broad scope ranging from single molecules and cells to individual species, species communities, ecosystems, and their functioning on the planet. Simply speaking "Life in environmental context". By combining SciLifeLab infrastructures, and the data-driven life science approach, the capability will create opportunities with a strong impact on biodiversity oriented research (broadly defined). Taking advantage of SciLifeLab's national research infrastructure, technology, and scientific excellence, techniques such as imaging, microscopy, genomics, bioinformatics, metabolomics, proteomics, and big data analysis, for non-biomedical research will be used to shed light on all aspects of life on our planet.

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Key words: SciLife, Planetary Biology, Biodiversity, Capability, Platforms

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Abstract number: O36

Title: Characterisation and quantification of deleterious genetic variants in non-model organisms: from present to extinct species

Name: Julia Höglund

University: Stockholm University

Abstract:

Many animal populations are currently undergoing dramatic decline

Authors: Julia Höglund1,2, Seyan Hu1, Martijn Derks1, Love Dalén2, Mirte Bosse1,3

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Key words: when a population becomes smaller, threats affecting the species' genome become larger. A reduced population size increases the risk of inbreeding and loss of beneficial genetic variation, results in a worse ability to adapt to changes, and can potentially lead to extinction. Hence, there is a critical need to quantify damaging genetic variation to aid conservation efforts and understand past extinctions. By expanding previous species-specific models scoring genetic variants based on predicted deleteriousness, we created a model that is able to predict deleteriousness also across non-model organism. We trained the initial model using deep sequencing data from domesticated pig, and our next step is to compare it to a model trained on wild boar, using the same pipeline. By extending beyond model species, we enhance its applicability to several species, hopefully providing insights into the possible genetic factors underlying species decline.

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Abstract number: O37

Title: Loss of genetic variation and establishment of damaging variants in effectively small populations

Name: Martin Johnsson

University: Swedish University of Agricultural Sciences

Abstract:

Domestic animal populations, as well as many animal populations in the wild, are effectively small and shrinking. In particular, in domestic animals with breeding programs, there is very strong directional selection, while breeds without modern breeding tend to be fragmented and in decline. Large-effect deleterious variants at relatively high frequencies are common enough in domestic animals that they pose applied problems for breeders. In our work, we have combined genomic data analysis with a series of population genetic models to address the loss of genetic variation in effectively small and shrinking populations, and how large-effect deleterious variants establish themselves in small populations. The results suggest the presence of transient genetic variation, predicted to be gradually lost, and that balancing selection by heterozygote advantage, even temporarily through close linkage, makes establishment of new large-effect deleterious alleles likely.

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Key words: domestic animals, population genetics, deleterious variation

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Abstract number: O38

Title: The adaptive evolution of herring to different salinities

Name: Cheng Ma

University: Uppsala Universitet

Abstract:

Understanding the relationship between genetic and phenotypic variation is a fundamental goal in evolutionary biology. For marine organisms, salinity is a crucial environmental factor affecting survival and adaptation. However, the genetic mechanisms driving adaptive evolution to different salinity levels remain largely unexplored. Herring, which are widely distributed across high-salinity Atlantic Ocean and low-salinity Baltic Sea environments, serve as an ideal model for investigating salinity adaptation. Our research reveals that copy number variation (CNV) in hatching enzyme genes supports herring adaptation to diverse salinity conditions. Specifically, we discovered a significant expansion in the copy number of a gene encoding a hatching enzyme on chromosome 26 in Baltic herring. We hypothesize that this expansion is a selective response to the low salinity of the Baltic Sea, which likely reduces enzyme activity relative to the Atlantic's marine conditions. This CNV exemplifies an evolutionary mechanism that enhances herring survival and reproductive success.

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Key words: Adpative evolution, salinity, herring, hatching enzyme, CNV

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Abstract number: O39

Title: Toward predictive evo-devo: a data-driven approach to modeling phenotypic variation

Name: Lisandro Milocco

University: Stockholm University, SciLifeLab

Abstract:

Predicting evolution is crucial for tackling challenges like population survival under climate change and controlling emerging pathogens. However, it remains limited due to the difficulty in predicting the appearance of new phenotypic variation, generated by the notoriously complex process of development. Existing approaches to model phenotypic variation fall into two main categories: statistical models, which treat development as a black box—describing but not predicting variation—and mechanistic models, which require detailed developmental information that is rarely available. In this talk, I will present a data-driven framework that addresses these limitations by modeling the emergence of variation through time delay embedding of the developing system's states. I will share preliminary in silico results using a gene regulatory network and discuss ongoing efforts to apply this framework to empirical datasets, highlighting its potential to enhance our ability to predict evolution.

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Key words: evo-devo, prediction, development, time series

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Abstract number: O40

Title: Speciation and Temporal Dynamics of Female Sperm Management

Name: Dick Moberg

University: Stockholm University

Abstract:

Understanding how traits cause reproductive isolation between diversifying lineages is a central focus of evolutionary biology. However, mechanisms causing reproductive isolation early in the speciation process are seldom studied since research has primarily focused on already formed species in the late stages of speciation. In this study, we investigate mechanisms causing early postmating prezygotic (PMPZ) reproductive isolation between two populations of Drosophila montana. In this species, crosses between populations results in reduced fertilization. We therefore hypothesized that heteropopulation crosses would exhibit different rates of sperm utilization compared to conpopulation crosses. Our findings provide partial support for this hypothesis. We observed significant differences in sperm storage dynamics in one heteropopulation cross, which exhibited a slower rate of filling their sperm storage organs and retaining sperm for a longer period compared to other crosses. This suggests that inefficient sperm utilization may be a mechanism of PMPZ reproductive isolation, potentially influenced by mismatches in sperm and reproductive tract lengths or differences in seminal fluid composition.

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Key words: Speciation, Reproductive Isolation, postcopulatory mechanisms

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Abstract number: P1

Title: The evolution of thermal performance curves across the model genus yeast

Name: Jennifer Molinet

University: Stockholm University

Abstract:

Accelerating climate change and extreme temperatures highlight the urgent need to understand the evolutionary impacts on biodiversity to develop conservation strategies for at-risk species. This study assesses heat stress adaptation across eight Saccharomyces species with varying temperature preferences sourced from diverse global habitats. A long-term evolution experiment with gradual temperature increases (25-40°C) was conducted to simulate climate change. The results showed a ~30% fitness improvement at higher temperatures in evolved populations. While cold-tolerant species had greater fitness gains, they did not reach warm-tolerant species' limits. Evolutionary trajectories of TPCs varied, with some species showing a trade-off between thermal breadth and upper thermal limit, while others increased their optimal temperature and thermal tolerance. Two main trajectories emerged: broader TPCs for genotypes with higher thermal optima and increased CTmax at the cost of maximum fitness. These findings emphasize the complexity of microbial climate responses and the need to consider species diversity.

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Key words: Saccharomyces, thermal performance curve, thermal adaptation, experimental evolution, climate change

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Abstract number: P2

Title: The tempo and mode of toxicant sensitivity evolution

Name: Iain Moodie

University: Lund University

Abstract:

Chemical pollution is a critical driver of biodiversity loss, impacting ecosystems worldwide. Species differ remarkably in their sensitivities to environmental toxicants, and understanding why is crucial to better predict ecological risks and inform conservation strategies. By considering effect concentrations (the concentration of toxicant X that produces effect Y in species Z) as quantitative traits in a macro-evolutionary perspective, we can investigate how toxicant sensitivity evolves across diverse taxa. Here, we use large ecotoxicological databases of standardised effect concentrations (>1 million empirical results) for a wide variety of toxicants and species. Combined with time-calibrated molecular phylogenies, we use a data-driven phylogenetic comparative framework to elucidate the processes and patterns that have given rise to contemporary distributions of species' sensitivities. Our analysis revealed that the tempo and mode of toxicant sensitivity evolution differed across classes of toxicants, and recovered cases of convergent evolution across deeply diverged taxa.

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Key words: macroevolution, ecotoxicology, PCM (phylogenetic comparative methods)

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Abstract number: P3

Title: Chromosomal rearrangements in Ithomiini butterflies

Name: Karin Näsvall

University: Wellcome Sanger Institute

Abstract:

Chromosomal rearrangements can act as barriers to gene flow, promoting reproductive isolation and divergence between closely related species. However, their impact on speciation rates and importance in a macroevolutionary perspective remains unclear. Here, we focus on the South American Ithomiini butterflies, a diverse group of over 400 species with varying speciation rates among genera and highly variable karyotypes (n=5-120). We aim to develop high-quality chromosome-level assemblies for 200 taxa across the Ithomiini phylogeny to investigate the relationship between chromosomal rearrangements and speciation rates. Preliminary findings reveal that rearrangements are more extensive than previous chromosome counts indicated, primarily involving inter-chromosomal fusions and fissions. We also observed significant variation in genome size correlated with transposable element expansion. In addition, we explore how chromosomal rearrangements arise and increase in frequency by examining the relationship between rearrangement rates, genetic diversity, and transposable element dynamics.

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Key words: Speciation genomics, chromosomal evolution, structural variation, genome architecture

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Abstract number: P4

Title: The seasonal clock of animals: gaining insights via a molecular evolutionary analysis

Name: Saurav Baral

University: Stockholm University

Abstract:

The daily and seasonal cycles of all animals are controlled by their circadian clock, a dynamic network of interacting genes that keeps time. These clock genes, which are regulated by a complex transcription-translation feedback loop, are essential for synchronizing animal life cycles with favorable environmental conditions, such as resource availability. Unfortunately, for many animals, their circadian clocks are becoming desynchronized with resource availability due to anthropogenic factors such as light pollution and climate change. Worsening the issue is the limited understanding of how the circadian clock functions and evolves in most species. Here, I have analyzed clock genes from over a hundred different butterfly species to show that these genes are evolving at a far higher rate than expected. Although this is a conserved system present across all animals, it is also rife with adaptive evolution, altering complex interactions between different clock genes.

Authors: Saurav Baral, Stockholm University Christopher Wheat, Stockholm University

Key words: Clock gene, Molecular Evolution, Seasonal adaptaion

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Abstract number: P5

Title: Play ontogeny in young chickens - effects of domestication, tameness, sex, and the cognitive impact of play stimulation

Name: Rebecca Oscarsson

University: Linköping University

Abstract:

It is known that young chickens display different play behaviours, but the function of these are not fully understood. Moreover, domestication is believed to have increased playfulness, and tameness is hypothesized to be the main trait driving the domesticated phenotype. Furthermore, potential sex differences in play had not been investigated in chickens. Therefore, in three separate studies, we aimed to describe potential effects of (1) domestication, (2) tameness, and (3) sex, on chicken play ontogeny. First, we compared the ancestral Red Junglefowl (RJF) and the layer hybrid of White Leghorn (WL). Secondly, we compared Red Junglefowls selected for high (RJF HF) and low (RJF LF) fear of humans. Lastly, male, and female WL were compared. Finally, in a fourth study, the effects of play stimulation on the cognitive capacities of RJF and WL were explored. The results of these projects will be presented, and the function of play discussed.

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Key words: Play behaviour, domestication, tameness, sex differences, function of play

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Abstract number: P6

Title: Genomic Erosion Through the Lens of Comparative Genomics

Name: Carolina Pacheco

University: Lund University

Abstract:

Comparative genomic analyses provide key insights for conservation by revealing genomic erosion patterns across species with different evolutionary histories. Understanding the mechanisms driving genomic erosion is crucial for species like the Mauritius parakeet, Mauritius kestrel, and pink pigeon, where conservation efforts led to demographic recovery, but genetic diversity keeps declining. Comparing the genomes of 39 bird species we found that species with larger historical effective population sizes have greater heterozygosity, but carry higher masked load, highlighting the importance of historical demography to assess species vulnerability to genomic erosion. We identified significant differences in realized load between taxonomic groups of our target species, possibly due to differences in life history traits. Structural variation analyses revealed differences in transposable elements and genomic rearrangements between groups. Our findings underscore the value of multispecies comparisons in understanding the evolutionary dynamics of genomic erosion and its relevance for biodiversity conservation.

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Key words: Genomic erosion, comparative genomics

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Abstract number: P7

Title: Have sponges stolen gene to survive without oxygen?

Name: Sofia Paraskevopoulou

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Abstract:

In animals, new phenotypic traits often emerge through gene duplications, splice variation, recombination, or even gene loss. Lateral Gene Transfer (LGT), the movement of genetic material across species borders, is another potential mechanism but is rare in animals due to constrains on vertical transfer of foreign DNA to offspring. Preliminary data from our lab suggests a potential LGT event in freshwater sponges, where the RQUA gene, likely transferred from anaerobic microbes, enables the synthesis of an anaerobiosis-specific cofactor rhodoquinone (RQ). This is unexpected, as no other animal encodes RQUA and those animals that can synthesize RQ use alternative splicing to yield a new gene product of an unrelated protein COQ2. Phylogenetic analysis suggests that freshwater sponges acquired RQUA via LGT, possibly from an euglenid protist. While RQUA expression in microbes is regulated by environmental oxygen levels, we observed subtle gene expression changes in sponges under varying oxygen conditions. Given that sponges experience tissue anoxia during contractions and asexual reproduction, we hypothesize that tissue hypoxia may drive RQ upregulation.

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Key words: gene expression, transcriptomics, confocal microscopy, sponge phenotype

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Abstract number: P8

Title: Elevated temperature changes behaviour, selection and mating system landscapes

Name: Matilda Pembury Smith

University: Stockholm University

Abstract:

Climate change-induced heat stress can impair fertility and reproductive behaviour in both sexes, with intensified effects in monogamous species due to the risk of an exclusive pairing with a non-fertile individual. Shifts in mate choice and selection for polyandry have been theorised as population fitness rescue mechanisms under climate change. However, the impact of heat stress on mating behaviour in both sexes remains poorly understood. Here, we tested how elevated developmental temperature influences reproductive behaviour using isofemale lines of the typically monandrous species Drosophila subobscura, where males provide a nuptial gift. Heat stress significantly changed male gift presentation and female acceptance, impacting mating probability and reproductive output. Additionally, female remating probability rose significantly after copulating with a heat-stressed sterile male, with remating propensity varying across genotype. These findings suggest developmental heat stress affects multiple aspects of sex-specific reproduction, underscoring how climate change may influence sexual selection and mating system evolution.

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Key words: sexual selection, mate choice, nuptial gift, temperature, mating system

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Abstract number: P9

Title: The stability of evolvability over 60 million years of Primate evolution

Name: Anna Penna

University: Lunds Universitet

Abstract:

The ability of evolving systems to change (evolvability) is deeply connected to the structure and amount of phenotypic variation transmitted from generation to generation (G-matrix). The G-matrix captures a population's immediate ability to evolve by selection and drift, making it a central parameter in quantitative genetics. Still, whether and how G evolves over prolonged evolutionary time scales is unclear. Here, we apply a comparative evolutionary quantitative genetics approach to investigate the stability of G in the primate radiation by comparing phenotypic covariance matrices (P-matrices). Based on 37 homologous 3D landmarks captured on the skull of 309 species ($N = 9868$ specimens), we estimated and compared P of 55 genera under a Bayesian framework. Our results show high levels of similarity, both in their variance structure and how they respond to selection. These findings suggest that even different shapes are governed by similar developmental systems.

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Key words: G-matrix

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Abstract number: P10

Title: Context Dependent Male Mate Choice Copying in a Livebearing Fish

Name: Arezo Shamsgovara

University: Stockholm University

Abstract:

Mate choice drives evolution, often requiring costly assessment of ornamentation, which is indicative of mate quality. To avoid these costs, individuals can copy the mate choices of conspecifics. The phenomenon of mate choice copying is well established in females, yet its occurrence in males remains controversial. Male mate choice copying could offer benefits, such as identifying receptive females, but it also involves risks, such as increased sperm competition when choosing previously mated females. In this study, we explored male mate choice copying in a livebearing fish, pygmy halfbeak (Dermogenys colletei) using a dichotomous choice assay to see if a rival male's presence affects choices. Results suggest that male halfbeaks may copy the choice of conspecifics, but that this behaviour depends on social and ecological factors. This study sheds light on the context in which males mate choice copy, offering insights into the evolution of complex male mating behaviours.

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Key words: Sexual selection, Mate choice, Mate Choice Copying, Male Mate Choice, Ornament

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Abstract number: P11

Title: Nuclear Cooperation as a Driver of Evolutionary Transitions in Fungi

Name: Mattias Siljestam

University: Stockholm University

Abstract:

The evolution of complex life has been shaped by transitions in individuality, where distinct entities combine to form higher-level organisms. In fungi, heterokaryosis—a condition where genetically distinct nuclei coexist in the same cytoplasm—provides an ideal system to study such transitions. My research focuses on Neurospora tetrasperma, a species that transitioned from homokaryosis to heterokaryosis approximately one million years ago. Using mathematical modelling within an evolutionary invasion analysis framework, I investigate how cooperation between different nuclear types drive this evolutionary shift. The study explore the conditions under which nuclear cooperation is favoured, providing insights into the mechanisms behind evolutionary transitions in individuality.

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Key words: Neurospora, Adaptive Dynamics, Evolutionary Transitions, Multilevel selection

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Abstract number: P12

Title: NA

Name: Rike Stelkens

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Abstract:

Accelerating climate change and extreme temperature events urge us to better understand the potential of populations to tolerate and adapt to new thermal challenges. Interspecific hybridization can facilitate adaptation to novel or extreme environments. However, predicting the long-term fitness effects of hybridization remains a major challenge in evolutionary and conservation biology. My lab uses experimental evolution with the powerful microbial model system budding yeast to track adaptive processes across hundreds of generations in real-time. We investigated the thermal adaptation dynamics of four species of budding yeast and their interspecific F2 hybrids, for 200 generations under extremely cold (5°C) and warm (31°C) conditions. We found significant variation in the evolutionary potential of species and hybrids. Cold-tolerant species showed larger fitness increases in warm temperature, whereas warm-tolerant species showed larger fitness gains in cold temperature. By far the largest fitness improvements occurred in hybrids, with some populations nearly quadrupling in fitness in the cold environment over the course of experimental evolution. Some hybrids exceeded both their parents in thermal adaptive potential. Reciprocal transplanting of evolved populations from the endpoint of evolution into opposite temperatures revealed that hybrids generally have greater resilience than their parents when challenged with sudden temperature shifts. Our results highlight that hybridization alters the fitness outcomes of long-term adaptation to extreme environments and may render populations more resilient to sudden environmental change, presenting both opportunities and challenges for conservation and sustainable agriculture.

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Key words: climate change, experimental evolution, fitness, hybridization, yeast, thermal adaptation

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Abstract number: P13

Title: Codon Usage Bias and Selection Patterns in Atlantic Herring

Name: Leyi Su

University: Uppsala University

Abstract:

Codon usage bias, which describes differences in the frequencies of occurrence of synonymous codons in coding sequences, is a prevalent finding in most organisms. The extent of codon usage bias is determined by many factors including gene expression level, GC content, tRNA abundance and effective population size. The Atlantic herring (Clupea harengus) is a model organism for exploring the genetic basis of ecological adaptation on account of its large effective population size. Our codon usage analyses demonstrate that the Atlantic herring shows stronger codon usage bias compared with Zebra fish and human. We then classified the synonymous mutations into three groups based on the direction of codon changes and found different selection patterns in the Site Frequency Spectra based on these three categories. However, the codon usage is largely affected by the GC3 content, so the drivers of observed stronger codon usage bias in Atlantic herring still requires more research.

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Key words: Codon Usage Bias, GC content, Genome Evolution, Site Frequency Spectrum, Natural Selection

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Abstract number: P14

Title: Natural and sexual selection in wild populations of tortoise beetles

Name: Maja Tarka

University: Lund University

Abstract:

Populations differ in their ability to adapt and evolve as a response to a changing environment. Understanding how and why these differences arise will be crucial for predicting their future. We use a novel study system for eco-evolutionary dynamics, the green tortoise beetle Cassida viridis, to understand how natural and sexual selection fluctuates between and within populations. By monitoring free ranging individual beetles in their natural habitat, we show that individuals are surprisingly sedentary, and this allows us to track them over their lives. This enables us to study how the environment, the host plant composition and phenotypic traits affect beetle survival and mating success. Our study provides valuable insights into the processes of fluctuating selection and adaptive strategies, elucidating the microevolutionary dynamics in wild insect populations.

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Key words: microevolution, quantitative genetics, insects, survival and mating, phenotyping

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Abstract number: P15

Title: Population structure and isolation in different Swedish pollinator groups

Name: Isolde van Riemsdijk

University: Lund University

Abstract:

Insect numbers and diversity are in rapid decline, also within protected areas, endangering the ecosystem functions that insects provide and conflicting with societal commitment to protect biodiversity. Functional connectivity (the degree to which landscapes facilitate the movement of organisms, and the resulting fitness effect on populations) is crucial for population persistence, enabling three major evolutionary processes

Authors: van Riemsdijk, Isolde, Nolen, Zachery, Runemark, Anna et al. Lund University, Sweden

Key words: 1) re-colonization following stochastic extinctions

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Abstract number: P16

Title: Biodiversity Genomics Intitatives - sequencing life for the future of life

Name: Olga Vinnere Pettersson

University: SciLifeLab

Abstract:

Biodiversity genomics projects, in particular sequencing reference genomes, provide an open data resource to biologists worldwide. Reference genomes of eukaryotic life enable answering a plethora of biological questions. This resource enables ground-breaking research on, e.g. evolution of functions, conservation of endangered species, understanding the basic biology, etc. In this talk, I will present the international initiatives that Sweden is involved in, as well as give several examples of applications of reference genome sequencing for understanding of evolutionary processes.

Authors: Olga Vinnere Pettersson (UU-SciLifeLab, Sweden), Robert Waterhouse (SIB, Switzerand)

Key words: Genomics, open data, evolution, biodiversity

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Abstract number: P17

Title: Inbreeding preference emerges in female guppies during more ecologically relevant mate encounters

Name: Amanda Viving

University: Stockholm University

Abstract:

Inbreeding is expected to reduce offspring fitness, known as inbreeding depression. Mate choice could help animals avoid inbreeding, but recent studies suggest that animals rarely use mate choice to avoid relatives, even when inbreeding is costly. Here, we examined the roles of sex, mating status, and social complexity on precopulatory inbreeding avoidance in guppies (Poecilia reticulata), a species experiencing inbreeding depression. Virgin and experienced male and female guppies were tested for their preference between related and unrelated partners in two experimental setups: (1) dichotomous choice and (2) free-swimming arena. In the dichotomous setup, neither sex preferred unrelated partners, but in the socially complex free-swimming arena females directed more sexual behaviors toward relatives. Mating status did not influence mate preference in either sex regardless of the experimental setup. These findings question the idea that mate preference shifts with sexual experience and underscores the importance of experimental design in researching mate choice.

Authors: Amanda Viving, Léa Daupagne, John Fitzpatrick. Stockholm University, Sweden

Key words: inbreeding avoidance, precopulatory mate choice, sex, mating status, social complexity

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Abstract number: P18

Title: Evolution and fine-scaled temperature variation in insect pest projections

Name: Loke von Schmalensee

University: Uppsala University

Abstract:

Climate change has caused changes in species' distributions, both in time and space. These shifts are projected to continue in the future, raising concerns about the spread of agricultural pests. Most climate projections are done by integrating phenotypic reaction norms with coarse climate projections, failing to incorporate evolutionary responses and important fine-scale temperature variation. Harnessing data from long-term experimental evolution under different thermal regimes in the insect pest, Callosobruchus maculatus, we project its future population growth and agricultural impact using 1-hour resolution thermal regimes, across 20 Californian sites. We use our framework to elucidate the relative contribution of evolution in different life-history traits to pest impact in a warmer world.

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Key words: Thermal adaptation, Climate change, Agricultural pests, Temporal variation

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Abstract number: P19

Title: eDNA in terrestrial animal monitoring

Name: Beilun Zhao

University: UPPSALA UNIVERSITY

Abstract:

Environmental DNA (eDNA) has become an invaluable tool for monitoring terrestrial animals, particularly for species that are challenging to detect through traditional methods. However, effective monitoring hinges on selecting appropriate sampling substrates and methods aligned with research objectives. The choice of substrate can influence species detection accuracy, affecting rates of false positives and negatives and capturing the spatiotemporal distribution of species. Our study investigates the detection biases introduced by substrates in assessing insect diversity, comparing eDNA substrates like anthill, sediment, soil, spiderweb, water, and decayed wood with traditional Malaise traps, commonly used to capture flying insects. Our analysis reveals that each substrate captures a unique taxonomic profile, with notable differences in diversity levels and species representation, underscoring the role of substrate choice in shaping biodiversity assessments. This study highlights the benefits of combining multiple substrates to reduce detection biases, enhance insect biodiversity assessments for improved ecological management and conservation strategies.

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Key words: Insect Diversity, Environmental DNA (eDNA), Malaise Traps, Substrate Bias, Biodiversity Assessment

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Abstract number: P20

Title: Understanding mitonuclear co-divergence through functional difference in Ficedula flycatchers

Name: Yishu Zhu

University: Uppsala University

Abstract:

Mitonuclear coevolution ensures metabolic function in organisms. Rapid-evolving mitochondrial genes is predicted to take the lead in this co-evolution and favour changes in nuclear alleles that either compensate for deleterious mitochondrial mutations ("nuclear compensation theory") or reinforce favourable mitochondrial mutations that ensure adaptation to new environmental conditions ("nuclear reinforcement theory"). Here, I report co-divergence of mitonuclear OXPHOS genes encoding proteins building Complex I of the OXPHOS pathway in two flycatcher species as predicted by both hypotheses. However, high-resolution phenotypic data on cellular metabolic function reveal functional differences of Complex I activity that is more in line with the "nuclear reinforcement theory" and divergent climate adaptation in these wild populations. Such mechanism could contribute to speciation through the arise of mitonuclear incompatibility between lineages.

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Key words: evolutionary biology, mitonuclear coevolution, ficedula, nuclear compensation

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Abstract number: P21

Title: Do Sharks Respond to Eyespots?

Name: Madicken Åkerman

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Abstract:

Animal colourations and patterns exemplify evolutionary adaptations driven by predation to enhance prey survival. Eyespots, characterized by concentric rings of contrasting colours, have long been assumed to reduce predation by deceiving predators, and their anti-predator role has been demonstrated repeatedly. However, although well-studied in terrestrial environments, their impact on marine predators remains largely speculative. In this study, we demonstrate that eyespots elicit different responses in terrestrial predators (red junglefowl) and marine predators (brown-banded bamboo sharks and lemon sharks). Our findings reveal that terrestrial predators hesitate when confronted with eyespotted prey, whereas marine predators show accelerated attack responses. These contrasting behaviors suggest that eyespots function differently across environments, acting as deterrents in terrestrial settings but potentially attracting marine predators. Our study demonstrates that the function of eyespots varies across predator types and environments, emphasizing the need for further exploration in marine ecosystems where the function of eyespots is less understood.

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Key words: conspicuous markings, detection-hypothesis, anti-predator colouration

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Abstract number: P22

Title: The role of a structural variant for seasonal camouflage evolution in hares

Name: Huijuan Bi

University: Stockholm University

Abstract:

Close to 21 species of mammals and birds have convergently evolved the ability to seasonally change color, but it is unclear if the molecular mechanisms underlying this phenotype are also convergent across species. Previous genomic work in hares linked white to brown variation in winter coats to pigmentation gene ASIP. We revisited this genomic data and identified an indel in ASIP associated with the ability to change color in hares. We use comparative genomics to confirmed the presence of this indel in the new PacBio reference-genome of the mountain hare. To explore the regulatory role of this mutation for the ability to change color, we annotate transcription factor binding sites (TFBS) in the indel region that are shared across color changing species. We identified several shared TFs in winter white hares, notably RBPJ, which is involved in maintaining proper hair pigmentation, and Prdm1, which plays a role in photoreceptor regulation.

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Key words: seasonal camouflage, ASIP, transcription factor

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Abstract number: P23

Title: NA

Name: Omolola Afolabi

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Abstract:

NA

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Key words: NA

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Abstract number: P24

Title: On the origin of an insular hybrid butterfly lineage

Name: Jesper Boman

University: Uppsala Universitet

Abstract:

We report the discovery of a European hybrid butterfly lineage, a finding that can be considered surprising given the intense and long-term study of European butterflies. The lineage we describe is mainly inhabiting an island in the Baltic Sea and was previously designated as a subspecies (horkei) of one of the parental species (Aricia artaxerxes). By analysing whole-genome resequencing data, we determine that horkei originated by hybridization between the non-sister species A. artaxerxes and A. agestis. This hybridization event occurred approximately 54,000 years ago, predating the last glaciation of the current distribution range. Horkei must therefore have persisted long enough to be able to colonize its current range, despite that this area lies between the current distributions of the parental species. The hybrid origin, the maintenance of genomic integrity across times of dramatic climate change suggest that horkei could be in the process of hybrid speciation.

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Key words: Biodiversity, Speciation, Hybridization, Hybrid speciation, Butterflies

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Abstract number: P25

Title: NA

Name: Andre Bourbonnais

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Abstract:

Insect herbivores exhibit remarkable diversity, with most species specializing on specific host plants. The intricate relationships between these herbivores and their host plants are strong drivers of insect diversification and speciation. Although the influence of microbial symbionts on these evolutionary processes is acknowledged, it remains unclear whether symbionts act as leading or adaptive factors in host divergence when adapting to new ecological niches.

To investigate the evolutionary processes that act on the symbiont as its host adapts to a novel host plant, I assembled and analyzed the metagenome-assembled genome (MAG) of the unculturable symbiont, Candidatus Stammerula tephritidis (Stammerula), which is maternally transmitted by the two host races in Tephritis conura (Diptera:Tephritidae). The assembled MAG showed characteristic signs of genome reduction typically found in obligate symbionts. In this study, the MAG of Stammerula was annotated and compared across different populations.

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Key words: metagenomics, population genetics, symbiont, ecological speciation

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Abstract number: P26

Title: Long-term genetic consequences of admixture in a sand lizard population

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Abstract:

The sand lizard (Lacerta agilis) occurs in fragmented populations in southern Sweden, including small, isolated populations that are of conservation concern. These populations have low genetic diversity and show signs of inbreeding depression. The semi-natural population of Stora Keholmen was established approximately 20 years ago by interbreeding different Swedish sand lizard populations. Stora Keholmen appears to have recovered from the inbreeding depression of its main parental population and has comparatively high genetic diversity. Here, we use whole genome sequencing to compare genetic diversity of the main parental population, the inbred Asketunnan population, to the admixed Stora Keholmen population. We determine genomic diversity within and between both populations and identify regions of high diversity in the admixed population. Similarly, we determine if the inbred population has retained diversity in some genomic regions, which may indicate ongoing selection.

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Key words: Comparative genomics, admixture, conservation

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Abstract number: P27

Title: The Swedish Reference Genome Portal: A new service facilitating access and discovery of genome data studied in Sweden

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Abstract:

The Swedish Reference Genome Portal (https://genomes.scilifelab.se/) is a new service aiming to facilitate access and discovery of genome data of non-model eukaryotic species studied in Sweden. For each species, the portal aggregates taxonomic data, genome assemblies and annotation tracks, metadata, and links to external resources in a single place. The genome data is displayed in an embedded JBrowse 2 genome browser, allowing for visual representation of a variety of data types, and sharing of sessions between users. With this service, we aim to make genomics data more accessible for all users regardless of their prior level of bioinformatics knowledge, and promote FAIR data sharing. The poster will introduce key features of the Genome Portal and illustrate how researchers affiliated to Swedish institutions can submit their data. We are always interested in new additions to the portal! If you are interested, please contact us at dsn-eb@scilifelab.se.

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Key words: genomics

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Abstract number: P28

Title: Temporally stable parallel color cline in the shell of a marine gastropod from four coastal inlets

Name: Juan Gefaell

University: Lund University

Abstract:

The evolutionary ecology of L. saxatilis' shell color polymorphism has been relatively little studied. Here I describe a repeated color cline in the populations of L. saxatilis from the Rías Baixas (NW Iberian Peninsula), a series of four coastal inlets that arose from immersion of river valleys around 3000 years ago. We provide direct evidence that this color cline has remained relatively stable during the last 46 years. I also show, based on an analysis of snails from 55 localities across the four Rías Baixas, that there is a strong statistical association between the most prevalent color morphs and a suit of environmental and shell morphological variables, pointing to strong ecological selective pressures maintaining the cline and trait covariation. As the populations of L. saxatilis from the Rias Baixas got isolated relatively early, this putative example of parallel evolution has a bearing on discussions about predictability and contingency in evolution.

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Key words: L. saxatilis, evolutionary ecology, color polymorphism, gastropod shell, parallel evolution

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Abstract number: P29

Title: Synonymous site constraint in mammals supports the unwanted transcript hypothesis

Name: Matthew Christmas

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Abstract:

It is known that selection acts on synonymous sites in mammals, but the functions held by synonymous sites are largely unresolved. Recently, the unwanted transcript hypothesis (UTH) has been presented as a potential explanation for evolutionary constraint at synonymous sites in species with low effective population sizes, such as humans. Selection for higher GC content and against mutations that alter splicing in native transcripts is predicted to shape synonymous site content and protect against unwanted transcripts. Utilising the Zoonomia alignment of 240 placental mammal genomes and single-base resolution constraint scores, we interpret mammalian synonymous site constraint in this context. We show that 20.8% of four-fold degenerate (4d) sites are under significant constraint, with a strong GC bias. We see evidence for higher 4d constraint in species with lower effective population sizes and greater genome transposable element content, as predicted by the UTH. Genes enriched for synonymous site constraint are integral to organismal viability through their involvement in embryo development and transcriptional regulation. Overall, our results provide support for the UTH and we conclude that it is the most viable model for explaining selection on synonymous sites in mammals

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Key words: Evolutionary constraint, synonymous sites, mammals, GC content

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Abstract number: P30

Title: NA

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Abstract:

NA

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Abstract number: P31

Title: NA

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Abstract:

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Abstract number: P32

Title: Habitat complexity alters the strength of sexual selection on brain size in male and female halfbeaks (Dermogenys collettei)

Name: Léa Daupagne

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Abstract:

Animals often reproduce in complex environments, which should generate selection for increased detectability in signaling traits. However, the extent to which sexual traits have evolved to overcome the challenges of interacting in complex environments remains understudied. We examined whether habitat complexity influences sexual selection in the Pygmy Halfbeak, Dermogenys collettei, a small livebearing freshwater fish. Using free-swimming arenas, we created low- and high-complexity environments and observed mating behaviors in mixed-sex groups of three males and three females. While the opportunity for sexual selection did not differ significantly between environments for either sex, we detected positive selection for both male and female brain size in open arenas, but not in complex habitats. Interestingly, no clear selection on male or female ornamentation was detected in either environment. Our findings suggest that habitat complexity may limit selection pressures on cognitive traits, such as brain size, without affecting visual ornamentation's role in mating success.

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Key words: Sexual selection, habitat complexity, mate choice

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Abstract number: P33

Title: NA

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Abstract:

NA

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Key words: NA

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Abstract number: P34

Title: Innovative helment complexity is phylogenetically conserved

Name: Marisol De la Mora Curiel

University: UNAM/ENES Juriquilla

Abstract:

The genomic data from ultraconserved elements were used to determine the evolutionary relationships among species of membracids, representing taxonomic diversity within the subfamilies and utilizing fresh specimens. The question of interest is whether the complexity of the helmet has evolved multiple times, or if organisms with similar helmet shape have a close evolutionary relationship, suggesting that the shape may be derived from a common ancestor. Our results show concordance with evolutionary relationships in previously published works

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Key words: the clades have a bootstrap support of 100, and the morphogeometric data support the hypothesis that similar pronota are found among phylogenetically close organisms

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Abstract number: P35

Title: Evolution of sexual dimorphism in resource use

Name: Stephen De Lisle

University: Karlstad University

Abstract:

Sex differences in ecologically important traits are common in animals and plants, and prompted Darwin to first propose an ecological cause of sexual dimorphism. Yet a role for ecological resource competition in the evolution of sexual dimorphism has never been directly demonstrated and remains controversial. I used experimental evolution in Drosophila melanogaster to test the hypothesis that resource competition can drive the evolution of sex differences in diet. Over just a handful of generations, offspring from flies evolved in low-resource, high-competition environments show elevated sexual dimorphism in diet preference compared to both the ancestor and populations evolved on high-resource availability. Expanding this design to include a manipulation of sex ratio indicates that over longer timespans diet evolves in predictable ways in response to operational sex ratio. These results indicate an important role for both ecology and mating system in driving the evolution of sexual dimorphism in ecologically important traits

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Key words: Sexual dimorphism, evolutionary ecology, quantitative genetics

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Abstract number: P36

Title: Exploratory behavior in the hybrid Italian sparrow (Passer italiae) and its parental species

Name: Samantha Duhé Jones

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Abstract:

To address how behavioral traits evolve in hybrid lineages, we use the homoploid hybrid Italian sparrow (Passer italiae), whose parental species are the commensal house sparrow (P. domesticus) and non-commensal Spanish sparrow (P. hispaniolensis). We use a novel environment test to investigate whether exploration in hybrids is intermediate, mosaic, or transgressive using lineages of Italian sparrow from Crete, Corsica, and Sicily, differing in parental genetic contribution, as well as the two parental species and male F1 hybrids. We recorded time spent on features, latency to first feature, number of unique features visited, total visits, and two principal components derived therefrom. Across measurements, the most important predictor is the interaction of population with sex. House sparrows and Italian sparrow females are more active than Spanish sparrows and Corsican and Sicilian males, while Cretan males are transgressively active. In conclusion, both commensal Italian sparrows and F1 males generally have intermediate exploratory behavior.

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Key words: hybridization, behavior, commensalism, intermediacy, transgression

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Abstract number: P37

Title: Discovering genotype-phenotype relationships with machine learning and the Visual Physiology Opsin Database (VPOD)

Name: Seth Frazer

University: University of California Santa Barbara

Abstract:

Predicting gene function from genetic variation is crucial for fields like bioengineering and evolutionary biology. Opsins, light-sensitive proteins affecting phenotypes like color vision, are a well-studied model gene family. However, existing opsin data is scattered and inaccessible, hindering systematic analysis.

We introduce the Visual Physiology Opsin Database (VPOD), compiling 1211 unique opsin genotypes and corresponding light absorption phenotypes (lambda-max) from 111 publications. Using VPOD and machine learning, we demonstrate accurate lambda-max prediction, accounting for non-additive mutation effects, and identification of critical amino acid sites.

This ability to predict gene function from sequence alone allows exploration of molecular evolution, ecological connections, and protein design. VPOD and our models provide a foundation for future research on gene families with quantifiable phenotypes.

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Key words: Machine learning

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Abstract number: P38

Title: Can co-flowering species influence on each other's evolution? Insights from food-deceptive orchids in Öland

Name: Yedra García

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Abstract:

Interactions between co-flowering species for shared pollinators are common and can influence plants' reproductive success and ultimately natural selection acting on floral traits. However, studies testing for pollinator-mediated reproductive interactions in local communities are rare mainly due to lack of appropriate statistical methods. Here, we applied recent statistical models within the Hierarchical Modelling of Species Communities (HMSC) framework to test for pollinator-mediated interactions among three co-flowering species and estimate phenotypic selection on floral traits simultaneously on the three species. To do that, we recorded phenotypic traits, flower abundance and reproductive fitness of three food-deceptive co-flowering orchid species across 75 1m2 patches with varying species composition. Our study showed species-species associations influencing the reproductive fitness of plant species at local communities and yield new insights on the biotic factors influencing the success of food-deceptive pollination systems. Moreover, our work provides a promising approach towards understanding natural selection at the community level.

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Key words: reproductive interactions, pollinators, natural selection, orchids, community

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Abstract number: P39

Title: Taming Evolution

Name: Johanna Gjøen

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Abstract:

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Authors: The impact of selection and domestication on behaviour in Red Junglefowl

Key words: We investigated long-term selection effects on tameness in Red Junglefowl (Gallus gallus), at the 13th generation, using 40 birds: 20 from each line, with equal male-female distribution in the high-fear line, and 12 males and 8 females in the low-fear line. Previous studies have shown significant differences in cerebellum size and neuron density between Red junglefowl selected for high or low-fear of humans. Hence, we focused on traits associated with the cerebellum, including motor coordination, balance, as well as social navigation, to assess selection impacts. Behavioural tests (obstacle course, rotarod, and Y-maze) were used to explore the correlation between tameness levels and cerebellar function. Preliminary observations indicate potential motor and social trait differences between selection lines, offering insights into cerebellar adaptability under selective pressures. Complete results will provide more insight into the relationship between cerebellum-linked behaviours and selection, as well as cerebellar adaptation in evolutionary processes.

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Abstract number: P40

Title: Meta-analytical evidence for frequency-dependent selection across the tree of life

Name: Miguel Gómez

University: Karlstad University

Abstract:

Explaining the maintenance of genetic variation in fitness-related traits within populations is a fundamental challenge in ecology and evolutionary biology. Frequency-dependent selection (FDS) is one mechanism that can maintain such variation, especially when selection favours rare variants (negative FDS). However, our general knowledge about the occurrence of FDS, its strength and direction remain fragmented, limiting general inferences about this important evolutionary process. We systematically reviewed the published literature on FDS and assembled a database of 747 effect sizes from 101 studies to analyse the occurrence, strength, and direction of FDS, and the factors that could explain heterogeneity in FDS. Using a meta-analysis, we found that overall, FDS is more commonly negative, although not significantly when accounting for phylogeny. An analysis of absolute values of effect sizes, however, revealed the widespread occurrence of modest FDS. However, negative FDS was only significant in laboratory experiments and non-significant in mesocosms and field-based studies. Moreover, negative FDS was stronger in studies measuring fecundity and involving resource competition over studies using other fitness components or focused on other ecological interactions. Our study unveils key general patterns of FDS and points in future promising research directions that can help us understand a long-standing fundamental problem in evolutionary biology and its consequences for demography and ecological dynamics.

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Key words: frequency dependent selection

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Abstract number: P41

Title: Unravelling the Cost of Pigmentation: Gene Knockouts and Their Effects in Pieris brassicae

Name: Eleine Gómez Sundberg

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Abstract:

Butterflies are known for their vibrant colouration, but the costs of producing these colours is not well understood. Pieris brassicae use pteridine for their white pigments, which are stored in pigment granules known as pterinosomes. Transport of pteridine precursors is mediated by an ABC transporter complex formed through the heterodimerization of white and brown. In lepidoptera, the ok gene, a paralog for brown also heterodimerize with white. To explore the functional role of these genes, we used CRISPR/Cas9 to knockout white, brown, and ok in P. brassicae embryos. Mutant phenotypes resulted in various developmental and pigmentation defects (translucent larval epidermis, pupal colour disruption). Adult butterflies displayed suppressed wing development, and absence of wing pigmentation, along with distinct eye colour changes. These findings reveal the relative roles of the genetic mechanisms behind butterfly pigmentation and ultimate shed light on the cost of producing colour.

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Key words: Pteridine Transport, Butterfly coloration, ABC transport complex, CRISPR/Cas9

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Abstract number: P42

Title: Lens canariensis - Two millennia of lentil cultivation on the Canary Islands

Name: Jenny Hagenblad

University: Linköping University

Abstract:

During more than a millennium, agriculture in the Canary Islands relied on a limited number of crop species. During this time the islands were isolated from each other and the mainland making each island an independent evolutionary replicate of crop plant - human - nature interrelations. The European discovery and conquest of the islands in the 15th century turned a Neolithic society into a globalisation hub between the old and new world with dramatic consequences for the human population and for agriculture.

Through genetic analyses of present-day genebank accessions, combined with aDNA analyses of specimens more than a millennium old, the evolution of the Canarian lentil has been investigated. The results show the consequences of isolation and globalisation as well as the effects of both climate and human society and hint to a role of Canarian lentils in the cultivation and consumption of lentils far beyond the Canarian archipelago.

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Key words: aDNA, crop evolution, agrarian history, plant - human interrelations

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Abstract number: P43

Title: Cost of spontaneous dispersal is not sufficient to drive adaptive evolution in a spatially structured habitat

Name: Subhasish Halder

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Abstract:

How populations adapt to the ecological challenges related to spatial-structuring— a common attribute of most naturally occurring populations, is poorly understood. Previously, using laboratory adapted populations of Drosophila melanogaster I have shown fitness cost of living under spatial-structuring owing to sex-biased spontaneous dispersal. Here, I took an experimental evolution approach to investigate the evolvability of spontaneous dispersal. Following 30+ generations of maintenance in a structured habitat with inter-patch movement, I found experimental and control populations do not differ in dispersal related traits. Females from experimental populations continued to pay reproductive and survival costs when subjected to experimental habitat structuring, indicating no sign of adaptation to population structuring. I argue that adaptation to habitat structuring depends on the intricate details of an ecology and discuss the problems in the detection of heritability in spontaneous dispersal including non-transitivity in dispersal syndrome, and the caveats and confounds of my experimental paradigm.

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Key words: Population spatial-structuring, Sex-biased dispersal, Experimental evolution

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Abstract number: P44

Title: Adapting fast and slow: The repeatability and molecular basis of plastic and genetic responses to temperature extremes

Name: Alex Hart

University: Uppsala University

Abstract:

Theory predicts that phenotypic plasticity can play a pivotal role in evolution by impeding or facilitating genetic adaptation. Thus, to predict how populations will respond to climate change, we need to understand how plastic and genetic responses interact during thermal adaptation.

We used experimental evolution in seed beetles to unravel plastic and genetic responses to temperature stress. Replicate lines were generated from three geographic origins, and then adapted to cold, ancestral, or hot temperature for ~100 generations. Gene expression was then measured at the three temperatures.

In line with previous findings, genetic changes in expression often counteracted immediate plastic responses, suggesting that genetic compensation is a major mode of thermal adaptation across the transcriptome. However, this pattern was much stronger and more repeatable across genetic backgrounds for cold-adaptation compared to heat-adaptation. We harness pool-sequencing and phenotypic data from the same lines to explore the underlying mechanisms behind these qualitative differences.

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Key words: genomics, climate change, thermal adaptation, genetic plasticity

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Abstract number: P45

Title: Gone with the wind: exploring a vanished African rock doves hybrid zone in the Sahara Desert

Name: Germán Hernández Alonso

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Abstract:

A previous genomic study of rock doves (Columba livia) identified a genetically distinct population in West Africa, possibly representing a new species. This divergence is hypothesized to have arisen through cycles of allopatry during the dry and wet Sahara periods. Based on the Refugia Theory and observed admixture patterns, it was proposed that a hybrid zone existed in the Sahara during its last green period. This project aims to test the existence and location of this extinct hybrid zone by analyzing whole-genome sequences from six historical rock doves from previously unsampled populations in the Central Sahara and West Africa, in addition to existing genomic data. The findings confirm the presence of the hybrid zone, with a likely location in the mountainous and hilly regions of northwest Africa. Additionally, the results reveal a strong population structure and confirm the genetic divergence of West African rock doves.

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Key words: Population Genomics, Columba livia, Speciation, Refugia theory

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Abstract number: P46

Title: NA

Name: Amparo Herrera-Dueñas

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Abstract:

NA

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Key words: NA

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Abstract number: P47

Title: Genetic Mechanisms of Host Shifting in Acrocercops transecta: A Linkage Map Analysis Using Gras-Di

Name: Bin Hirota

University: Kyoto Prefectural University

Abstract:

Host shifts in phytophagous insects often leads to genetic divergence between populations and adaptation to a novel host plant can promote speciation. A leaf-mining moth, Acrocercops transecta, consists of two host races that are associated with either Juglandaceae or Lyonia ovalifolia (Ericaceae). To understand the genetic background of shifting to Lyonia, backcross hybrids were propagated between the two host races. Genotyping by Random Amplicon Sequencing-Direct (Gras-Di) was used to construct a linkage map and to identify genetic regions responsible for oviposition preference and larval performance. We will show the genomic architecture of host shifting between distatly related host plants and discuss its consequences for ecological speciation in A. tranescta.

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Key words: host race, speciation, phtophagous insects, larval performance ,oviposition preference

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Abstract number: P48

Title: Skull bones of contrasting developmental origins influence both micro- and macroevolution in lacertid lizards

Name: QUENTIN HORTA-LACUEVA

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Abstract:

Vertebrates are remarkable for their diversity of skull shapes, the evolvability of which might be determined by the specific variational properties of bones conferred by two types of embryonic tissues (the neural crest vs. the mesoderm). We tested this hypothesis by studying skull shape in the highly diverse family of Lacertid lizards, using X-ray microtomography-based (CT) 3D morphometric analyses. At the microevolutionary scale, we quantified variation in skull shape across populations of European wall lizards (Podarcis muralis) known to exhibit extreme morphological variations. At the macroevolutionary scale, we compare skull shape across more than 150 lacertid species. We quantified the contribution of the main skull bones to patterns of variation with regards to their neural crest or mesoderm origin. Family-level disparity patterns concordant with the variability observed in P. muralis< would reveal if and how the neural crest biology underlies the possible integration of micro- and macroevolutionary processes.

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Key words: skull mophology, developmental biases, micrevolution, macroevolution, geometric morphometrics

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Abstract number: P49

Title: NA

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Abstract:

Understanding how environmental signals are sensed by organisms and how such signals lead to regulatory variation that induce changes in phenotypes are important if we are to understand how organisms adapt to changing environments. In many insects a particular case of this is wing polyphenism, the environmentally induced development of small or large wings. This is observed in several different waterstriders and we have combined tissue specific transcriptomic analyses with functional genomic tools to demonstrate that the Fat/Hippo pathway control this wing polyphenism in Gerris buenoi. How this occur is however unknown and here we examine the potential role of alternative splicing as well as hormonal assays to try to identify the upstream regulator of Fat/Hippo. Our results implicate the involvment of a new GRN in wing polyphenism and demonstrate the diversity of regulatory mechanism involved, despite a shared phenotypic basis across hemimetabolous insects for wing polyphenism.

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Key words: phenotypic plasticity, gene regulation, developmental plasticity, alternative splicing

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Abstract number: P50

Title: Conservation genomics of wall lizards (Podarcis muralis) in the UK

Name: Santiago Jose Avila Quintero

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Abstract:

Small populations experiencing inbreeding depression may initiate a purging process, where natural selection gradually eliminates strongly deleterious mutations. Introduced populations frequently exhibit a lag phase proceeding their expansion, which may involve purging. Here we studied wall lizards (Podarcis muralis) in the UK, where multiple introductions from France and Italy have given rise to isolated, small populations. These offer a unique opportunity to study their population genomics and test for purging of deleterious mutations using independent replicates. We will present our initial results on the genetic structure of these populations, using analyses based on whole-genome data from both introduced and native populations. These analyses will help identify the precise origins of the introduced populations. Additionally, we are assessing genomic diversity and investigating signs of inbreeding across these populations. Our ongoing exploration includes examining deleterious mutations and potential purging effects, providing unique insights into the genetic status of these populations.

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Key words: Conservation genomics, evolutionary genomics, introduced species, Wall lizards, purging.

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Abstract number: P51

Title: Metagenomic reconstruction of the mammoth steppe flora from 48,000 BP based on the steppe bison intestinal content

Name: Chenyu Jin

University: Centre for Palaeogenetics

Abstract:

During the last Pleistocene cold stage (115,000 - 11,700 years ago), the non-glaciated part of Arctic Eurasia exhibited a distinctive plant composition consisting of steppe and xerophilous arctic plants adapted to a dry and cold climate. This vegetation formed the Pleistocene mammoth steppe, which provided a habitat for large herbivores like mammoths (Mammuthus primigenius) and steppe bison (Bison priscus). In this study, we analyzed a plant paleo-community of the Arctic mammoth steppe through DNA sequencing of the well-preserved intestinal content in a bison ice mummy, known as the Alazeya steppe bison, which was discovered in the Kolyma Lowlands in northeast Russia in 2009 and dated to >48,000 14C years before present. We leveraged the power of plant genome-wide and skim genome accessions to maximize the retrieval of the sequence reads belonging to plant genera. Macrofossil analysis of this sample revealed a plant composition resembling a saline meadow. In line with macrofossil evidence, we identified alkali grass (Puccinellia sp.) indicating high salinity, and Larch (Larix sp.) in the DNA data of the steppe bison sample. The Larch (Larix) and the range of most likely species of willow (Salix) are indicative of cold temperatures and paludification. We also confirmed the presence of plant genera typically associated with arid soil conditions such as Artemisia and Koeleria, while genera Phippsia, Alopecurus, and Festuca could suggest high soil water content, at least seasonally. Some of these taxa were not previously identified in this material by macrofossil analyses. Hence, the use of metagenomic approaches combined with comprehensive reference databases allows us to obtain a more detailed view of the mammoth steppe vegetation and provides extended interpretations of soil conditions.

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Key words: shotgun sequencing, metagenomic, Middle Pleistocene

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Abstract number: P52

Title: Long-term use of Concept Inventory of Natural Selection on Swedish University students shed light on difficult concepts and identifies improved English skills over the years

Name: Anna M Johansson

University: Swedish University of Agricultural Sciences

Abstract:

A concept inventory is a set of multiple-choice questions, where the wrong answers correspond to common misconceptions. We translated the Concept Inventory of Natural Selection (CINS) to Swedish and used have used the English and Swedish versions since 2012. The concept ”Change in a population” has consistently been most difficult for the students with the misconception ”Learned behaviors are inherited” getting the most answers alongside “Mutations occur to meet the needs of the population”. Interestingly, the same question asked about different species indicates that choice of species in a question can have an impact on how students perceive a concept. Overall, there are differences between students that gets the questions in Swedish or English. During the first years it took the students longer time to answer questions posed in English than in Swedish. In recent years the difference in answering time has disappeared, indicating an improved ability to read English.

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Key words: evolution, education, language

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Abstract number: P53

Title: Avian cognition: the influence of sleep

Name: Robin Johnsson

University: Franklin & Marshall College

Abstract:

Cognition, encompassing the processes through which animals acquire, store, and use information, is vital for survival across taxa. Notably, cognitive functions vary both between and within species, yet the underlying mechanisms remain largely unexplored. This presentation focuses on sleep, a critical but often overlooked neurophysiological phenomenon. Remarkably, despite a separation of 300 million years of evolution, both mammals and birds have independently evolved two unequivocal sleep states: non-rapid eye movement (NREM) sleep and REM sleep. Research indicates that these sleep states enhance cognitive processes in both groups, particularly in relation to learning and memory consolidation. During wakefulness, new memory traces are acquired and encoded in the brain, and subsequent sleep stabilizes and enhances newly formed memories. Conversely, sleep loss can hinder these neurological processes, resulting in impaired cognitive functions required for ideal behavioural performance. In this presentation, I will summarize the current research on sleep-dependent cognition in birds.

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Key words: cognition, sleep, birds

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Abstract number: P54

Title: NA

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Abstract:

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Key words: NA

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Abstract number: P55

Title: The role of chromosomal inversions in adaptation to salinity stress in Atlantic cod

Name: Rebecca Krohman

University: University of New Brunswick

Abstract:

Recombination is suppressed within inversions allowing these chromosomal regions to evolve separately and causing them to spread quickly through populations if they allow an individual to adapt better to local conditions. Individuals who contain an inversion with locally adapted alleles will be more likely to survive in a population exposed to environmental stressors. Atlantic cod is an ecologically, culturally, and economically important species and classified as endangered due to previous overfishing. Cod contains multiple inversions throughout its genome. Using common garden experiments, I will identify when mortality occurs and how inversion genotype frequencies change when the early life of cod are exposed to salinity stress. This study will directly test which genomic regions influence the survival of early life stages of cod in specific environmental conditions, allowing for strong inferences regarding which genotypes are adaptive. My results will help inform management and conservation strategies to increase cod population size.

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Key words: Atlantic cod, Chromosomal inversion, salinity stress, common garden experiment

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Abstract number: P56

Title: The frequency, drivers and consequences of introgression among Swiss ants revealed by large-scale genotyping

Name: Guillaume Lavanchy

University: Lund University

Abstract:

Hybridization and the resulting introgression are increasingly recognized as major forces driving species and genome evolution, but estimating its frequency in nature is challenging. Here, we genotyped over 4100 individuals belonging to 40 species from seven ant genera using ddRAD sequencing to screen for signatures of admixture, indicative of contemporary introgression. We found that the proportion of species engaging in introgression is much higher than previous estimates, but the amount of introgression is very low in most cases. This suggests that many species introgress a little, contrasting with previous findings of abundant hybridization between only a few species. We found support for the prediction that introgression is more frequent between species with overlapping mating phenology and low genetic divergence, indicating that both behavioural barriers (pre-mating) and incompatibilities (post-meiotic) play important roles in shaping introgression in these ants. Introgression contributed to overall genetic diversity, but moderately in most cases.

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Key words: introgression, hybridization, evolutionary genomics

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Abstract number: P57

Title: Investigating the segregation patterns of gCNVs

Name: Freja Lindstedt

University: Uppsala University

Abstract:

Gene copy number variations are pervasive in eukaryotic genomes, but understudied. Open evolutionary questions include gCNV duplication rates, segregation patterns and impact on recombination. Previously we identified gCNVs across 25 Brassicaceae species. Using this, I have designed crosses to investigate the evolution of target gCNVs in Capsella rubella.

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Key words: gCNVs, evolution, Brassicaceae

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Abstract number: P58

Title: NA

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Abstract:

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Abstract number: P59

Title: Flower allometry and its relationship with pollinators along an altitudinal gradient

Name: Sissi Lozada Gobilard

University: Lund university

Abstract:

Flower traits have been shown to be related to breeding systems (outcrossing vs. selfing), pollinators and can vary along environmental gradients. Environmental variation along altitudinal gradients is commonly associated with changes in the diversity of plants and animals, making them ideal systems to study variation in flower traits and its relationship with pollinators. We measured flower traits of 20 plant species and observed their pollinators (flower visitors that touched reproductive parts of the flower) along an altitudinal gradient (1000-4500m) in the tropical Andes of Bolivia. Flower traits included flower size, entrance diameter, flower length and anther-stigma distance. In particular, we compared allometries of stigma-anther height along the gradient. In this study we test the hypothesis that anther-stigma correlations is stronger at higher altitudes, assuming that at higher altitudes the conditions are harder, pollination is less reliable and therefore selfing plants species would be more common. Additionally, we tested whether allometric slopes for fit traits are shallower than size traits, and how they vary among pollinators.

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Key words: Flower traits, flower evolution, altitudinal gradient, tropical Andes, Bolivia

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Abstract number: P60

Title: Single-cell sequencing suggests a conserved function of Hedgehog-signalling in spider eye development

Name: Brenda Irene Medina Jiménez

University: Stockholm University

Abstract:

Spiders evolved different types of eyes, commonly called primary and secondary eyes. Arthropod eye development is best understood in the vinegar fly Drosophila melanogaster, which evolved three types of eyes, the larval eyes, ocelli and compound eyes. The gene regulatory networks that underlie their development exhibit a conserved core network that attest of similarities between these eyes. Using members of this core network as candidate genes, studies have revealed crucial differences such as the apparent lack of some key factors in some groups of arthropods, including spiders. By analysing cell transcriptomes from spider embryos undergoing organogenesis, we found that Hedgehog (Hh)-signalling seems to be involved in eye development in the spider Parasteatoda tepidariorum and demonstrated that this involvement is conserved in spiders. Additionally, we identified genes that are expressed in the developing eyes of spiders, but that have not been studied in this context before.

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Key words: Arthropod Evolution, Arthropod Head Development, Eye Development, Visual System Development

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Abstract number: P61

Title: Comparative genome annotation for gene family evolution analysis

Name: Milena Trabert

University: Uppsala University

Abstract:

Gene duplications and deletions are common in many eucaryotes, and their effect on phenotypic evolution is of great interest. The statistical framework for these analyses has been developed when the first whole genome sequences became available, and corresponding software is well established. Thanks to the increasing amount of whole genome sequences and annotations available across the whole tree of life, this type of analysis is becoming very accessible and shines new light on many previously unknown examples of phenotypic evolution through gene family expansion or contraction. Unfortunately, the results can be biased through the input data, since it is difficult to distinguish for example if a gene was deleted or merely not annotated in a species. In my work, I am evaluating different annotation methods and different types of reference data for a uniform annotation pipeline to assess the effect of the input data on gene family birth-death dynamics.

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Key words: genome annotation, comparative genomics, gene family evolution

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Abstract number: P62

Title: Visual opsin expression in the damselfly Ischnura elegans

Name: Natalie Roberts

University: Lund University

Abstract:

Visual opsins affect color vision in animals. The damselfly, Ischnura elegans, relies on vision for mate detection and their eyes are characterized by numerous opsin gene duplicates. Female I. elegans express three genetically determined color morphs, with the two most common morphs in Sweden being characterized by blue and green thorax coloration (androchromes and infuscans, respectively). Previous studies have found that exposure to androchrome or infuscans females increases male preference for those morphs and that, in the field, males prefer the most common morph in their population. To assess whether opsin genes are differentially expressed based on previous experience, which may explain male preference based on previous exposure, we quantified opsin gene expression in males that had encountered either androchrome or infuscans females for a 2-day period. Results can explain how visual based mate preferences in this dynamic, polymorphic species.

Authors: Roberts, Natalie; Lund University; Sweden Svensson, Erik; Lund University; Sweden

Key words: opsin genes, mate choice

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Abstract number: P63

Title: Impact of Domestication, Recent Selection, and Interactions on Behavioural Synchronisation in Dogs and Wolves

Name: Lina Roth

University: Linköping University

Abstract:

This study explored how dogs synchronise their behaviour with their owners, focusing on immediate interactions, breed, and domestication effects. Conducted in outdoor enclosures, the test involved 30 seconds of walking and 30 seconds of standing still. Three studies were performed: Study A tested 20 companion dogs after Ignore, Pet, and Play treatments, showing dogs adjusted their movements to match their owners regardless of treatment. Study B involved 24 ancient breed dogs, 17 solitary hunting dogs, and 20 companion dogs, all synchronising their movements with their owners. Study C tested six socialised pack-living wolves and six pack-living dogs, finding no movement synchronisation with handlers. The results suggest that dogs living with humans synchronise their movements with their owners, while pack-living wolves and dogs do not, indicating that interspecies behavioural synchronisation may depend on the extent of human interaction.

Authors: Jasmine Heurlin, György Barabás, Lina S V Roth

Key words: Domestication, Behavioural synchronisation, Wolves, Dogs

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Abstract number: P64

Title: New genomic data of the Levant confirm mobility patterns beyond the regions of West Asia

Name: Tina Saupe

University: Uppsala University

Abstract:

With the growing availability of ancient human genomes worldwide, researchers of different disciplines have been increasingly interested in linking changes in genetic-related ancestries, socio-cultural-related patterns, and linguistics focusing particularly on West Asia as the bridge between the geographical regions. Genetic studies have shown that genetic-related ancestries in West Asia were introduced mostly during the Bronze-Iron Age transition, hence the variety of genetic-related ancestries for the North of the Levant is still unclear. Here, we want to present newly generated genetic data of archaeological sites located in the Levant and place them in context with published ancient genomes focusing on possible mobility patterns throughout West Asia. Due to the rather bad preservation of human skeletal remains from this geographical region, we focused firstly on the improvement of the laboratory workflow by applying a target enrichment via in-solution hybridisation on selected individuals. Our first observations of the genetic results have shown a similar picture of genetic-related ancestries supporting previous findings.

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Key words: ancient DNA, Levant, Bronze Age, Target Enrichment

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Abstract number: P65

Title: Heritability of shield size and shape in the green tortoise beetles Cassida viridis

Name: Erica Winslott

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Abstract:

The amount of additive genetic variance affects how fast a population can respond to selection, but how additive genetic variance varies over time and space in wild populations is not well understood. One way to assess additive genetic variance is by estimating heritability. We used the green tortoise beetle, Cassida viridis, a novel system for studying evolutionary potential in the wild, to address trait and population differences in heritability. Our traits in focus were the size and shape of the extended elytra and pronotum (the shield), which the beetles use as protection from predators. Preliminary results indicate a higher heritability of the beetle shield area than the shield shape. Furthermore, we found potential differences in heritability between two populations, and in some cases these differences depended on the parents' sex. These results suggests that traits and populations might differ in their evolutionary potential.

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Key words: Heritability, Quantitative genetics

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Abstract number: P66

Title: Does size matter? Female mate choice and positive size-assortative mating in the Common Blue-tailed Damselfly (Ischnura elegans)

Name: Frida Sevrell

University: Lund University

Abstract:

Mate choice is a dynamic process allowing individuals to selectively mate with members of the opposite sex displaying preferred traits or higher fecundity. In many species males compete for mating and female mate choice is a powerful mechanism of sexual selection. However, the mechanisms and population consequences of female mate choice remain unclear. Here we explore the role of female mate choice behind size-assortative mating in the common blue-tailed damselfly (Ischnura elegans). We found positive assortative mating in four natural populations across many years, whereas the strength of assortment varied between populations. We also performed mate choice experiments in these four populations and demonstrated a shared female preference for larger males. In contrast, smaller males more frequently approached and presumably harassed females compared to larger males, demonstrating a conflict between male and female mate choice. Our findings highlight the importance of female mate choice in shaping mating patterns in nature.

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Key words: Female mate choice, Size-assortative mating, Sexual selection, Ischnura elegans

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Abstract number: P67

Title: Rack and romance: The evolution of deer antlers - correlations, causations or coincidence?

Name: Samanvitha Santusht

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Abstract:
The antlers of deer (family Cervidae) have become a classic example of trait evolution through female mate choice and male-male competition (e.g., sexual selection). Past studies have focused on few aspects of antler morphology, such as length. However, Cervidae exhibit a vast array of diversity in shape, form and structure . This raises the question - under what circumstances do different aspects of antlers become the target of selection, even if sexual selection is the general underlying driving force? My study aims to bring together the social mating systems, sexual size dimorphism (SSD), breeding group sizes, habitat and phylogeny as the variables that potentially influence and drive antler evolution in deer. In my presentation, I will focus primarily on SSD and the proxies for the intensity of sexual selection collected from museums specimens and through literature survey, including those of the extinct species—the Irish elk.

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Key words: Cervids, antler morphometrics, sexual size dimorphism, breeding group sizes, social mating system, Irish elk

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Abstract number: P68

Title: Sex- and morph-biased gene expression across development in the Common Bluetail Damselfly (Ischnura elegans)

Name: Pelle Van Hilst

University: Lund University

Abstract:

Studying differential gene expression (DGE) changes throughout the ontogeny can elucidate developmental mechanisms of morphs and sexes. Gene expression data can also reveal if genes with limited expression to certain phenotypes experience weaker selection by studying population genomic parameters like π, Tajima's D and dN/dS.

Here we present a study on DGE in the Common Bluetail Damselfly (Ischnura elegans), an insect with a female limited color polymorphism, where one of the three female morphs is a male mimic. Among nymphs, 93% of the sex-biased genes are exclusively differentiated at this stage. The number of sex-biased genes was substantially higher between the nymph and adult life-stages than between the adult phenotypes suggesting adaptive decoupling. Unexpectedly, the male mimic showed higher differential gene expression against males, than the two other female morphs. We will further investigate the links between intralocus conflict and DGE by estimating between-sex-Fst and identifying candidate loci.

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Key words: DGE, intralocus conflict, insect

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Abstract number: P69

Title: ANTSR is an ancient sex-determining locus in ants and bees

Name: Tilman Rönneburg

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Abstract:
Haplodiploid sex determination systems are found in all species of Hymenoptera. However, the molecular genetic mechanisms that specify sex are highly diverse and have only been discovered in a small number of species. In many haplodiploid taxa, the initial trigger is a complementary sex determination (CSD) locus, in which heterozygosity initiates a molecular pathway to generate females. In the honeybee Apis mellifera, the CSD locus overlaps an exon of a protein-coding gene and affects its amino acid sequence whereas in the ant Linepithema humile it affects expression of the lncRNA gene ANTSR. Here, we map a single CSD locus in the genome of the red mason bee Osmia bicornis. The region is orthologous to the CSD locus identified in L. humile. We identify elevated levels of genetic diversity in the ortholog of the locus in other bee genera, suggesting that it may govern sex determination widely in bees.

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Key words: mapping, sex determination, haplodiploidy

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Abstract number: P70

Title: Conservation genomics of Anthophora bees

Name: Demetris Taliadoros

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Abstract:

Solitary bees are vital components of the ecosystem, but population declines have been reported for many species. Three species from the genus Anthophora -Anthophora quadrimaculata, Anthophora retusa, and Anthophora plagiata - are present widely in Europe. In Sweden, A. plagiata and A. retusa have experienced declines in recent decades to the point of local extinction, but substantial recovery has been reported in the case of A. retusa. Population resequencing of 140 samples from throughout Sweden revealed that A. plagiata has extremely low genetic variation. In contrast, A. retusa does not exhibit reduced genetic variation. Using MSMC, we find evidence for gradual long-term population declines for all species since the end of the Pleistocene and evidence that effective population size in A. plagiata has been historically low. These results are concordant with those from other insect species indicating that many threatened species have experienced population declines that predate the modern era.

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Key words: Conservation genomics, solitary bees, demography, local extinction

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Title: Impacts of Feralization on the Horse Gut Microbiome

Name: Madeleine Van Well Bergström

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Abstract:

Feralization is a process where a domesticated species is returned to wild conditions and can be explained as the reverse of domestication. The process involves a sudden shift from artificial to natural and sexual selection, which can lead to changes in for instance species morphology, physiology, and behavior. Despite intense focus on genetic and microbial changes associated with domestication, we know little about how feralization affects animal microbiomes. Feralization thus provides a unique opportunity to observe the genomic, phenotypic, and microbiota responses to selection from a known (domesticated) standpoint. In this study, we investigate the impacts of feralization on two populations of feral Pottoka horses in central and northern Spain. We sequenced their gut microbiomes using 16S rRNA metabarcoding. Variation in gut microbiome composition and diversity was evaluated across individuals and between feral and domesticated horses. These results will enable a better understanding of the process of feralization as microbes can more rapidly adapt to new environmental challenges. Feralization of domestic species with an extinct ancestral wildtype, such as horses, facilitates opportunities to bring back equivalents to restore ecosystem function in benefit of biodiversity.

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Key words: Microbiome, Feralization, Horse gut microbiome

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