

Swiss Conference on Organismal Biology

BIOLOGY 23

16-17 February 2023

Sciences II building
University of Geneva

Invited speakers

Sonya Clegg University of Oxford

Elena Conti University of Zurich

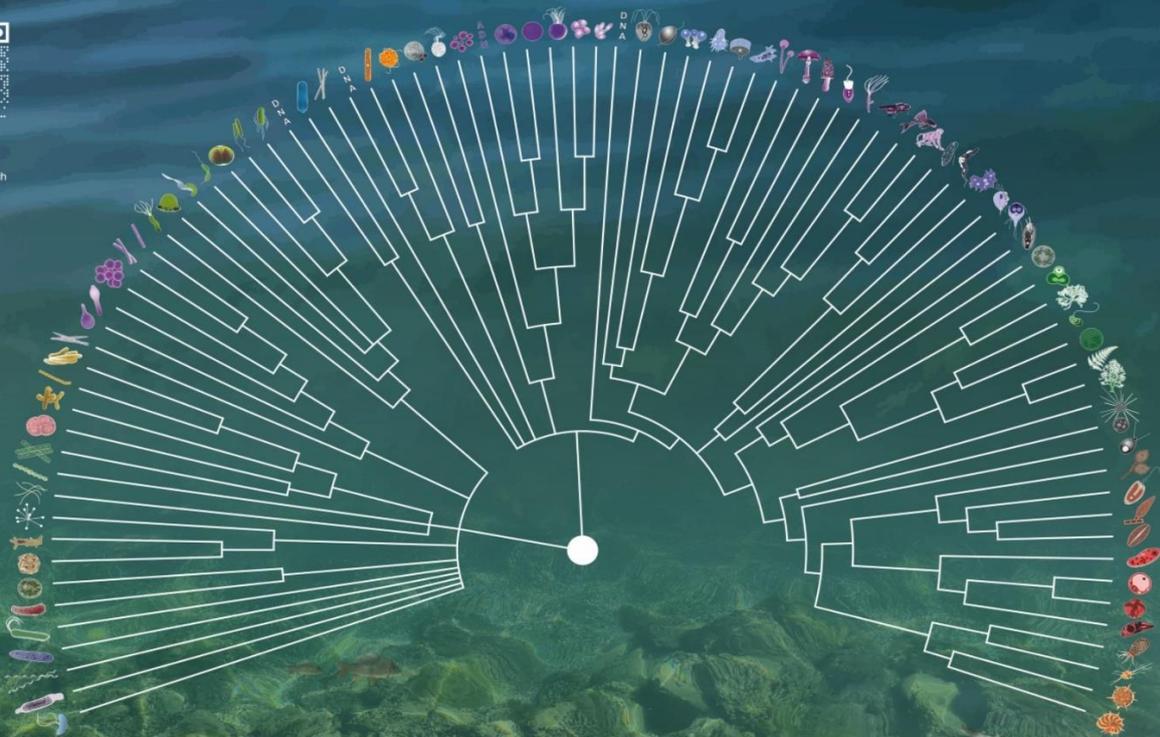
Tim Coulson University of Oxford

Laurent Excoffier University of Bern

Catherine Graham WSL, Birmensdorf, Zurich



biology23.unige.ch



Partner organisations
and financial support:

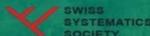


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WHERE ARE WE AND HOW TO FIND US?

Conferences

Sciences II

Quai Ernest-Ansermet 30

1205 Genève

Closest bus / tram stops

Sainte-Clothilde (3min)

Jonction (6min)

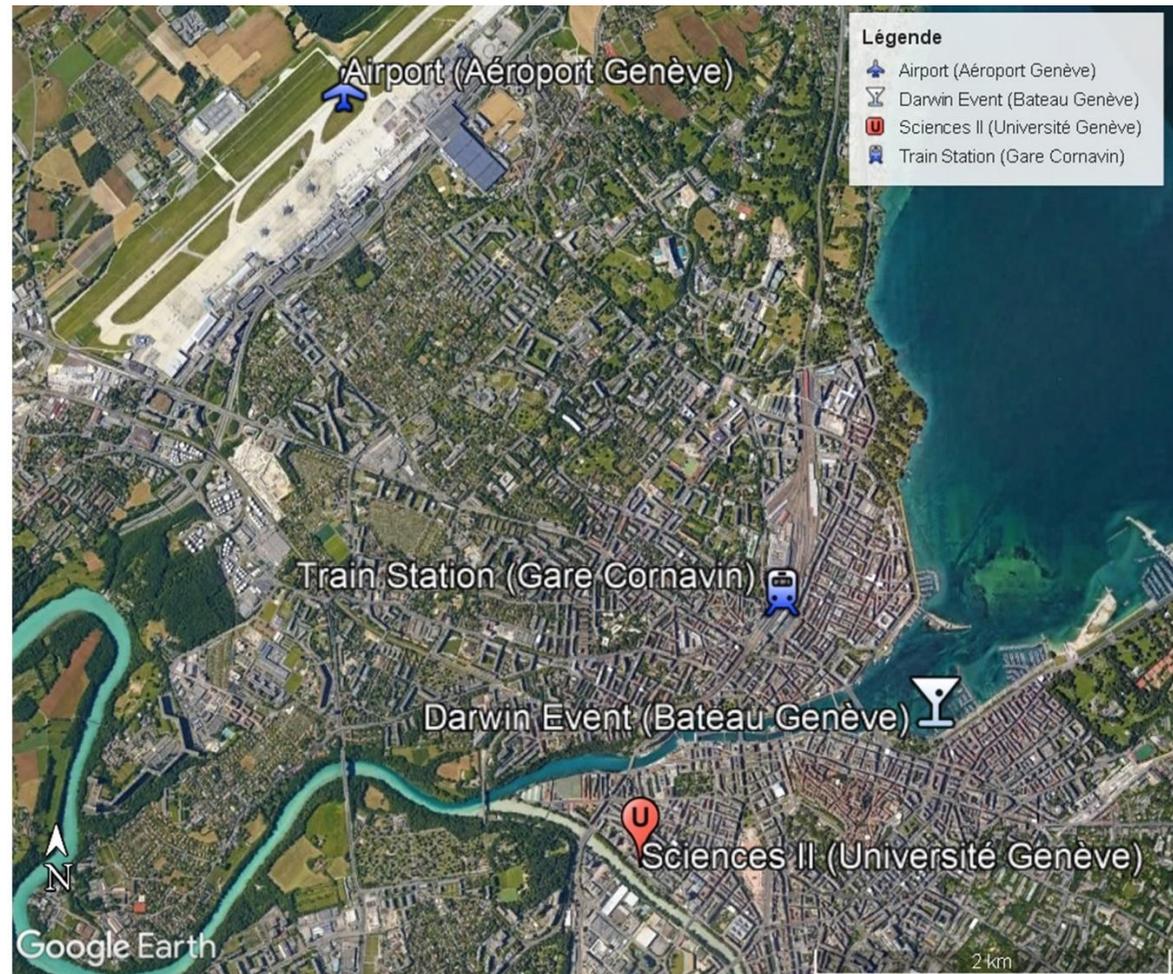
Ecole de Médecine (10min)

From the Train station (Cornavin)

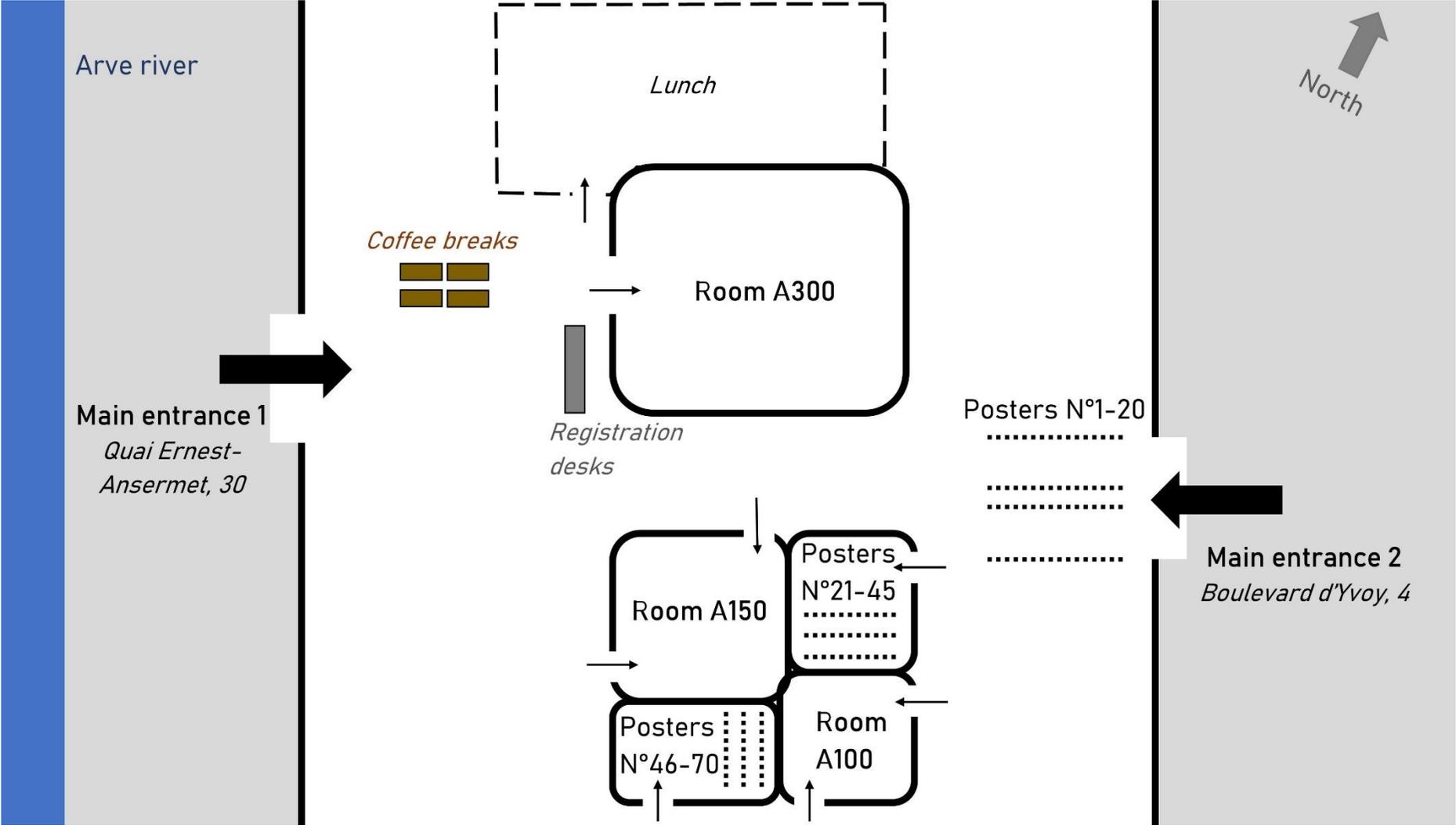
- Tram 14 direction Bernex Vailly
to *Jonction* (5 stops)

- Bus 1 direction Thônex
to *Ecole de médecine* (4 stops)

- Bus 19 direction Onex, cité
to *Sainte-Clothilde* (6 stops)



SCIENCES II – MAP OF THE CONFERENCE



THE DARWIN EVENT- HOW TO GET THERE?

Darwin Event at « Bateau Genève »

Quai Gustave Ador 1

[Quai Marchand des Eaux-Vives]

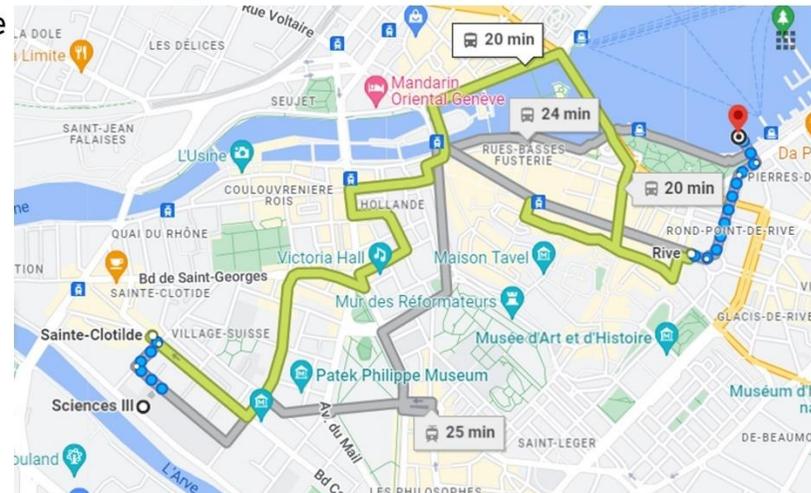
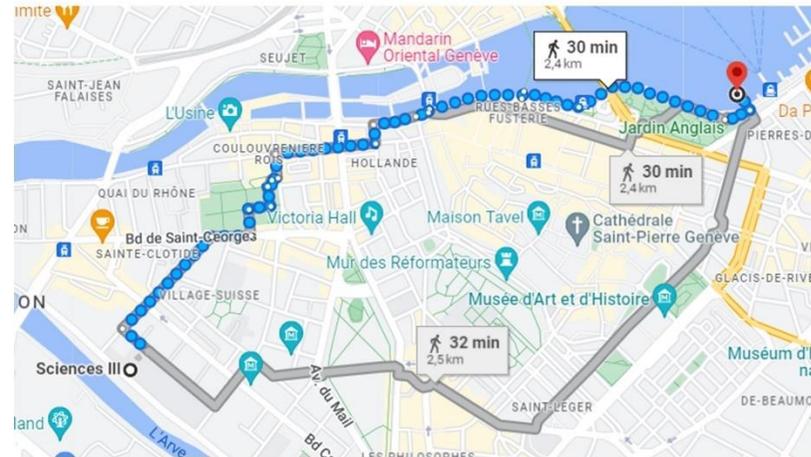
1207 Genève

<https://www.bateaugeneve.ch>

How to get there ? From Sciences II

30min walking

Bus 2 from stop *Sainte-Clotilde*, direction Genève Plage
to stop *Rive* (7 stops)



KEYNOTE PRESENTATIONS

Time and Location	Presenter	Title
Plenary I (16.02.23) <u>Room:</u> A300, <u>Time:</u> 10:30	Elena Conti	<u>Comparative Genomics elucidates the convergent origins of floral heteromorphism.</u>
Plenary II (16.02.23) <u>Room:</u> A300, <u>Time:</u> 13:15	Laurent Excoffier	<u>Demographic inference from ancient human genomes.</u>
Darwin Event (16.02.23) Le Bateau de Genève 20:00	Sonya Clegg	<u>Tales of the South Pacific: the evolutionary ecology of island colonising birds.</u>
Plenary III (17.02.23) <u>Room:</u> A300, <u>Time:</u> 09:15	Tim Coulson	<u>Unifying ecology and evolution to understand why very large and very small species exist.</u>
Plenary IV (17.02.23) <u>Room:</u> A300, <u>Time:</u> 13:00	Catherine Graham	<u>The importance of temporal dynamics in species interactions for community structure and stability.</u>



Comparative Genomics elucidates the convergent origins of floral heteromorphism

Elena Conti

University of Zürich

Convergent evolution is one of the most fundamental yet contentious issues in evolutionary biology. The rapid accumulation of high-quality reference genomes and transcriptomes now enables us to re-examine evolutionary convergence and parallelism in a new framework: Does convergence at the phenotypic level correspond to convergence or deep homology at the genotypic level? Do the same genes and genetic architectures underlie convergent traits, or can different genes be recruited to achieve the same phenotypic outcome? I will discuss these questions focusing on heterostyly in Primulaceae but within the broader framework of flowering plants. Heterostyly evolved three times independently in Primulaceae, namely in *Primula*, *Hottonia*, and *Androsace*. Heterostylous taxa of Primulaceae typically comprise two different types of plants with distinct floral morphs characterized by reciprocally placed sexual organs and a heteromorphic incompatibility system that blocks self- or intra-morph fertilization. Heterostyly thus promotes cross-fertilization while preventing the harmful effects of self-fertilization, and it evolved at least 14 times in angiosperms. A supergene known as the S locus operates the genetic control of heterostyly. Despite the numerous genetic, morphological, and reproductive studies on heterostyly over the past 150 years, the molecular nature and evolutionary origins of the S locus remained unknown until recently. What are the genes and genetic architectures of the S locus? Are they the same in independent origins of heterostyly? Did the S locus evolve through a single, large duplication followed by loss of intervening genes or through multiple, asynchronous gene duplications followed by translocations? We addressed these questions by generating highly contiguous, chromosome-scale, haplotype-phased assemblies of heterostylous and homostylous genomes of Primulaceae and performing comparative genomic analyses across Ericales, the order that includes Primulaceae. Primulaceae thus represent an ideal system to study evolution on repeat in the genomics era, clarifying the connections and disconnections of evolutionary convergence from the genotypic to the phenotypic level and back.



Demographic inference from ancient human genomes

Laurent Excoffier

University of Bern

Reconstructing the demographic history of our species is important not only for satisfying a legitimate curiosity about our origins, but also because it can allow us to better infer past episodes of selection and correctly interpret observed patterns of genomic diversity. In the last 10 years, ancient DNA has revolutionized the way we can reconstruct the settlement history of modern humans, as it gives us direct access to the genomic identity of the first colonizers of different regions of the world. However, most ancient genomes are only partially sequenced, which limits their use for demographic inference as the retrieved information suffers from ascertainment bias. However, investing in good quality ancient genomes allows one to use sophisticated inference methods developed for the analysis of modern genomes. These ancient genomes can thus be used as anchor points in the analysis of modern genomes, or be analyzed on their own to provide new insights about past settlement processes. I will illustrate this point by showing how they have allowed us to provide new insights about the exit of modern humans out of Africa, the settlement of northeastern Siberia and the relationships between early farmers and hunter gatherers from western Eurasia.



**Tales of the South Pacific: the evolutionary ecology
of island colonising birds**

Sonya Clegg

University of Oxford



Unifying ecology and evolution to understand why very large and very small species exist

Tim Coulson

University of Oxford

Ecological changes can result in evolution of phenotypic traits and life history, which can impact population and community dynamics. These two processes interact to generate eco-evolutionary feedbacks. I will explain how we can empirically quantify and theoretically model these feedbacks by drawing on my research into the ecosystems of Yellowstone National Park and Trinidad's freshwater streams. Although the framework I describe has had some success in linking population ecology, population genetics, life history theory, and quantitative genetics, one of the drawbacks of the approach I will describe is models can become quite complicated making them hard to analyse. I will describe a novel approach I have pioneered to simplify models to gain general, novel, ecological and evolutionary insight. I will illustrate the approach by demonstrating how to evolve both species with very large body sizes and slow life histories, and those with small body sizes and fast life histories.



The importance of temporal dynamics in species interactions for community structure and stability

Catherine Graham

Swiss Federal Institute for Forest, Snow and Landscape Research (WSL)

Species interactions are dynamic in nature, and yet, all too often we evaluate interactions with data summarized over time. By evaluating summarized data, we likely miss key mechanisms governing species interactions and community stability. Here we explore fine grained (monthly) plant-hummingbird interaction data gathered across multiple sites and over several years to describe how interaction and network structure changes across time and evaluate mechanisms that influence this variation. We show, for instance, that different factors influence resource specialization across time (2 years of monthly sampling) and space (11 sites along an elevation gradient). In addition, we use theoretical models to show that temporal dynamics in hummingbird-plant assemblages increases community stability. This combination of long(ish) term empirical data collection and both statistical and theoretical models provides new insight into the importance of considering temporal dynamics when studying species interactions and community stability.

THURSDAY 16.02.2023 – Morning Sessions

Room: **A300**, Subject: **SYSTEMATICS AND MACROEVOLUTION**

Chair: Yamama Naciri

- | | | |
|-------|--------------------|---|
| 11:15 | Alexandra Viertler | No DNA? No problem: How to phylogenetically place fossil Darwin wasps (Ichneumonidae). |
| 11:30 | Kimberley Kissling | The bony labyrinth of the extinct Steller's sea cow, the largest known marine herbivore. |
| 11:45 | Cody R. Cardenas | Using integrative phylogenetics to clarify evolutionary relationships in Adephaga: Characterization of targeted genomic loci. |

Room: **A150**, Subject: **BIODIVERSITY AND CONSERVATION**

Chair: Lionel Di Santo

- | | | |
|-------|------------------|--|
| 11:15 | Sébastien Miche | Phylogenomics for regional biodiversity assessment in the Canton of Geneva. |
| 11:30 | Noëlle Klein | Does agricultural management promote Swiss agricultural priority species? A spatial approach. |
| 11:45 | Shaquille Matthy | Multi-criteria assessment of control methods for the invasive <i>Trachemys scripta</i> in Switzerland. |

Room: **A100**, Subject: **RADIATION AND SPECIATION**

Chair: Alice Cibois

- | | | |
|-------|--------------------|--|
| 11:15 | Noah Meier | One or two species? Genomics provide insight in the systematics of the Green Whip Snake (<i>Hierophis viridiflavus</i>). |
| 11:30 | Théo Gaboriau | Host use drives convergent evolution in clownfish and disentangles the mystery of an iconic adaptive radiation. |
| 11:45 | Dario N. Neokleous | The diversification and biogeographic history of <i>Limnonectes</i> "kuhlii"-like and <i>L. palavanensis</i> fanged frogs on Borneo. |
-

No DNA? No problem: How to phylogenetically place fossil Darwin wasps (Ichneumonidae)

Alexandra Viertler¹, Karin Urfer, Georg Schulz, Seraina Klopstein, and Tamara Spasojevic

¹ *Ecology and Evolution, University of Bern; Life Sciences, Natural History Museum Basel.*

The parasitoid Darwin wasps are among the most poorly studied groups of organisms. Their fossil record is even more poorly understood than their extant diversity but is fundamental for reconstructing the evolutionary history of the group. One of the prerequisites to improve its quality, is a reliable taxonomic placement of newly described fossils.

Here, we perform a total-evidence phylogenetic analysis, which combines morphological and molecular data, extant and fossil taxa, to aid taxonomic placement of four new fossil Darwin wasp species in amber. We based our analysis on a published total-evidence dataset for Ichneumonidae, that contains 222 morphological characters and 10 molecular genes. However, we revised the morphological matrix and extended it with nine newly defined characters (225 in total) and 20 fossil and extant species (230 in total) relevant for the placement of the new fossils. To increase the number of scored characters for the fossils, we also performed micro-CT scans and 3D reconstructions. For the newly added extant taxa, we amplified three (28S, COI, CAD) out of the 10 genes.

A Bayesian total-evidence analysis was performed using RevBayes and the trees from posterior distribution were used to summarize the attachment probability of the fossils to branches in the phylogeny with RoguePlots.

We show that a total-evidence phylogenetic analysis, based on a careful assessment of morphological characters from fossils and their micro-CT scans, can significantly improve taxonomic placement of amber fossils. Increasing the precision of fossil placement is key to improving parameter estimates in dating and diversification analyses.

The bony labyrinth of the extinct Steller's sea cow, the largest known marine herbivore

Kimberley Kissling¹, Kévin Le Verger¹, Lionel Hautier², Loïc Costeur³, and Gabriel Aguirre-Fernández¹

¹ *Paleontological Institute and Museum, University of Zurich, Karl-Schmid-Strasse 4, 8006, Zurich, Switzerland.*

² *Institut des Sciences de l'Evolution de Montpellier (ISEM), CNRS, IRD, EPHE, Université de Montpellier, Place Eugène Bataillon, 34095 Montpellier Cedex 5, France.*

³ *Naturhistorisches Museum Basel, Augustinergasse 2, Basel.*

Sirenians (dugongs, manatees, and their extinct relatives) are obligate aquatic mammals with a rich fossil record extending back 56 million years. Among aquatic mammals, they are unique because of their strict herbivory. Sirenians have acute hearing and communicate with conspecifics via calls. The bones of the ear are well preserved throughout their history and offer the best chance of tracing the evolution of sirenian senses. Hearing in sirenians is poorly understood from a functional viewpoint and it is important to consider the effect of size on the shape. Here, we analysed morphological variation of bony labyrinth endocasts in a sample of thirteen extant and fossil sirenians. Three-dimensional models were rendered from computer-tomography scans for anatomical comparisons and shape analyses. The inner ear shape was predominantly uniform over time and species, despite their dramatic body size range. We focus on the Steller's sea cow, the largest sirenian (and with 9 m length, larger than an orca), and on what the inner ear can tell us about the environment and behaviour of these fascinating mammals.

Using integrative phylogenetics to clarify evolutionary relationships in Adephaga: Characterization of targeted genomic loci

Cody Raul Cardenas¹ and Emmanuel F.A. Toussaint

¹ *University of Geneva.*

The use of phylogenetic data generated with high-throughput sequencing has revealed fascinating biographic and evolutionary histories while resolving historically intractable phylogenetic relationships. The second largest beetle suborder, Adephaga (Coleoptera), has been studied in depth in recent years. Consisting of over 45,000 species and found worldwide, this suborder includes important predators in terrestrial and aquatic ecosystems. However, limited taxonomic sampling in important clades muddles our understanding of the diversification and systematic relationships in this group. To test recent hypotheses of lineage relationships in the suborder, we will integrate multiple genomic data-collection strategies that have been used and produce the most complete phylogeny of Adephaga to date. Previously used methods including anchored hybrid enrichment of exons (AHE), whole genomes, transcriptomes, and ultra-conserved elements (UCEs). Recently some UCE datasets have been described to target more than one loci on the same gene and are composed of off-target loci (e.g., fungi or bacteria). This fundamentally alters interpretations of phylogenetic relationships and complicates investigations of evolutionary history. Because of these pitfalls, it is necessary to characterize and identify the genetic composition of genomic-data used in phylogenetic analyses. Preliminary analyses using two different UCE kits suited to Adephaga phylogenetics suggests that multiple UCE loci are found on the same gene. Additionally, there is evidence these UCE loci may have been generated using contaminated genomes. Preliminary phylogenetic results indicate that all data-collection strategies can be successfully integrated. Further bioinformatic work characterizing the genomic loci used will improve phylogenetic models and future evolutionary investigations.

Phylogenomics for regional biodiversity assessment in the Canton of Geneva

Sébastien Miche^{1,2}, Camille Christe², Charles Pouchon², Nicolas Wyler², and Mathieu Perret^{1,2}

¹ *Department of Plant Sciences, University of Geneva, 30 quai Ernest-Ansermet, 1211 Genève 4, Switzerland.*

² *Conservatoire et Jardin Botaniques de Genève, 1 Chemin de l'Impératrice, 1292 Pregny-Chambésy, Switzerland.*

Monitoring variation of phylogenetic diversity across space and time is critical to understand the effect of species extinction and distribution changes on the loss of evolutionary history. However, measuring accurate phylogenetic-diversity indexes within local species assemblages remains problematic because of the poor resolution and uncomplete sampling of the tree-of-life at the species-level. Here, we demonstrate the feasibility of using high-throughput genome sequencing and target-enrichment of 353 nuclear genes to estimate phylogenetic relationships among all species of the Geneva flora (1126 species). Our results show that, despite a significant taxonomic effect on gene capture efficiency, this method provides a more resolved phylogenomic tree at the species level than synthetic phylogenies available in the “Open Tree of Life” project. This new genomic reference for plants will be used in combination with occurrence data (>200'000 observations) to accurately quantify and model variation in evolutionary history of the Geneva flora across different floristic communities, habitats and time periods. Ultimately, this new layer of phylogenetic information will be integrated in the calculation of the Canton's green infrastructure for long-term conservation of biodiversity.

Does agricultural management promote Swiss agricultural priority species? A spatial approach

Noëlle Klein^{1,2}, Adrienne Grêt-Regamey², Felix Herzog¹, Philippe Jeanneret¹, Maarten van Strien², Antoine Adde³, Sonja Kay¹

¹ *Agricultural Landscapes and Biodiversity, Department of Agroecology and Environment, Agroscope, Reckenholzstrasse 191, 8046 Zurich, Switzerland.*

² *Chair of Planning of Landscape and Urban Systems (PLUS), Institute for Spatial and Landscape Planning, Department of Civil, Environmental and Geomatic Engineering, ETH Zürich, Stefano-Franscini-Platz 5, 8093 Zürich, Switzerland.*

³ *Institute of Earth Surface Dynamics, Faculty of Geosciences and Environment, University of Lausanne, Lausanne, 1015, Switzerland.*

European biodiversity has been shaped by agriculture. However, intensified agriculture has severely affected biodiversity, as many priority species depend on extensive land use and mosaic structures. Different payment-based biodiversity-promotion-schemes have been implemented to combat biodiversity losses on various spatial scales. Nevertheless, as agricultural land surface is decreasing, the conflict of interest between efficient food production and habitat quality for biodiversity is increasing in farming landscapes. One approach to preserve priority species, can be to adapt agricultural management regionally. In this Swiss-wide study, we used a life-cycle-assessment method to assess the direct impacts of fieldbased management on birds/butterflies, as indicator species groups (map A). We also used stacked species distribution models of agricultural priority species to estimate their theoretical distribution potential (map B). Using spatial hotspot analyses, we were able to determine significant hot-/ and cold spots for both maps and assess their spatial overlap. The result is a high-resolution Swiss-wide spatial analysis of the potential of agricultural land-use management to support Swiss agricultural priority species realise their potential distribution. Our results highlight areas with high or low potential for agricultural priority species, combined with the impact of the respective land management on the different indicator groups. This allows for spatially explicit comparisons across regions and land management, to identify areas where land-use management should be adapted. Optimised land use of agricultural land can help to improve the status of the declining species in the future.

Multi-criteria assessment of control methods for the invasive *Trachemys scripta* in Switzerland

Shaquille Matthys¹, Charlotte Ducotterd, Sylvain Ursenbacher, Benedikt Schmidt, and Stefano Canessa

¹ *Conservation Biology, Institute of Ecology and Evolution, University of Bern.*

Invasive alien species (IAS) are a major cause of biodiversity loss, impacting endemic species via predation, competition for resources, habitat alteration and hybridization. There are numerous approaches to control IAS, but their success can vary widely depending on the target species and management context. A formal evaluation of different methods is helpful when dealing with limited resources and complex ethical implications of lethal and non-lethal control methods.

This study focuses on control methods for the pond slider *Trachemys scripta*, one of the 100 most invasive species according to the IUCN. The presence of *T. scripta* can have negative ecological impacts to native European pond habitats, particularly through competition with the European pond turtle (*Emys orbicularis*). In Switzerland the species already occurs and reproduces in several locations.

Our project assesses some common methods for *T. scripta* control in Switzerland, in terms of biological effectiveness, costs and welfare implications. For effectiveness, we have built a population model to project *T. scripta* population dynamics under different control methods, using a mix of existing data from previous projects and novel collected data. Based on the modelling results, we then estimate the total management costs for each method. Finally, for each control method we are collecting information about the physical conditions of turtle capture, transportation, and captivity; here we present preliminary results and the framework for this welfare assessment.

Through this assessment, we aim to facilitate rational planning, balancing ethical and financial constraints against biological evidence, allowing for optimal protection of native species.

One or two species? Genomics provide insight in the systematics of the Green Whip Snake (*Hierophis viridiflavus*)

Noah Meier^{1,2}, Kay Lucek¹, Marco A. L. Zuffi³, Federico Storniolo⁴, Marcello Mezzasalma⁵, Philippe Geniez⁶, Sylvain Dubey^{7,8}, Roberto Sacchi⁴, Stefano Scali⁹, and Sylvain Ursenbacher^{1,10}

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² Naturhistorisches Museum Basel, Augustinergasse 2, CH-4001 Basel, Switzerland.

³ Museum of Natural History, University of Pisa, Via Roma 79, 56011 Calci (Pisa), Italy.

⁴ University of Pavia, Dipartimento di Scienze della Terra e dell'Ambiente, Viale Taramelli 24, 27100 Pavia, Italy.

⁵ Department of Biology, Ecology and Earth Science, University of Calabria, Via P. Bucci 4/B, 87036 Rende, Italy.

⁶ CEFÉ, Univ Montpellier, CNRS, EPHE-PSL University, IRD, Biogéographie et Ecologie des Vertébrés, 1919 route de Mende, 34293 Montpellier Cedex 5, France.

⁷ HW Romandie SA, Avenue des Alpes 25, 1820 Montreux, Switzerland.

⁸ Department of Ecology and Evolution, University of Lausanne, 1015 Lausanne, Switzerland.

⁹ Natural History Museum of Milan, Corso Venezia, 55, 20121 Milano, Italy.

¹⁰ info fauna CSCF & karch, Avenue de Bellevaux 51, CH-2000 Neuchâtel, Switzerland.

The two subspecies of the Green Whip Snake *Hierophis viridiflavus viridiflavus* and *H. v. carbonarius* represent an interesting model system to study speciation. Indeed, they likely evolved during glacial periods due to isolation by distance. Recent studies show that even though these subspecies belong to different mitochondrial lineages, a single tested nuclear gene and morphological traits display overlapping character states. Moreover, little is known whether these two subspecies are reproductively isolated from each other. Furthermore, it is unknown how the complete or partial melanism of the subspecies *carbonarius* is regulated and why it is restricted to this eastern subspecies only. Therefore, we evaluated the amount of gene flow within two transects across the contact zone of the subspecies with a genomic approach using double-digest restriction site-associated DNA (dd-RAD). Our molecular samples, including 148 individuals from the contact zones and further away, were genotyped on 24,817 single nucleotide polymorphisms (SNP). Admixture analysis supports the existence of two well-defined clades corresponding to both subspecies. However, a high gene flow between both subspecies was observed within a cline of 300 km. Moreover, associations between phenotypic characters and genomic markers were investigated by quantifying the amount of yellow coloration and by applying geometric morphometrics on the head shape and pholidosis. We conclude that the two subspecies represent evolutionary significant units (ESU). Due to the extensive hybridization zone, it seems that reproductive barriers have not evolved (yet). On a taxonomic basis, we suggest continuing treating the two ESU as subspecies.

Host use drives convergent evolution in clownfish and disentangles the mystery of an iconic adaptive radiation

Théo Gaboriau¹, Anna Marcionetti Alberto Garcia-Jimenez, Benjamin Titus, Lucy Fitzgerald, Sarah Schmidt, Baptiste Micheli, and Nicolas Salamin

¹ *Université de Lausanne, DBC.*

Clownfish (Amphiprioninae) are a fascinating example of a marine adaptive radiation. From a central pacific ancestor, they quickly colonized the coral reefs of the Indo-Pacific and diversified independently on each side of the Wallace line. The association with the venomous sea anemone is often thought to be the key innovation that allowed the clownfish radiation. However, this intuition has little empirical or theoretical support given our current knowledge of the clade. Our synthetic work aims at filling this gap by testing the influence of anemone host-use on gene selection and on genetic and phenotypic divergence. We gathered multiple in-situ pictures of clownfish individuals in their host for each clownfish species, from which we estimated variation in coloration patterns, morphology and host use. We significantly updated known clownfish-host associations based on this new data. We also sequenced whole-genomes for each clownfish species and reconstructed the most up-to-date phylogenetic tree for the Amphiprioninae. In the light of this new data, we found robust evidence for convergent evolution of morphology and coloration driven by differential host-use. Clownfish colonized the same hosts in parallel in different regions and evolved the same phenotype in both replicates of similar events. We also identified several genes under positive selection during host shifts events. We provide empirical evidence of an adaptive radiation triggered by a key innovation and isolate genetic markers involved in this mechanism.

The diversification and biogeographic history of *Limnonectes* “*kuhlii*”-like and *L. palavanensis* fanged frogs on Borneo

Dario N. Neokleous¹ and Stefan T. Hertwig

¹ Natural History Museum Bern (Department of Vertebrates), University of Bern (Institute of Ecology and Evolution).

Borneo is among the biggest islands of our planet, showing extraordinary species richness of frogs. Many genera include species with low morphological differentiation, which are thus regarded as “cryptic”. *Limnonectes kuhlii* was long seen as a single, widespread species. Recent studies have shown that there are many evolutionary lineages hidden under this name, especially on Borneo. Almost two dozen unnamed lineages exist there, forming an endemic clade that is the sister group of species from mainland Asia. We can confirm these findings and show that sympatry is very common for two or more Bornean lineages at a particular location, with some places harbouring up to six clades. We also show that there is another *Limnonectes* radiation on the island: *L. palavanensis* is recovered as a species complex containing eight clades, including the type locality on Palawan. Major groups diversified in the Oligo- and Miocene with inter- and intra-lineage splits occurring in the Pleio- and Pleistocene. In both radiations, coexisting lineages are distant relatives with p-distances higher than 5%, indicating the presence of separate species. However, future studies focusing on gene flow, morphology and bioacoustics are necessary to accurately study the diversity of these groups and to infer species that deserve description.

THURSDAY 16.02.2023 – Early Afternoon Sessions

Room: **A300**, Subject: **EVOLUTIONARY GENETICS AND GENOMICS**

Chair: Estella Poloni

- | | | |
|--------|----------------------|--|
| 14:30 | Enrique A. Dominguez | A Tool for Visual Exploration of Linkage Disequilibrium in Highly Polymorphic Systems of Loci. |
| 14: 45 | Tristan Cumer | The genomic architecture of a continuous color polymorphism in the European barn owl (<i>Tyto alba</i>). |
| 15:00 | Sandra Grünig | Adaptation in diploids and tetraploids of <i>Biscutella laevigata</i>. |
-

Room: **A150**, Subject: **SPECIES INTERACTIONS**

Chair: Isabel Blasco-Costa

- | | | |
|--------|------------------------|---|
| 14:30 | Bruno Camargodossantos | Cannabidiol improves Nile tilapia cichlid fish welfare. |
| 14: 45 | Corina Maurer | Abundant generalist pollinators prevent a rapid decline in interaction diversity upon landscape simplification. |
| 15:00 | Franziska Brenninger | Optimal immunity shaped by life both before and after infection. |
-

Room: **A100**, Subject: **ECOLOGY AND EVOLUTION**

Chair: Charles Pouchon

- | | | |
|--------|----------------|---|
| 14:30 | Chongmeng Xu | Developmental process and the occurrence of cell death in the ant defense organ revealed by gene expression patterns. |
| 14: 45 | Marius Roesti | Causes and consequences of habitat selection in lake-stream stickleback. |
| 15:00 | Abhishek Meena | Do frequent heatwaves damage male reproductive tissue? |
-

Tool for Visual Exploration of Linkage Disequilibrium in Highly Polymorphic Systems of Loci

Enrique Alanis Dominguez¹, Da Di¹, David Roessli¹, Alicia Sanchez-Mazas¹, and José Manuel Nunes¹

¹ *Laboratory of anthropology, genetics and peopling history, Department of Genetics & Evolution, University of Geneva, Switzerland.*

Linkage disequilibrium (LD) refers to the non-random association between genetic variants at distinct loci within a population. Understanding the patterns of LD can provide insights into the demographic history and evolution of populations, besides helping in the identification of genes or markers associated with some diseases or traits of interest. However, to analyse LD patterns between highly polymorphic pairs of loci can be challenging, in particular when many haplotypes are present.

To manage such a wealth of information, we present a Shiny application that allows users to interactively visualize LD patterns in one or several populations using a circular graph representation. Thanks to this app, the users can dynamically control the number of haplotypes displayed by setting thresholds on relevant parameters such as haplotype frequency or intensity of LD deviation, but also ignore some loci, loci pairs or populations if desired. While the inputs are simple plain text files, graphical and numerical outputs are easily obtained in well-known open formats. This interactive tool is currently used to explore and analyse LD patterns in highly polymorphic multiallelic loci such as HLA (human MHC), where it allows identifying specific patterns resulting from populations' demography or natural selection.

This new Shiny application reveals the advantages of interactive data visualisation and exploration, in particular for the analysis of complex, non-intuitive, parameters such as LD between highly polymorphic loci. Being particularly user-friendly, it will be most useful to researchers working in a variety of scientific domains such as systemic biology, genetics and population genetics.

The genomic architecture of a continuous color polymorphism in the European barn owl (*Tyto alba*)

Tristan Cumer^{*1,2}, Ana Paula Machado^{*1,2}, Luis M. San-Jose^{*3}, Alexandre Roulin¹, and Jérôme Goudet^{1,2}

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** equally contributing*

Color polymorphism, and the mechanisms that allow its maintenance in populations, have fascinated evolutionary biologists for decades. Studies of the variation of coloration in wild populations often focus on discrete color traits exhibiting relatively simple inheritance patterns, while studies on continuously varying traits remain rare. Here, we studied the continuously varying white to red color polymorphism in the Western palearctic barn owls (*Tyto alba*), ranging from pale white in the south to reddish dark in the north of its distribution. By using a Genome Wide Association approach on whole genome data of 75 barn owl individuals sampled across Europe, we identified, on top of the previously known MC1R mutation, two other regions involved in this color polymorphism. We estimated the amount of variation linked to these QTL variants, and show the combination of the tree variants explain about 80% of the color variation. Among the two newly identified regions, a region on the sexual chromosome (Z) shows a large signal of differentiation on the Swiss populations when controlling for the MC1R genotype, and we suggest it may play a role in the sexual dimorphism observed in the species. These results uncover two new genomic regions and provide keys to better understand the molecular bases of the color polymorphism as well as the mechanisms responsible of the maintenance of the color polymorphism in the European barn owl at both continental and local scales.

Adaptation in diploids and tetraploids of *Biscutella laevigata*

Sandra Grünig¹ and Christian Parisod¹

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Whole genome duplication (or autopolyploidy) can drive plant speciation, although adaptive underpinnings remain debated. Polyploids have been postulated to adapt faster to environmental changes than their diploids relatives. Additionally, selection is expected to act differently according to the ploidy. However, empirical evidences addressing adaptation to environment across different ploidies are still scarce. Taking advantage of the well-resolved evolutionary history of the diploid-autotetraploid species complex *Biscutella laevigata* (Brassicaceae), we address the genomic signatures of adaptation among pairs of diploid and tetraploid populations from contrasted elevations. Genome scans using whole-genome sequences of 91 individuals from 12 populations sampled in a factorial design highlighted candidate genes underlying adaptation to elevation and ploidy. In particular, window-based tests of isolation by distance and isolation by elevation characterize within each ploidy whether loci were predominantly shaped by spatial vs environmental reduction of gene flow.

Cannabidiol improves Nile tilapia cichlid fish welfare

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In artificial environments, it is common for animals to experience negative states that compromise their welfare. Therefore, investigating ways to improve captive animals' welfare is an urgent concern. A substance that has the potential to increase reared animals' welfare is cannabidiol (CBD). CBD is derived from the *Cannabis sativa* and is widely studied in medicine to control human neural diseases. Besides positive effects on humans, CBD presents anxiolytic properties, regulates reproduction, and decreases aggressiveness and stress in mammals. Therefore, we tested the effect of different CBD doses (0, 1, 10, and 20 mg/kg) on aggressiveness, stress, and reproductive development of the Nile tilapia (*Oreochromis niloticus*), a fish reared worldwide for farming and research purposes. CBD mixed with fish food was offered to isolated male Nile tilapias for five weeks. The 10mg/kg dose efficiently decreased the fish's aggressiveness over time, while the 20mg/kg dose attenuated the non-social stress. Both doses decreased the baseline cortisol level of fish and increased the testis size (gonadosomatic index). However, CBD 1 and 10 mg/kg doses decreased the spermatozoa number. No CBD dose affected any feed ingestion or growth variables, showing evidence that it is not harmful to the meat production amount. Thus, despite the effect on spermatozoa, CBD supplementation exhibits a high potential to increase animals' welfare in artificial environments. Therefore, we showed for the first time that CBD could be used as a tool to increase non-mammal welfare, presenting the great potential to be explored in other husbandry and captivity species.

Abundant generalist pollinators prevent a rapid decline in interaction diversity upon landscape simplification

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Landscape simplification is considered a major factor in reported declines in plant and pollinator diversity in agroecosystems. Most flowering plant species benefit from animal pollination, whereas pollinators are dependent on floral resources. However, it is barely investigated how landscape simplification affects the diversity of plant-pollinator interactions. It may not only depend on the cascading effects of altered plant and pollinator diversity but also on changes in interaction structure, such as altered diet generalisations of interacting species, with implications for network stability and functioning. We therefore analysed the flower-visitation networks (focusing on bees and hoverflies) of 24 agricultural landscapes along gradients of landscape simplification in France, Germany, and Switzerland. We assessed the impact of landscape simplification on species and interaction diversity, as well as the robustness of the plant-pollinator networks. We found that interaction diversity decreased at a similar rate as pollinator species diversity along the landscape simplification gradient. The decrease in interaction diversity was buffered by the persistence of abundant, well-linked generalist pollinators in simplified landscapes, which resulted in pollinator communities in simplified landscapes being nested subsets of communities in complex landscapes. Regardless of landscape simplification, the presence of a few highly abundant pollinators made the networks very robust against predicted loss of visited plant species from the network due to pollinator loss. This was primarily due to the nested network structure through which these dominant pollinators also visited rather poorly linked plant species in all landscapes, thereby likely providing an important insurance function for pollination services in simplified landscapes.

Optimal immunity shaped by life both before and after infection

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¹ *University of Zurich.*

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Immunocompetence varies not only between host-pathogen settings, but also within species. Theory suggests that differences in the strength of immunity are shaped by competing life history demands, reflected in a trade-off between investing resources into reproduction and into immune defense. Earlier exploration of this trade-off has typically focused on explaining sexual dimorphism in immunocompetence. In order to maximize lifetime reproductive success, organisms that experience strong sexual selection (typically males) are expected to decrease investment into immune defenses in favor of reproductive effort. However, in reality, time to infection is stochastic. Therefore, some lucky individuals may be poorly equipped to deal with a parasite, yet reproduce just fine for a while. The theoretical ramifications of this remain unexplored, as do the system-specific fitness consequences of infection: not all infections kill, or stop the host from reproducing. To fill in these knowledge gaps, we derive optimal resource investment strategies into immune defense vs. reproductive effort for varying levels of parasite pressure and severity when individuals accrue fitness both before and after infection. Further, we explore the impact of sexual selection on this trade-off, in combination with varying levels of resistance against, and tolerance of, parasites. Our results confirm that optimal investment into immunity changes depending on the intensity of mating competition. Interestingly, organisms divert energy away from immunity not only when parasites are rare, but also when they are very common – though the latter case only appears when sexual selection is strong, yielding a ‘live fast, die young’ life history solution.

Developmental process and the occurrence of cell death in the ant defense organ revealed by gene expression patterns

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Plants using ants as anti-herbivore agents are common in tropical regions. They provide ants with food and nesting sites, called domatia. Domatia are hollow structures that host ants and are key traits for the evolution of ant-plant interaction. However, the morphology and molecular mechanisms of domatia development have rarely been studied. We studied stem domatia of well-known ant plants, the genus *Macaranga*, using comparative transcriptomic and morphological analyses. The results indicated that programmed cell death, a suicide procedure in the ultimate step of cell-specific differentiation, developed hollow cavities. We also found three possible procedures of the domatia formation: (i) stem expansion, in which proliferates pith cells occur; (ii) programmed cell death, which forms cavities; and (iii) secondary cell wall deposition, which shapes the physical structure. These findings provide new evidence for the domatia development and enhance our understanding of protective ant-plant interaction.

Causes and consequences of habitat selection in lake-stream stickleback

Marius Roesti¹, Nicole Nesvadba, Thor Veen, Keila Stark, Mackenzie Kinney, Jeffrey Groh, Daniel Bolnick, Yoel Stuart, and Catherine L. Peichel

¹ *Institute of Ecology and Evolution, University of Bern.*

Adaptive population divergence is commonly ascribed to selection favoring different individuals in different habitats. Random migration between habitats, and hence gene flow between populations, should thus counteract adaptive divergence. Yet, population divergence could also occur from different individuals selecting different habitats. In case of such individual habitat selection, gene flow between habitats would not be random and could help maintain or even promote population divergence. In this project, we evaluate this overall idea by testing for the causes and consequences of habitat selection using a pair of directly adjacent but phenotypically distinct populations of lake and stream threespine stickleback. A mark-transplant-recapture experiment using wild-caught stickleback reveals phenotype-dependent native habitat selection. To test for a genetic basis of habitat selection, and to find traits and genomic regions associated with habitat selection, we then gave laboratory-raised purebred stickleback (from lake-lake and stream-stream crosses) and lake-stream F2 hybrids the choice between the same natural lake and stream habitats. Purebred stickleback showed increased preference for the native habitat of their parents, indicating a genetic basis to lake-stream habitat selection. In this talk, I will present first results from the analysis of 800 lake-stream F2 hybrids that either selected the lake or stream habitat. Furthermore, I will present our results from a follow-up fitness enclosure experiment conducted with a subset of these hybrids, in which we asked whether the selection of a certain habitat by an individual is associated with increased fitness in that habitat.

Do frequent heatwaves damage male reproductive tissue?

Abhishek Meena¹, Alessio De Nardo¹, Komal Maggu¹, Jeannine Roy¹, Sonja Sbilordo¹, Rhonda Snook², and Stefan Lüpold¹

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² *Department of Zoology, Stockholm University, Sweden.*

Extreme weather events are a threat to biodiversity. Studies on the consequences of climate change on biodiversity tend to focus on where and how species can survive. However, the persistence of a species depends not only on survival but also on reproduction. Fertility is often more sensitive to heat stress than survival, as damage to gametes can occur at sublethal temperatures. Thermal sensitivity usually varies between life stages. Most previous studies focus on one stage and/or sex at one point just after the heat stress or without including genetic variation. However, there is still a lack of understanding of the fitness consequences of heatwaves in multiple life stages and the underlying genetic variation. Therefore, to address these issues, we investigated the following questions: (i) how heatwaves impact male reproduction during the developmental and/or the adult stage in *Drosophila melanogaster*, (ii) whether males' reproductive capacity can recover from such a heatwave and to what extent. We found a significant interaction between larval and adult heat stress on male reproductive tissue, resulting in a decline in fertility, hatching success, and fecundity even after a recovery period. Extreme heat waves seem to have a damaging effect on male reproductive function. This study illustrates the severe impact of heat stress on male reproductive traits. It could speed up population declines through fertility loss, highlighting the need to include effects on reproduction in studies of biodiversity loss. This study is especially important for insects, given their fast global decline and direct dependence on the temperature of their environment.

THURSDAY 16.02.2023 – Late Afternoon Sessions

Room: **A300**, Subject: **EVOLUTIONARY GENETICS AND GENOMICS**

Chair: Mathias Currat

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|-------|-------------------|---|
| 16:00 | Marion Talbi | Fine-scale recombination maps: From simulation to empirical data. |
| 16:15 | Thibault Latrille | Up to 25% of beneficial mutations in protein sequences are not adaptive innovations in mammals. |
| 16:30 | Leo Zeitler | Genetic purging due to self-fertilization does not prevent accumulation of expansion load. |
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Room: **A150**, Subject: **BEHAVIOUR**

Chair: Lionel Cavin

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|-------|-------------------------------|---|
| 16:00 | Océane Ferreira | Does the early social environment influence behavioural flexibility in cooperative breeding cichlids? |
| 16:15 | Francesca N. Angiolani-Larrea | Oviposition location is key for offspring fitness. |
| 16:30 | Marina Garrido-Priego | Caring is sexy: Females of <i>Hyalinobatrachium valerioi</i> prefer males with clutches. |
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Room: **A100**, Subject: **COMMUNITY ECOLOGY**

Chair: Isabel Blasco-Costa

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|-------|---------------------|--|
| 16:00 | Flavien Collart | Ecological and biological indicators of the accuracy of species distribution models: lessons from European bryophytes. |
| 16:15 | Seraina L. Cappelli | Undersown plant species affect disease severity in barley through aboveground processes. |
| 16:30 | Elie Tièche | Agricultural practices shape fungal communities at microgeographic scales. |
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Fine-scale recombination maps: From simulation to empirical data

Marion Talbi¹ and Milan Malinsky

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Meiotic recombination is one of the central evolutionary parameters. While until recently technological challenges limited empirical estimation of fine-scale recombination rates, sequencing technology and method development now allow us to infer its variations on a genome-wide scale.

Genetic polymorphism within population provides information on linkage disequilibrium among loci and permits the inference of recombination history, including in non-model species. However, this information is sensitive to other evolutionary processes: e.g., changes in demography, selection, or migration. Disentangling the relative contribution of each of these phenomena on the linkage and diversity patterns is of prime importance when looking at the effect of recombination in evolutionary studies, for example while studying speciation or adaptation. Simulations are a strong tool to obtain a neutral expectation against which to compare empirical results and gain a better understanding of the processes shaping them.

In this talk, I propose to evaluate how good is inference of fine-scale recombination maps based on population genetic data. I am going to use and compare: (i) fine-scale recombination maps obtained from two ecotypes of the cichlid fish species *Astatotilapia calliptera*, that are on the path to speciation, and (ii) simulation-based maps obtained under matching evolutionary parameters (divergence time, gene flow, demographic history). I will then use this comparison to interpret the difference in fine-scale recombination maps between the two ecotypes. In addition, I am going to focus on the effect of selection on recombination inference, as reflected in the pattern of genetic differentiation between the ecotypes (e.g., F_{st} and D_{xy}).

Up to 25% of beneficial mutations in protein sequences are not adaptive innovations in mammals

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In this work based on genome-wide studies across species and populations, we estimated the proportion of beneficial mutations in protein coding sequences that are not adaptive innovations. Our study is based on the premise that slightly deleterious mutations scattered across the genome are reaching fixation due to genetic drift. These mutations are then subsequently reverted by beneficial back-mutations, generating a balance at which genomes are constantly both damaged and repaired simultaneously at different loci. Even though the existence of these back-mutations is predicted by the nearly neutral theory, they have been largely overlooked, and positive selection has been countlessly interpreted as adaptation to changing environments. In this work, we integrated datasets across the entire exome of 96 species at the mammalian scale, with polymorphism for 28 populations from 6 genera (*Equus*, *Bos*, *Capra*, *Ovis*, *Chlorocebus* and *Homo*). We then estimated selective effects of mutations inside mammalian protein coding sequences, under a model assuming no adaptation at the phylogenetic scale. We finally estimated the proportion of beneficial mutations that are not adaptive innovations among all beneficial mutations at the population scale. Our work confirms that deleterious substitutions have accumulated in mammals and are currently being eliminated. In modern humans, it results in around 25% of beneficial mutations that are not adaptive innovations, but instead are repairing previous deleterious changes.

Genetic purging due to self-fertilization does not prevent accumulation of expansion load

Leo Zeitler¹, Christian Parisod¹, and Kimberly Gilbert¹

¹ *University of Fribourg, Fribourg, Switzerland.*

Mating system and demography shape genetic diversity within a population. Self-fertilization tends to occur more frequently towards species' range edges since mate reassurance that comes with selfing is a favorable trait for colonization. The accumulation of genetic load during range expansions may be combated in selfers due to increased homozygosity resulting in purging. While the effect of range expansions on genetic load is well described, the combined consequences of complex demography and mating system shifts are less clear. We investigate this question by integrating forward-time simulations of range expansions with empirical data collected from more than 500 genomes across a post-glacial expansion of *Arabis alpina*, a mixed mating plant. Simulation show that irrespective of self-fertilization, the expansion results in elevated genetic load in marginal populations. Selfers also expand their range faster, indicating fewer generations subject to genetic drift and a reduced Allee effect. We detect a reduction of recessive lethals in edge populations with increased selfing. However, this purging is not sufficient to prevent expansion load. Empirical results show substantial load still accumulated in selfing range-edge populations compared to outcrossing, range-core populations. Our results demonstrate that self-fertilization can alter the signature of genetic load in expanded populations, potentially providing an additional benefit of purging along with mate reassurance. Complicated factors such as local adaptation at the range edge may force slower expansion and therefore limit the benefit of selfing and subsequent escape from accumulating genetic load.

Does the early social environment influence behavioural flexibility in cooperative breeding cichlids?

Océane Ferreira¹; Birgit Szabo¹, and Barbara Taborsky¹

¹ *Division of Behavioural Ecology, Institute of Ecology and Evolution, University of Bern, Bern, Switzerland.*

To flexibly adapt one's behaviour to the current environmental conditions can be crucial for survival, reproductive success and social integration in group living animals. Flexibility has been widely demonstrated in the animal kingdom in both social and non-social contexts, but the factors driving variation in flexibility remain poorly understood. The early social environment is one important driver of variation in cognitive abilities and of flexibility in the social context. Here, we ask whether the early social environment also affects flexibility in a non-social context. We investigated this question in *Neolamprologus pulcher*, a cooperatively breeding cichlid living in stable social groups with division of labour. In this species non-social helping tasks are modulated by social behaviours; therefore, it is possible that the early social environment influences non-social flexibility later in life. To test this hypothesis, we compared the performance of individuals raised during their first two month of life either in large groups of 10 fish or small groups of three fish across three non-social flexibility tasks: innovation, reversal learning and set shifting. Flexibility in non-social contexts was demonstrated in all tasks, but there was no evidence for a long- term effect of the early social environment. While previous studies have demonstrated that developmental plasticity induced by the early social environment affects cognition in the social domain, these results suggest that early social experience does not affect the non-social domain likewise.

Oviposition location is key for offspring fitness

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Animals have evolved different behavioural, physiological, or morphological adaptations to increase survival and fitness of their offspring. Amphibians exhibit huge diversity in reproductive strategies, which are largely driven by oviposition site selection. A clear example of this are glassfrogs, where clutches are laid in species-specific conditions including exact positioning on leaves. Hence, we raise the question of how important is oviposition location for offspring survival and development. To tackle this question, we used *Teratohyla spinosa*, a Neotropical glassfrog that lays its jelly rich eggs on the edge at the underside of leaves. As clutches are in constant contact with dripping water canalized by the leaf's surface, we hypothesized that *T. spinosa* strategically chooses these locations to ensure clutch hydration during embryo development. We experimentally relocated clutches to the central part of leaves and compared their hydration status, embryonic development, predation rate, and hatching success to control clutches. Our preliminary results show that mortality was not affected by clutch location on the leaf, however, hydration conditions differed considerably between test and control clutches, especially when located on big leaves. Overall, our results demonstrate that parents can increase offspring fitness by strategic oviposition site choice even species that show no extended parental behaviour.

Caring is sexy: Females of *Hyalinobatrachium valerioi* prefer males with clutches

Marina Garrido-Priego¹, Moric Toszeghi, Francesca Angiolani-Larrea, Anyelet Valencia-Aguilar, Max Ringler, Jennifer Stynoski, and Eva Ringler

¹ *Institute of Ecology and Evolution, University of Bern.*

In many animal mating systems, females prefer to mate with males that feature certain morphological or behavioral traits. However, in species where males provide parental care, it is still relatively unknown whether females also evaluate male parental performance when selecting between suitable mating partners. In this study, we assessed male mating success in the glass frog *Hyalinobatrachium valerioi*. Males take care of the eggs and they stay with clutches until they hatch, while females leave immediately after oviposition. Previous studies suggest that females prefer males with multiple clutches. Here, we aimed to test this hypothesis and assess whether they also take into account the level of care. For 62 days during the peak of their breeding season (Sept-Nov of 2021), we conducted night and morning surveys at Quebrada Negra, Costa Rica. We recorded individuals' positions on a digital map, took pictures for individual identification, and assessed the number of current clutches and their parental behavior. In total, we sampled 102 individuals, 43 males, and 54 females. We combined behavioural observations, GIS, parentage, and statistical analysis to get deeper insights into individuals' movement and behavior. We found that the likelihood of getting a new clutch on a given night is bigger in males that were present in the oviposition site the previous night, that call and that already have clutches.

Ecological and biological indicators of the accuracy of species distribution models: lessons from European bryophytes

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³ *Institute of Botany, University of Liège, Liège, Belgium.*

** equally contributing*

The predictive power of species distribution models (SDMs) substantially varies among species depending on their ecological and life-history traits, but which of these traits are the most relevant and how they influence species 'predictability' remains an area of debate. Here, we address these questions in bryophytes. SDMs were calibrated for 411 species in Europe and externally evaluated using an independent dataset in southern Belgium. Predictors included macroclimatic, topographic and edaphic variables. Eleven species traits describing ecological preference, niche breadth and life-history were scored to determine whether they could help interpreting variation in model accuracy among species. A substantial drop in predictive power was observed when moving from internal to external model validation, emphasizing the relevance of external model validation. SDM accuracy substantially varied among species. This variation was significantly explained by species characteristics, including life-history traits, ecological preference and niche breadth, supporting the hypothesis that the strength of species–environment correlations is affected by characteristics of the species themselves. Species ecological preferences, and in particular, pH and nitrogen preference index, were by far the variables most contributing to relation between predictive performance and species traits. SDM accuracy tended to decrease in widespread generalist species. The fact, that model accuracy was higher for species from oligotrophic, and hence, more restricted habitats, is important in a conservation context as ubiquitous species from eutrophic environments are precisely the ones of lower conservation relevance.

Undersown plant species affect disease severity in barley through aboveground processes

Seraina L. Cappelli^{1,2}, Luiz A. Domeignoz-Horta², Jussi Heinosalo¹, and Anna-Liisa Laine^{1,2}

¹ *University of Helsinki.*

² *University of Zürich.*

From theoretical and experimental studies in model systems it is well established that species rich ecosystems are better at providing ecosystem functions such as biomass production, pollinator abundance, pest suppression or carbon sequestration than species poor ecosystems. Modern agroecosystems are depleted of diversity, heavily dependent on external inputs and notoriously sensitive to pathogen outbreaks. In the TWINWIN field experiment we study the potential of different undersown plants to provide a multitude of ecosystem functions in agroecosystems. When barley was grown with a diverse set of undersown species it suffered less from pathogen infection (mostly net blotch disease) and had lower proportions of damaged seeds (mostly insect larvae) than when grown alone or with only few undersown species. Most undersown species contributed to reduced disease pressure, but single undersown species varied greatly in their impact on barley yield. A pot experiment showed that reduced pathogen infection with increasing undersown diversity was mostly mediated through aboveground processes, while belowground processes were less important. Understanding how diversification in general and single undersown species in particular affect different ecosystem functions, is crucial to design sustainable agroecosystems in the future.

Agricultural practices shape fungal communities at microgeographic scales

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² *Computational and Molecular Population Genetics, Institute of Ecology and Evolution, University of Bern.*

Soil fungal communities play an essential part in nutrient cycling and carbon storage and are thus critical for the functioning of terrestrial ecosystems. Anthropogenic disturbances such as tillage, fertilization, and crop rotation have been identified as main drivers of biodiversity loss in soils. However, the extent of this effect on fungal communities is still underexplored. Here, we addressed the impact of agricultural practices on the biodiversity of topsoil fungal communities at different spatial scales. High-throughput sequencing of the ITS2 region was used to characterize abundance, diversity and community compositions along the border of low-disturbance grass verges and the adjacent croplands. We identified a total of 4'651 fungal ASVs in the Swiss lowland agricultural landscape. Alpha diversity did not differ among sampling localities or land uses. However, beta diversity analyses showed that fungal community structures are sensitive to agricultural management. Croplands harboured a greater proportion of pathotrophic and saprotrophic taxa with Ascomycota being the most dominant phylum across all samples. Community dissimilarity was best explained by different land use of pairwise samples collected within croplands and grass verges within a distance of only 1 m. Our results show that agricultural practices can be key drivers in shaping fungal communities even at microgeographic scales. This brings forth a necessity to take into consideration a broader range of geographic scales to appropriately contextualize community variations among fungal communities in ecological settings.

FRIDAY 17.02.2023 – Morning Sessions

Room: **A300**, Subject: **ECOLOGY AND EVOLUTION**

Chair: Claudio Quilodràn

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|--------|--------------------------|--|
| 11:00 | Alexandros Tsoupas | Spatially explicit simulations unveil the population dynamics along the Danubian route during the Neolithic. |
| 11: 15 | Judith Schepers | Effect of heat and drought on plant performance at rear range limits. |
| 11:30 | Carlos Rodríguez-Ramírez | The contribution of alternative splicing to adaptation in threespine stickleback. |
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Room: **A150**, Subject: **BIODIVERSITY AND CONSERVATION**

Chair: Arthur Sanguet

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|--------|---------------------------|--|
| 11:00 | Gesa von Hirschheydt | How many lichens can you find? - Accounting for imperfect detection in a standardized survey. |
| 11: 15 | Damian O. Ortiz Rodriguez | Habitat network models to predict species occurrence and their sensitivity to changes in maximum dispersal distance. |
| 11:30 | Ines Carrasquer Puyal | Museomics to the rescue: Unraveling the insect decline across the 20th century in Switzerland. |
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Room: **A100**, Subject: **SEX EVOLUTION**

Chair: Alice Cibois

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|--------|-------------------|--|
| 11:00 | Emelyne Gaudichau | Elucidating molecular mechanisms of sex determination in stick insects. |
| 11: 15 | Zuyao Liu | The fourspine stickleback (<i>Apeltes quadracus</i>) has an XY sex chromosome with polymorphic inversions. |
| 11:30 | Ewan Flintham | The maintenance of genetic variation in polygenic sexually antagonistic traits. |
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Spatially explicit simulations unveil the population dynamics along the Danubian route during the Neolithic

Alexandros Tsoupas¹ and Mathias Currat¹

¹ *Department of Genetics and Evolution, University of Geneva, Switzerland.*

The genetic diversity of modern Europeans has been greatly influenced by the transition of the way of life from hunting and gathering to farming, known as the Neolithic Transition. This change was facilitated by the arrival in Europe of Farmer populations from the Eastern Mediterranean through two main axes: along the Mediterranean coastline and along the Danube. In our study we investigate this transition specifically along the Danubian expansion axis, by using genomic data from 59 newly sequenced and 10 published ancient genomes. We use spatially explicit simulations to simulate different models of interactions between migrating Farmers and local Hunter-Gatherers and compare them with Approximate Bayesian Computations. In addition, we infer demographic characteristics of the Neolithic Transition, such as the effective population sizes of the two groups, and the levels of admixture and competition between them. Our results suggest that Long Distance Dispersal events were essential for the spread of Farmers along the Danubian route, the competition between Farmers and Hunter-Gatherers was low, at least in Central Europe, and the rate of admixture between the two groups was not constant in time. Our study sheds more light on the Neolithic Transition in Europe by describing with more details some demographic processes and characteristics of that era, helping to better understand modern European genetic diversity.

Effect of heat and drought on plant performance at rear range limits

Judith Schepers¹, Jessica Heblack¹, and Yvonne Willi¹

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Climate has been long known to impact species distribution. However, it is not always clear which aspects of the environment are the most restricting (Hargreaves et al., 2014). A recent literature study documented that cold ends of species' distributions were most often affected by temperature, whereas warm ends of many species were shaped by moisture and temperature, apart from biotic interactions (Paquette & Hargreaves, 2021). Many species seem to withdraw from their warm end of distribution associated with climate warming (Rumpf et al., 2018), suggesting that warmer or hot-dry conditions reach levels outside of the ecological niche. In a greenhouse experiment, we tested whether the effects of heat and drought expected at warm range edges under climate warming were deleterious to plant performance, as well as if and how the effects interacted. We exposed one center and four range edge populations of the North American plant *Arabidopsis lyrata* to heat and drought, as it is increasingly experiencing these conditions at the rear range edge under climate change, and studied their effect in separation and in combination on plant traits and plant performance. Differences were tracked as reaction norms in response to stress treatments from the germination until reproduction. Here we present the results of this study, highlighting interaction effects between heat and drought on performance and the role of plastic trait changes.

Literature

Hargreaves, A. L., Samis, K. E., & Eckert, C. G. (2014). Are species' range limits simply niche limits writ large? A review of transplant experiments beyond the range. *American Naturalist*, 183(2), 157–173. <https://doi.org/10.1086/674525>

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The contribution of alternative splicing to adaptation in threespine stickleback

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Alternative splicing regulates which parts of a gene are kept in the messenger RNA and has long been appreciated as a mechanism to increase the diversity of the proteome within a species. Recently, it has also been suggested as a mechanism underlying adaptation and phenotypic evolution. Consistent with this prediction, there are a few cases in which alternative splicing has been shown to mediate specific phenotypic differences within species or to differ more broadly between populations adapted to different environments. However, the overall contribution of alternative splicing to phenotypic evolution and adaptation is unknown. In this study we asked whether alternative splicing played a role in adaptation to divergent marine and freshwater habitats in threespine stickleback (*Gasterosteus aculeatus*). We examined both differentially expressed and differentially spliced genes (DEGs and DSGs) between pairs of marine-freshwater stickleback across the northern hemisphere and compared the overlap of these genes with genomic regions of high differentiation between marine and freshwater populations. Thus far, we find that both DEGs and DSGs are enriched in these regions, but differentially spliced genes are more enriched than differentially expressed genes. Although further work is needed, these data suggest that differential splicing may play an important role in adaptation to divergent marine and freshwater habitats in threespine stickleback.

How many lichens can you find? - Accounting for imperfect detection in a standardized survey

Gesa von Hirschheydt¹, Marc Kéry, Stefan Ekman, Silvia Stofer, Michael Dietrich, Christine Keller, and Christoph Scheidegger

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While imperfect detection has been thoroughly studied in animal and plant surveys, there are only few studies quantifying detection probability in lichens. Here, we explore detectabilities in a standardized lichen survey of 826 sampling plots across Switzerland. These data provide the statistical base for population size estimates on which the national Red List assessment will rely. Failing to account for detection probability in this survey can therefore have significant consequences for the conservation status of lichens. Across 373 corticolous (tree-inhabiting) species we found an average detection probability of 52 %, with conspicuous lichens showing greater probabilities of detection (61 %) than inconspicuous lichens (43 %). Previous experience of an observer with a species also significantly increased detection probability. There were, however, differences between observers that could not be attributed to experience. We illustrate a simple way to include these three influences in a model to correct estimates of species occurrence with detection errors. Our study confirms the findings from other organisms that detection probability is often far from perfect, even when standardization of sampling reduced detection errors. The conservation relevance of this (and similar) surveys makes it particularly important to account for such detection errors.

Habitat network models to predict species occurrence and their sensitivity to changes in maximum dispersal distance

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Presence or absence (occurrence-state) of a species is highly relevant for conservation. To predict occurrence-state, network models can be used, with suitable habitat patches as nodes, connected by potential species dispersal. A threshold is set at the species' maximum dispersal distance to define connections. However, for most animal species there are no trustable maximum dispersal distance estimates. This hinders the development of accurate network models to predict species occurrence-state. We present a sensitivity analysis of the performance of network models to different maximum dispersal distance settings. Our approach, applied on six amphibians in Switzerland, used habitat suitability modelling to define habitat patches, linked within a dispersal distance threshold to form habitat networks. We used network topological measures, patch suitability, and size to explain species occurrence-state through boosted regression trees. We performed these modelling steps on each species for different maximum dispersal distances, including a literature-derived species-specific value. We evaluated predictive performance and predictor importance among network models. We found a positive relation between predictive performance and dispersal distance, and that species-specific values from literature rarely yielded the best performance. With increasing dispersal distance, the habitat-quality-related variable decreased in importance, while it increased for topology-related predictors. We conclude that model sensitivity to the dispersal distance parameter stems from the contrasting topologies formed with different movement assumptions. Most reported maximum dispersal distances are underestimated, presumably due to leptokurtism. Therefore, caution should be taken when selecting a dispersal distance threshold, considering higher values than those from field reports to account for long-distance dispersers.

Museomics to the rescue: Unraveling the insect decline across the 20th century in Switzerland

Ines Carrasquer Puyal¹, Nadir Alvarez, and Jeremy Gauthier

¹ *Department of Genetics and Evolution, University of Geneva.*

The large-scale decline of insects in the past decades starts to be widely documented. However, the mechanisms, the kinetic and the causes of this decline, and in particular the role of anthropogenic activities, remain poorly understood. Indeed, studies documenting this decline are based on recent trends, since the 1970s, and rely on biomass estimations that do not fully reflect the state of populations. However, samples are available to undertake a large-scale study, both spatially (Switzerland) and temporally (throughout the 20th century). The museum collections contain insects collected throughout this period and form real time series. Thanks to recent developments in museomics, it is now possible to access the genetic information carried by these samples and thus to study their demographic evolution over time. Here we investigate population trends of ten widely distributed insects using museum specimens. To that aim, we selected specimens constituting populations sufficiently sampled in the past and we apply the HyRAD protocol, a cutting-edge museum genomics method. By using population genetic estimators, notably the genetic diversity, the inbreeding coefficient and the effective population size, it will thus be possible to finely assess the population dynamics and the mechanisms involved.

Elucidating molecular mechanisms of sex determination in stick insects

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Sex determination is a key process in animal development, triggering the differentiation of primary and secondary sexual traits essential for reproduction. In insects, sex determination is controlled by different cascades of genes that evolved around two genes called transformer and doublesex. Detailed molecular studies of these two genes in holometabolous insects suggested that insect sex determination is generally controlled via sex specific splicing. However, recent studies of a wider range of insect species challenge this assumption. Here, we investigated sex-specific splicing and expression patterns of the genes doublesex and transformer in stick insects, a hemimetabolous insect order. Interestingly, we found a duplication of the gene doublesex with both copies featuring similar expression patterns between the sexes and across tissues, and no evidence for sex specific splicing. A knockdown experiment targeting one of the two copies via RNAi did not reveal any effect on male or female secondary sexual traits. Furthermore, we also did not find any evidence for sex specific splicing of the gene transformer. In combination with new findings in other hemimetabolous insect orders, our data show that sex determination mechanisms in these orders differ strikingly from those in holometabolous insects. Thereupon, the study of non-model organisms reveals how mechanisms believed to be highly conserved feature extensive variation among species.

The fourspine stickleback (*Apeltes quadracus*) has an XY sex chromosome with polymorphic inversions

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Upon formation of a new sex chromosome pair, recombination is often suppressed, leading to subsequent degeneration. Although inversions are proposed to cause recombination suppression on sex chromosomes, there is still little empirical evidence that inversions drive the early stages of sex chromosome evolution. Species with young and polymorphic sex chromosomes might provide insights into the initiation of sex chromosome evolution. To better understand the early evolution of sex chromosomes, we used fourspine stickleback (*Apeltes quadracus*) as a model. Whole-genome sequencing of males and females from three wild populations and genetic crosses from the same populations revealed *A. quadracus* has an XY sex determination system on chromosome 23. Across all three populations, there is a shared 1 megabase (Mb) region of divergence between males and females that contains several novel candidate sex determination genes. However, there are also different patterns of divergence between males and females in each of the three populations. In one population, there is an inversion on the Y chromosome that suppresses recombination between the X and the Y across 8 Mb. In another population, there is an inversion on the X chromosome that suppresses recombination between the X and the Y across 4 Mb. Although there is not extensive degeneration, these recent inversions are associated with the accumulation of premature stop codons, suggesting that degeneration has already begun on these young sex chromosomes. Our results therefore provide an opportunity for further investigation of the role of inversions in the early stages of sex chromosome evolution.

The maintenance of genetic variation in polygenic sexually antagonistic traits

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Selection often favours different characteristics in males and females, leading to genetic conflicts across the sexes. Theory suggests that these conflicts can maintain genetic variation by generating balancing selection, especially under specific patterns of allelic dominance. However, so far, most of this theory has neglected the genetic complexity of polygenic traits, where phenotypes may be determined collectively by alleles carried across many genetic loci. Consequently, the influence of sexual antagonism on genetic variation in the many traits that show such multilocus genetic architecture remains poorly understood. Here, we use mathematical modelling and computer simulations to investigate the evolution of a polygenic trait that has different optima in males and females. We show that the conditions necessary to maintain variation across multiple loci are significantly more restrictive than at a single locus, with very strong sexual conflict typically required. This is because fitness landscapes that typically favour polymorphism at a single locus (through their effects on dominance), also generate patterns of epistasis across the loci encoding a polygenic trait, with such interactions tending to favour the fixation of a single genotype. Together our results indicate that sex-specific selection is not a straightforward source of balancing selection in polygenic traits, and that instead sexual antagonism should be most prolific in maintaining genetic variation when traits are determined by a single large effect locus.

FRIDAY 17.02.2023 – Early Afternoon Sessions

Room: **A300**, Subject: **SPECIES INTERACTIONS**

Chair: Mathieu Perret

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|--------|---------------------|--|
| 13:45 | Thais Guillen Otero | <u>Facultative mycorrhizal fern? A close-up to the response of <i>Struthiopteris spicant</i> (L.) Weiss and its fungal partners to nutrients and light limitation.</u> |
| 14: 00 | Christina Tadiri | <u>Evidence for Density-Dependent Transmission of an Environmentally-Borne Parasite.</u> |
| 14:15 | Morgane Massy | <u>Phylogenetic history, host-specificity, and genetic structure in Spinturnicidae bat mites from the Baja California peninsula.</u> |
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Room: **A150**, Subject: **EVOLUTIONARY GENETICS AND GENOMICS**

Chair: Alicia Sanchez-Mazas

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|--------|------------------|--|
| 13:45 | Thomas Grubinger | <u>Herbarium specimens shed light on the origins and flavour of early European tomatoes.</u> |
| 14: 00 | Manuel Poretti | <u>Chromosome rearrangements and evolutionary diversification of duplicated genomes.</u> |
| 14:15 | Kenneth Kim | <u>Comparative gene expression analysis of moulting in Insect and Crustacean lineages.</u> |
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Room: **A100**, Subject: **COMMUNITY ECOLOGY**

Chair: Lionel Cavin

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|--------|------------------------|--|
| 13:45 | Thu Zar Nwe | <u>Impacts of nitrogen addition and plant diversity on soil fauna in grassland ecosystems.</u> |
| 14: 00 | Marianna Tzivanopoulou | <u>Assessing the reliability of citizen-science data for the study of ant species' environmental niches and distributions.</u> |
| 14:15 | Mikko Tiusanen | <u>Reproductive investment of plants changes along the elevation gradient.</u> |
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Facultative mycorrhizal fern? A close-up to the response of *Struthiopteris spicant* (L.) Weiss and its fungal partners to nutrients and light limitation

Thais Guillen-Otero¹ and Michael Kessler¹

¹ *Department of Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland.*

The establishment of mycorrhizal relationships between a fungus and a plant usually provides an ecological advantage for the latter while securing a carbon source for the fungus. However, under a particular set of environmental conditions, the resources invested in the fungi's growth and maintenance surpass the benefits obtained by the host. In cases where mycorrhization has a negative impact, facultative mycorrhizal plants are capable of inactivating the symbiosis and surviving. While this phenomenon has been documented and studied in angiosperms, little is known about its occurrence and dynamic in ancient vascular plants. The present study analyzed the response of a particular fern species (*Struthiopteris spicant* L. Weiss) to light and nutrient limitations in terms of growth, mycorrhizal colonization, and leaf nutrient content. We conducted a greenhouse experiment with 80 specimens of *S. spicant* to test the influence of three factors (light availability, phosphorus, and nitrogen fertilization) in their relationship with arbuscular mycorrhizal fungi. Our results indicated significant differences among treatments regarding the richness and relative abundance of Glomeromycota fungi and the C:N ratio on the leaves. Light seemed to be the most crucial factor determining the establishment and maintenance of mycorrhizal relationships: uniquely plants receiving the greatest level of illumination developed associations with arbuscular mycorrhizal fungi.

Evidence for Density-Dependent Transmission of an Environmentally-Borne Parasite

Christina P. Tadiri¹ and Dieter Ebert¹

¹ *Department of Environmental Sciences, Zoology; University of Basel.*

For many infectious diseases, determining whether transmission is frequency- or density-dependent (i.e. whether the contact rate between susceptible hosts and the parasite change with host population density) is of crucial importance to understanding epidemic spread and dynamics. For environmentally borne parasites, especially those with a long free-living stage, the picture is particularly unclear. Here, we monitor transmissibility of an environmentally-borne bacterial parasite, *Pasteuria ramosa* in its host *Daphnia magna* over the course of a seasonal epidemic in a natural pond in Switzerland. Parasite transmission stages (spores) are released into the sediment when an infected individual dies and decomposes. Spores may survive for several years, thus it is assumed that the “spore bank” in the sediment is essentially limitless, and that most transmission in nature occurs from the sediment during grazing (i.e. should be frequency dependent). We here find that spores are present in the water column at infectious levels, and that their concentration in the water column fluctuates over the course of an epidemic, alongside the density of the host population and other invertebrates. As this parasite is not directly transmitted from host to host, we postulate that increasing “activity” in the pond as invertebrate populations grow stirs up spores from the sediment into the water column. We demonstrate experimentally that spores may remain suspended in the water column for long periods of time, thus increased disturbance to the sediment as populations grow may lead to high accumulations of spores in the water column, explaining the density-dependence we observed.

Phylogenetic history, host-specificity, and genetic structure in Spinturnicidae bat mites from the Baja California peninsula

Morgane Massy¹, Laura Najera-Cortazar, and Philippe Christe

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Parasites represent a large part of Earth's biodiversity. They play many essential ecological roles, notably in regulating food webs and driving species richness, and characterizing parasite communities is essential to studies of host-parasites interactions, evolution, and conservation. Bats carry numerous parasites with different levels of host-specificity and adaptations, but these parasitic communities remain poorly understood in many ecosystems. In this study, Spinturnicidae wing mites collected from bats along the Baja California peninsula and in northwestern Mexico were studied. Their mitochondrial COI and 16S gene and nuclear 18S gene were sequenced and Maximum-likelihood and Bayesian phylogenetic analysis were carried out to characterize species diversity. Host-specificity and phylogenetic congruency were measured for each mite species and median-joining haplotype networks were computed to investigate within species structure. Here we show that phylogenetic trees mostly support previously described morpho-species of Spinturnicidae mites. However, our phylogenetic analyses cluster *S. americanus* and *S. carloshoffmani* into a single monophyletic clade, indicating that they are more closely related than previously thought. Overall, Spinturnicidae mites were highly host-specific and had significant phylogenetic congruency with their bat hosts. However, species-level haplotype networks showed low differentiation between sampling sites and between hosts. This study is the first molecular characterization of North American Spinturnicidae mites, and it supports similar studies reporting high host-specificity in European Spinturnicidae. However, further work is needed to disentangle species-specific patterns of genetic structure and their causes.

Herbarium specimens shed light on the origins and flavour of early European tomatoes

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⁶ *Department of Evolutionary Anthropology, University of Vienna, Djerassiplatz 1, 1030 Vienna, Austria.*

When the cultivated tomato (*Solanum lycopersicum* L.) was introduced to Europe in the 16th century it showed large variation in fruit colour, shape and size. However, the geographic origins of these tomatoes have long been debated and their flavour remains unknown. To address these questions, we sequenced 21 herbarium tomatoes collected in Europe between 1596 and 1915 and accessed 166 published sequences from 20th-century Latin American tomato varieties. Evolutionary genomic analyses showed that all historical specimens were most closely related to either large-fruited or cherry-sized modern tomatoes from Mexico, which suggests Mexico as the immediate origin of European tomatoes and is consistent with the variation in fruit size reported in historical records. Sequence variation at 119 genes related to fruit yield and flavour revealed haplotypes private to subsets of historical specimens at 13.3% of the flavour genes, but only at 5.7% of the fruit-yield genes. Across putative causal variants underlying fruit size and fruit flavour, specimens with a higher percentage of fruit-size increasing alleles tended to have a lower percentage of alleles associated with favourable flavour, consistent with genetic constraints underlying a trade-off between fruit size and flavour. Sequence variation at the fruit-sugar gene LIN5 suggested that both historical and modern cherry-sized Mexican tomatoes are sweeter than their large-fruited counterparts. In contrast, variation at the ALMT9 gene controlling malic acid metabolism suggested that historical large-fruited tomatoes might have tasted better than modern ones. These results highlight the potential of herbarium genomics to explore hidden stages of plant domestication.

Chromosome rearrangements and evolutionary diversification of duplicated genomes

Manuel Poretti¹, Hussein Anani, Terezie Mandakova, Martin Lysák, and Christian Parisod

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Chromosome rearrangements (CRs) are known to promote the reduction of genome size and chromosome numbers (i.e. diploidization) in plants undergoing recurrent whole-genome duplications. Such phenomenon appears decisive for the evolutionary diversification of plants, however the genomic basis of chromosomal restructuring remains underexplored.

In our study, we combine cutting-edge sequencing technologies (Oxford Nanopore, PacBio Iso-Seq and Hi-C) to build, annotate, and compare chromosome-scale genome assemblies of closely related *Biscutella* species. These plant species diversified independently following a whole genome duplication event and colonized different environmental niches, making the *Biscutella* genus a unique system for understanding the impact of diploidization on plant adaptation in natural populations.

The availability of chromosome-scale genome assemblies is crucial for investigating structural variation. Although the complexity of large and repetitive plant genomes often hinders such analyses, we provide guidelines for the assembly and annotation of high-quality genomes and shed light on the molecular mechanisms underlying CRs (with a special focus on transposable elements). Through comparative genomics, we quantify the impact of different restructuring events on genome divergence and assess molecular processes that alter genome size and content, determining to what extent different types of restructuring events affect the gene space vs the repetitive fraction during diploidization and species diversification.

Comparative gene expression analysis of moulting in Insect and Crustacean lineages

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² *Swiss Institute of Bioinformatics, 1015, Lausanne, Switzerland.*

Pancrustacea (crustaceans and hexapods) is the most species-rich clade in the Arthropoda phylum, comprising the majority of animal species on earth. Arthropods such as Insects and crustaceans produce a hard chitinous exoskeleton that they need to shed in a process called moulting. This developmental process is conserved throughout Arthropoda, and yet the molecular processes underlying moulting and how it evolved in different arthropod lineages remain unclear. To examine the gene expression dynamics of moulting across different pancrustacean lineages, we analysed publicly available RNA-seq datasets from pre-moult and post-moult stages of several Crustaceans (*Litopenaeus vannamei*, *Parhyale hawaiiensis*, *Eriocheir sinensis*) and Insects (*Drosophila melanogaster*, *Bactrocera dorsalis*, *Zeugodacus cucurbitae*). Enrichment analysis reveals that differentially expressed genes before and after moulting are related to moulting pathways and structural processes such as chitin-based cuticle development, ecdysteroid metabolic process and chitin binding. Co-expression analysis of moulting across various pancrustacean lineages revealed two major clusters of orthogroups which reflect the transition from pre-moult to post-moult stage. We recovered genes that are likely involved in late-genes pathway such as chitin biosynthesis, which suggests that moulting processes other than the hormonal biosynthetic pathway are also conserved. Examining the specific gene families involved in the late-genes pathway and their evolutionary relationships in different taxa will be important to further elucidate the evolution of moulting in Arthropods.

Impacts of nitrogen addition and plant diversity on soil fauna in grassland ecosystems

Thu Zar Nwe¹, Santiago Soliveres¹, Anne Kempel¹, Eric Allan¹, and Nadia I. Maaroufi¹

¹ *Institute of Plant Sciences, University of Bern.*

Several studies have provided evidence that nitrogen enrichment can alter plant communities directly, or indirectly by changing plant richness and functional trait composition. However, it is unclear what the relative importance of these drivers is in affecting important soil fauna groups, detritivore and predatory mites, in temperate grasslands. We conducted a large grassland experiment that tested the effects of nitrogen addition, plant functional composition and diversity, and foliar pathogen presence (controlled by fungicide) on soil decomposer and predatory mites (total, adult and juvenile abundances and adult-juvenile relative abundance). We also examined effects of plant nutrient content and plant biomass (root and shoot). The results showed that nitrogen addition and high soil C:N ratio increased soil mite abundances (total, Oribatida juveniles and Mesostigmata adults). Further, high plant functional diversity increased total and adult predatory mite abundances, while fungicide application reduced the number of juveniles. We also found that the C:N ratio significantly decreased the proportion of Oribatida (detritivores), but increased Prostigmata-Astigmata abundances in fast-growing compared to slow-growing plant communities. The proportion of Mesostigmata (predators) was increased at high plant functional diversity. Interestingly, root biomass significantly increased adult Oribatida, while above-ground biomass increased overall mite abundances. Our results suggested that nitrogen addition and soil C:N ratio were key drivers of the abundance of soil mites and their trophic groups in temperate grasslands.

Assessing the reliability of citizen-science data for the study of ant species' environmental niches and distributions

Marianna Tzivanopoulou¹, Olivier Brönnimann, Tanja Schwander, Anne Freitag, and Antoine Guisan

¹ *Department of Ecology and Evolution, University of Lausanne.*

To obtain data at large spatial and temporal scales, scientists are increasingly taking advantage of citizen-science projects, where data collection is done by volunteers. However, the potential presence of bias due to differences in species detectability and sampling effort in space could affect the interpretation of scientific results. Quantifying such bias for different species groups is therefore key to using the full potential of citizen-science datasets. Here, we compare the environmental niches and predicted distributions of ant species in the canton of Vaud, Switzerland, based on quantitative inventories versus data from a large citizen-science project. For the majority of species (11 out of 15 from 6 different genera), we find significant overlap between the quantified environmental niches and a high correlation between model predictions based on the two datasets. Divergence in model predictions was observed mostly for species with low detectability or which occurred in both natural and urban habitats, because the latter were oversampled in the citizen-science project. Based on these findings we developed a method to correct for the spatial sampling bias of the citizen-science dataset. Applying this bias correction increased the niche overlap and prediction correlations. Our findings indicate that citizen-science data can reliably be used for species distribution modelling, as long as the characteristics of the species studied are considered. To take advantage of the abundance of citizen-science data when modelling the distributions of understudied species for conservation purposes, integrating scientific and corrected citizen-science data is recommended to minimize the risk of biased predictions.

Reproductive investment of plants changes along the elevation gradient

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Most plants are entomophilous, insect pollinated. Thus, attracting pollinators with flowers is a key for their reproduction. Producing flowers is costly and the optimal reproductive strategy may change depending on the environment. However, how the environment drives the reproductive efforts of plants, and their floral production is unclear. In addition, plants have innate functional traits, e.g., phenology and pace of life, that largely influence their capabilities to adapt to their environment. Still, the effects of interplay of the functional traits and environmental conditions on the reproductive efforts of the plants remain unexplored.

Here, we investigate how the vegetative cover of species influences the number of flowers produced and how this relationship changes along the elevation gradient. In addition, we study what is the role of the plant functional traits in their reproductive responses to the environment. For this, we combine data from surveys on vegetation cover and flower abundances collected between 600 and 1800 meters above sea level on Mt. Calanda, SE Switzerland.

We find a general decrease in the number of flowers towards the higher elevations. This effect is modified by the vegetative cover of the species: Highly abundant species invest relatively less into flowers at high elevations. These findings indicate that at the harsher conditions and shorter growing season of the high elevations, plants likely invest less resources into reproduction and more into survival. However, with the warming climate, increased investment into reproduction might become a better performing strategy at high elevations.

FRIDAY 17.02.2023 – Late Afternoon Sessions

Room: **A300**, Subject: **SYSTEMATICS AND MACROEVOLUTION**

Chair: Claudio Quilodràn

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|-------|--------------------------|--|
| 15:15 | Diana Isabel Rendón Mera | <u>Restrict and increase: a taxonomic revision of the jumping plant-louse genus <i>Leuronota</i> (Hemiptera: Psylloidea: Triozidae).</u> |
| 15:30 | Mathilde Ruche | <u>A novel understanding of peristome hygrosopic movements in mosses revealed by histological investigation.</u> |
| 15:45 | Vivien Louppe | <u>Impact of life cycle variation on lower jaw diversity in salamander and newts.</u> |
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Room: **A150**, Subject: **EVOLUTIONARY GENETICS AND GENOMICS**

Chair: Yamama Naciri

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|-------|------------------|--|
| 15:15 | Vitor Sudbrack | <u>Limited dispersal speeds up adaptation via non-additive genetic variants.</u> |
| 15:30 | Hanna Rosinger | <u>Not much of a muchness: Repeated freshwater adaptation - but distinct demographic histories of sticklebacks in Greenland.</u> |
| 15:45 | Anna Marcionetti | <u>Genomics of the diversification of the clownfish skunk complex (<i>Amphiprion akallopisos</i>, <i>A. sandaracinos</i> and <i>A. perideraion</i>).</u> |
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Room: **A100**, Subject: **COMMUNITY ECOLOGY**

Chair: Camille Christe

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|-------|---------------------------|--|
| 15:15 | Caroline Daniel | <u>Dynamic changes in plant species competition: effects of nitrogen and pathogens on multispecies competition networks.</u> |
| 15:30 | Roberto Rebollo Hernandez | <u>Flower color diversity in ecological communities: a case study in alpine grassland communities.</u> |
| 15:45 | Luiz Jardim de Queiroz | <u>Environmental niche sharing in the Alps depends on whether species arose through immigration or speciation.</u> |
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Restrict and increase: a taxonomic revision of the jumping plant-louse genus *Leuronota* (Hemiptera: Psylloidea: Triozidae)

Diana Isabel Rendón-Mera¹ and Daniel Burckhardt

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The plant-louse genus *Leuronota* Crawford currently includes species from America, Southeast Asia, and Oceania, though there is evidence supporting the monophyly of the American species but not for the genus as presently perceived. This assumption was, however, not tested, owing to the lack of a formal genus revision, inadequate original descriptions of many of the species and insufficient material in general. Thus, we conducted this long-pending revision of *Leuronota* to achieve a better resolution of the group and to explore its internal relationships, as well as to properly classify several apparently new species recently collected in Brazil and Costa Rica. To do so, we revised over 1,000 specimens including relevant type material. Species delimitation was based mainly on characters of the forewing and male terminalia and, to a lesser extent, the genal processes and female terminalia. We described, photographed, and produced drawings for all species, and constructed an identification key for adult specimens. As a result, we (1) transferred the non-American species to other genera; (2) synonymised two described species; (3) revised the generic diagnosis; and (4) formally described 30 new species. These results were also supported by our molecular data. Our study almost doubled the number of described species of *Leuronota*, highlighting the importance of taxonomy as a fundamental discipline not only for cataloguing biodiversity but also for understanding it. Furthermore, we created the foundation for examining the evolutionary patterns of insect-plant associations, an important question one could not answer without a sound taxonomic base.

A novel understanding of peristome hygroscopic movements in mosses revealed by histological investigation

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The peristome is located at the extremity of the sporophyte capsule and is considered as the most complex and conservative morphological structure in mosses. In the Arthrodontous mosses, defined by a peristome with one or two rings of articulated teeth made of remnants of thickened cell walls, this structure plays a key role in spore dispersal. Surrounding the opening of the capsule, the peristome teeth control spore release with hygroscopic movements in order to disperse the spores at the most appropriate time. The teeth respond to diverse humidity conditions and this mechanism results in opening and closing movements. These hygroscopic movements are due to the nature and architecture of the peristome. To better understand them, a thorough histological investigation of the Arthrodontous peristome was carried out across a large sampling of representative species in the Arthrodontous mosses. Longitudinal serially sectioned slices of the mature and developing peristome revealed the presence or absence of a hydrophobic layer in between the outer and inner faces of the peristome. To complement the anatomical dataset, we led a series of physiological tests to ascertain the function of this layer. Altogether, our combined histological and physiological data led to a novel understanding of the hygroscopic movements of peristomes.

Impact of life cycle variation on lower jaw diversity in salamander and newts

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Complex life cycles, involving fundamental morpho-functional and physiological changes during development, are widespread in the animal kingdom and are observed in most invertebrates and half of the known vertebrate species. These changes can induce significant selection pressures that may lead to divergent evolutionary trajectories, and thus promote the morphological diversification of organisms. In this study, we investigated how life cycle strategies foster morphological diversity among caudata using geometric morphometric analyses of the lower jaw in 218 species, covering the breadth of developmental strategies and ecological diversity across the group.

We investigated the influence of life cycle strategies on: 1) the variation in allometric patterns between the different species using multivariate analyses of covariance taking into account phylogeny; 2) the disparity in shape for each of the three bones of the mandible; 3) the morphological variation among and between life cycle strategies using classification algorithms.

Congruently with previous study of the cranium our results show that life cycle strategy significantly influences mandible shape. Paedomorphic species display a more disparate mandible shape, overlapping most of the morphospace displayed in biphasic, direct developing, and viviparous species. This high disparity in paedomorphs is mainly expressed in the dentary, while biphasic and direct-developers show higher disparity of the articular-angular complex. Overall, lower jaw morphologies appear more differentiated and phylogenetically structured in paedomorphs than in species undergoing complete metamorphosis, possibly resulting from the physical constraints linked to the aquatic environment in which all paedomorphic species live.

Limited dispersal speeds up adaptation via non-additive genetic variants

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The probability and the expected time for new beneficial alleles to fix via selective sweeps are two relevant quantities in population genetics. Such sweeps may be hard – where the fixing allele originates from a new mutation – or soft, in which the fixing allele comes from the species' pool of standing variation. The mean time taken by these different sweeps is well understood in well-mixed populations where individuals interact and compete randomly. Many natural populations, however, are subdivided and dispersal-limited. While such dispersal limitation is known to influence the probability that non-additive beneficial alleles will fix, its effect on the time taken by such fixation remains understudied. Here we show how limited dispersal and population subdivision affect the time scale of adaptation via hard and soft sweeps. We find that dispersal limitation always increases the time taken by an additive allele to sweep. In contrast, for sweeps of non-additive alleles, we find non-monotonic effects of dispersal limitation on the rate of adaptation: it decreases the time an allele takes to fix as dispersal is initially limited, but rises the time of sweeps if it is further limited past below a dispersal threshold. Regarding soft sweeps, we find that adaptation of recessive alleles no longer benefits from dispersal limitation. Overall, adaptation is faster under realistic dispersal rates when mutations have non-additive fitness effects. This work puts forward our understanding of the pace of genetic adaptation under the influence of limited dispersal, population structure and genetic dominance – in particular for non-additive alleles.

Not much of a muchness: Repeated freshwater adaptation - but distinct demographic histories of sticklebacks in Greenland

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Genetic diversity, which is critical for a population to adapt to changing environments, is shaped by a variety of demographic processes, such as population size, size of the founding populations, bottleneck strength during establishment of populations and migration rates between populations. Back-in time modelling permits us to efficiently test a variety of evolutionary scenarios and hence to gain insights about the demographic processes driven genetic diversity. Three-spined stickleback (*Gasterosteus aculeatus*) is an ancestral marine fish that has adapted to freshwater numerous times throughout the Northern hemisphere. The repeated and independent incidences of freshwater colonisation of sticklebacks enables us to study multiple replicated instances of freshwater adaptation and the demographic histories of those populations. Here we present a study of sticklebacks in Greenland, where a high number of lakes have been independently colonised and preliminary results revealed that stickleback populations differ in genetic diversity amongst those lakes as well as in phenotypes, typically associated with freshwater adaptation. Specifically, we utilised whole-genome-resequencing data from freshwater lakes in Greenland (6 individuals per population, 4 populations) and 20 marine individuals for demographic back-in time modelling (fastSimCoal2). Models were used to explain differences in genetic diversity among those lakes and how variation in demographic history influences freshwater adaptation of stickleback populations. The study provides detailed insights into the diverse nature of the demographic history of geographically close lakes and aims to broaden our understanding on the repeatability and speed of freshwater adaptation.

Genomics of the diversification of the clownfish skunk complex (*Amphiprion akallopisos*, *A. sandaracinos* and *A. perideraion*)

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Clownfish are an iconic group of coral reef fish that evolved a mutualistic interaction with sea anemones, which triggered the adaptive radiation of the group. Within clownfishes, the skunk complex is particularly interesting as, besides ecological speciation, hybridization events were suggested to shape the divergence of the group. Thus, we investigated here the mechanisms underlying the diversification of this complex. By taking advantage of their disjunct geographical distribution, we obtained whole-genome data of sympatric and allopatric populations of the three main species of the complex. We examined population structure, genomic divergence patterns, and introgression signals, and we performed demographic modelling to identify the most realistic diversification scenario. We excluded scenarios of strict isolation and of hybrid origin of *A. sandaracinos*, and we ruled out the presence of extensive gene flow in sympatry. However, we discovered moderate gene flow from *A. perideraion* and the ancestor of *A. akallopisos* + *A. sandaracinos* and weak gene flow between the species in the Indo-Australian Archipelago throughout the diversification of the group. We identified introgressed regions in *A. sandaracinos*, and we detected two large regions of high divergence in *A. perideraion*, likely maintained by the disruption of recombination. Altogether, these results show that hybridization events in the skunk complex are less pervasive than initially thought and suggest a role of host repartition in maintaining the genetic identity of the species in sympatry.

Dynamic changes in plant species competition: effects of nitrogen and pathogens on multispecies competition networks

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Plant competition is key to understanding processes such as population dynamics, maintenance of species diversity, or the assembly, stability and functioning of ecosystems. However, it has been challenging to study competitive interactions between multiple species in highly diverse systems. To go beyond the pairwise approach, network theory has developed a series of tools and metrics that characterise the structure of interactions among species. However, very few studies have explored how such networks vary with changes in resources and enemies, or how networks differ between species with different growth strategies (e.g., slow versus fast-growing species). We conducted a manipulative experiment with 18 perennial plants, which varied strongly in growth strategy, planting the species into neighbourhoods with different densities of each competitor and we followed their performance across two seasons. We did this within the context of the PaNDiv Experiment, near Bern in Switzerland, in which species richness, plant functional composition, nitrogen supply and foliar pathogen presence were manipulated. Our results show that nitrogen and fungicide (and to some extent seasonality) re-arrange the structure of plant interaction networks and decouple network metrics. Both the mean and the variance of the community specific leaf area (SLA), which is strongly linked to the growth strategies, impacted the structure of plant interactions. Competition networks can represent the overall structure of species interactions and can shed light on the mechanisms determining effects of global change on biodiversity.

Flower color diversity in ecological communities: a case study in alpine grassland communities

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Flowers exhibit an astonishing diversity of colors, which play important ecological roles such as attracting suitable pollinators. Studies started to document patterns of color diversity in various ecological communities. However, we still lack a mechanistic understanding of why communities harbor such a high diversity of flower colors.

In this study, we focus on alpine grassland communities that are known for their diversity of flowering species. We have measured flower color reflectance (using a spectrophotometer) for 65 plant species and gathered similar color data for 74 alpine species from the literature. These plant species can be categorized into communities based on their occurrence in typical phytosociological units.

By sampling random subsets of species belonging to either described communities or to the whole set of species, and calculating diversity measures, we ask whether observed alpine flower communities show higher color diversity than expected by chance (while controlling for the phylogeny of sampled species), and whether pollinator-mediated niche-partitioning may explain the high-color diversity in plants occurring in the same community.

Our preliminary results suggested that the colors are more diverse in observed communities than expected by chance. We are currently analyzing the data to answer the other question. Overall, we expect this work will bring novel insights for a better understanding on color diversity in plant communities.

Environmental niche sharing in the Alps depends on whether species arose through immigration or speciation

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The extent of niche conservatism and niche divergence between related taxa can be strongly influenced by ecological and evolutionary processes, such as immigration and speciation. However, the relative role of these processes on species niche sharing and whether they differ across taxonomic groups is little known. We addressed this issue by focusing on the Alps' biodiversity. We tested if the degree of environmental niche overlap depends on the process by which species arose in the regional pool (immigration or speciation). We reconstructed the environmental niche for 123 species of butterflies, 119 fishes, 26 amphibians, and 76 flowering plants. Then we estimated the degree of niche overlap between all within-taxa species pairs. To test whether closely related species have more similar environmental niches than unrelated ones, we correlated niche overlap with genetic distance (as a proxy for species relatedness). We found that species that have immigrated into the Alps, rather than speciated in situ, show a higher degree of niche overlap, independent of their relatedness. When we considered genetic distance, lacustrine fish that speciated in situ were the only group in which closer relatives had more divergent niches. We associate this pattern with adaptive radiation being more important in generating biodiversity in lacustrine fish than in the remaining taxa. Our findings reveal that despite shared biogeographic histories in the Alps, ecological and evolutionary processes contributed differently to the extent of niche conservatism and niche divergence between different taxonomic groups and habitats.

POSTERS

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2	Yann Fragnière	<u>Mapping habitats sensitive to overgrazing in the Swiss Northern Alps using habitat suitability modeling.</u>
3	Lorraine Hablützel	<u>The effect of life-history strategies on local adaptation.</u>
4	Kristine Jecha	<u>How Reliable are Morphological Criteria for Species Identification: a case study using ants of the <i>Lasius</i> genus.</u>
5	Gyda Fenn-Moltu	<u>Accidental biocontrol: human-mediated dispersal of insect parasitoids and predators.</u>
6	Vera Ogi	<u>Genomics of plant toxin resistance in entomopathogenic nematodes.</u>
7	Alessio De Nardo	<u>Context-dependent sexual selection in <i>Drosophila prolongata</i>.</u>
8	Baptiste Bovay	<u>Asynchronous migration of plants and butterflies: will butterflies choose new host plants from higher elevations?</u>
9	Daniel Rodrigues Nunes	<u>A biosystematic revision of the family Cribariaceae.</u>
10	Océane La Loggia	<u>Family matters: Early social complexity and development of social behaviour.</u>
11	Viviane Perraudin	<u>Ecological niche modeling for <i>Ptilostemon greuteri</i> (Asteraceae): implications for in situ conservation and future translocation.</u>
12	Nicolas Zurbuchen	<u>Intraspecific trait variation, local adaptation, and environmental conditions as drivers of host disease risk along an elevation gradient.</u>
13	Keerthi Divakaran	<u>Maize benzoxazinoid exudation in soil follows a diurnal rhythm.</u>
14	Isabelle Toussaint	<u>How changes in life cycle and associated environment foster functional diversity: A comparative analysis of prey capture kinematic in Caudata.</u>
15	Yan Yang	<u>Do pollen nutrients constrain the diet of wild bees in urban areas?</u>
16	Zixin Li	<u>Comparative and experimental evidence that sticklebacks cause benthic trophic cascades in Southern Greenland ponds.</u>

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17	Peter Lenart	Learning accelerates the evolution of slower aging, but constrains the evolution of negligible senescence.
18	Orlando Schwery	New Ways to Gain More Reliable Insights Into Adaptive Radiations - A Case in <i>Anoles</i>.
19	Mai Thu Nguyen	The genetic architecture of populations where females, males and hermaphrodites stably coexist.
20	Angelo Guadagno	Investigating cognitive flexibility using a full custom-made behavioural set-up.
21	Lauréline Humair	Can herbivorous insects in Switzerland provide insights into the biological control of <i>Robinia pseudoacacia</i> in South Africa?
22	Gerard Martínez-De León	Soil community responses to climate extremes at different elevations across seasons.
23	Soledad Santillán-Guayasamín	Effect of larval nutritional stress on wing morphology in <i>Culex pipiens</i>.
24	Dave Lutgen	Modular regulation and convergent evolution of ASIP underpins color variation in wheatears.
25	Kilian Perrelet	Engineering blue-green infrastructure for and with biodiversity in cities.
26	Elias Trachsel	Hybridization upon secondary contact - the purple-edged copper butterflies (<i>Lycaena hippothoe</i>) in the Swiss Alps.
27	Ehouarn Le Faou	The genetics of sex allocation evolution in a herbaceous plant: a sex chromosome introgression project.
28	Terezia Horvathova	Vertical, horizontal or environmental? Research on symbiont acquisition calls for proper controls.
29	Clara Castex	Host Specialization in Bat Parasites: Host Choice Experiment and Genetic Comparison of <i>Cimex lectularius</i>.
30	Luca Soldini	From a supergene to social polymorphism in fire ants.
31	Alice Pessina	Investigation of the host finding behavior of <i>Phytobius vestitus</i> for the biological control of the invasive weed <i>Myriophyllum aquaticum</i>.
32	Malin Röllin	Harvestmen communities of three vegetation stages in a revitalised pre-alpine riparian forest (Arachnida, Opiliones).

Location	Presenter	Title
33	Morgane Fournier	The role of life cycle variation on morphological diversity in European populations of salamanders and newts.
34	Jessica Heblack	Evolutionary constraints at low-latitude range edges under climate change.
35	Angela Meneses	Darwin wasps (Hymenoptera: Ichneumonidae) – little (known) fellows in nature conservation.
36	Gabrielle McLaughlin	Effects of local and landscape factors on pollinator genetic diversity and differentiation.
37	<i>Cancelled</i>	
38	Arletys Verdecia Moga	Characterization of maize plants response to entomopathogenic nematodes.
39	Cristina Llopis Belenguer	Host-parasite communities along a gradient of environmental disturbances preserve their structure but differ in driving factors.
40	Leslie McCluckie	Comparing the use of three different anesthetics on the freshwater snail <i>Radix balthica</i>.
41	Chiara Durrer	Biodiversity promotion areas improve diversity and richness of wild bee pollinators in nearby cherry orchards.
42	Tianyun Li	Contrasting plant community-mediated effects of herbivore grazing on plant diseases with different life history.
43	Hannah Inniger	Effects of population size on fitness traits in four common and four rare congeneric alpine plant species.
44	Aaditya Narasimhan	Life history trade-offs and genetic constraints at elevational range limits in <i>Cardamine hirsuta</i> (Brassicaceae).
45	David Marques	Unraveling the genomic origin of species in large white-headed gulls.
46	Sonia Sarmiento	Reference panel phasing for low-coverage sequencing imputation on non-model species barn owl (<i>Tyto alba</i>).
47	Gloria Animalesto	A New Species of <i>Haematoloechus</i> Looss, 1899 (Digenea: Plagiorchioidea) Infecting The Lung of Crab-Eating Frog <i>Fejervarya cancrivora</i> from Indonesia.
48	Lara Plattner	Effects of artificial light at night (ALAN) on the expression of floral traits in wildflower strips.

Location	Presenter	Title
49	Anne-Claire Fabre	Identifying how life cycle variation drives biodiversity in changing environments over space and time.
50	Moric Toszeghi	Brooding modulates the call of a glass frog with male parental care.
51	Bao Ngan Tu	Assessing the impact of glacier retreat on biodiversity and plant–insect interaction dynamics.
52	Vasco Lepori	Effects of varying niche width on eco-evolutionary dynamics and community properties.
53	Darina Koubínová	Resolution of phylogenetic relationships within the fern genus <i>Botrychium</i> s.s. (Ophioglossaceae) using target enrichment sequencing.
54	Anja Haefeli	Petrochromis sp. "kipili brown" a chocolate-coloured beauty from Lake Tanganyika.
55	Kora Klein	Why stick insects are perfect just the way they are: optimal sex ratios under facultative parthenogenesis.
56	Hiranya Sudasinghe	Genomic consequences of miniaturization in zebrafish relatives.
57	Viktor Kovalov	Fertility signaling games: should males obey the signal?
58	Julia Curty	Effects of artificial light at night and the differences between day and night on insect abundance.
59	Amira Sharief	One or Three: Empirical data facilitates conservation of musk deer suggesting only one species of musk deer in Western Himalayas.
60	Vincent Grognez	Switch off the light! Artificial light at night reshape floral traits of wild plants, with consequences for reproductive success.
61	Gregory Egloff	Small structures for mustelids.
62	Paul Himmighofen	Predator sensing by plants: Consequences for tri-trophic interactions.
63	Iris Prigent	The moulding of intra-specific diversity by selection under ecological inheritance.
64	Elizaveta Ermolaeva	Functional Approach Using Soil Protists as a Taxon-free Tool for Environmental Quality Assessment.
65	Graeme Wells	Molecular role of a <i>C. elegans</i> germline-specific RNA helicase.

Location	Presenter	Title
66	Yvonne Künzi	Are resistance and post-drought performance of temperate grassland species related to specific leaf area and drought length?
67	Luca Gabriel Champoud	Genetics of the <i>Calamagrostis stricta</i> (Poaceae) species complex in Europe, with special focus on the newly described <i>C. lonae</i>.
68	Dorothy Maushe	Benzoxazinoid metabolism by entomopathogenic nematodes.
69	Laura Fritschi	Testing the influence of masking factors on activity patterns of cichlids.
70	Tina Kiedaisch	The rust fungi collection in herbarium G: from unknown to becoming a world reference.

The threatened populations of *Clematis alpina* in Switzerland

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Clematis alpina (L.) Mill is a small arborescent liana of the Ranunculaceae family. The species has a scattered distribution between the French Alps and north-eastern Asia. Three subspecies are recognized. *C. alpina* subsp. *alpina* grows in the Alps, the Carpaths, the Balkan Peninsula and up to Poland and Ukraine. In Switzerland, *C. alpina* is mostly present in Engadin (eastern part of Grisons) where it grows up to 2350 m a.s.l. in *Larix decidua* or *Pinus cembra* forests. Several small relictual populations are found in western Switzerland such as in the Gasterntal in the Alps near Kandersteg (BE) or between Charmey and Boltigen in the Prealps (BE, FR). The species is protected entirely in the cantons of Tessin, Bern and Fribourg.

We present here an outline and preliminary results of a project done to study *C. alpina* in Switzerland and more precisely the situation of the threatened stands within the canton of Fribourg. The project aimed at making an inventory of the extant stations of *C. alpina* in the canton of Fribourg, assessing the ecological niche of the species throughout Switzerland and characterizing the genetic diversity at a population level in Switzerland and throughout Europe.

Mapping habitats sensitive to overgrazing in the Swiss Northern Alps using habitat suitability modeling

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Unsuitable livestock farming is considered as a main driver of biodiversity loss. In the high elevation areas across the world, many subalpine and alpine natural herbaceous communities are highly sensitive to sheep overgrazing. Such habitats of high biogeographic and conservation value are refugia for slow-growing, locally rare, and cold-adapted species. However, at a regional scale, no maps of these sensitive habitats exist that the authorities could refer to for regulating grazing. We therefore studied the possibility of using habitat suitability modeling (HSM) to map five selected habitats that are potentially threatened by overgrazing in the Northern Alps of the Swiss canton of Fribourg. For each habitat, we defined a group of characteristic species and gathered their occurrences from national data centers. These occurrences were pooled within each group and used as presences to calibrate the HSM. High-resolution predictors (10 m) were used to achieve fine-scale modeling. The models predicted accurate and ecologically relevant distributions for three of the habitats: alpine swards and heaths on exposed ridges and peaks, unstable calcareous screes and vegetated snow patches. These results show that habitats that are topographically and environmentally well-defined can be finely predicted by HSM using distributions of characteristic species for use in spatial conservation planning. In the context of summer pasture management, this helped us to translate the Swiss legal basis onto maps of authorized grazing pressure.

The effect of life-history strategies on local adaptation

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Natural populations typically experience heterogeneous environments and can adapt to their local conditions. The extent of local adaptation is influenced by the balance of divergent selection, gene flow and genetic drift. Here, we investigate the role of life history in this process. Life history can inform traits relating to a species' ecology, some of which could presumably impact the evolution of local adaptation. Using individual-based simulations, we explored the effects of different plant life-history strategies on local adaptation. The resulting levels of local adaptation were highly dependent on how often individuals passed through the processes pertaining to selection and dispersal. In particular, local adaptation was reduced in species with prolonged seed dispersal, and favoured in species with high generation times, where individuals experienced selection multiple times throughout their lifespan. In small populations, we saw how the effects of increased genetic drift could be offset, when life history led to large effective population sizes, such as in annuals with a high germination rate. Our results show how life history could affect the evolution of local adaptation, by influencing the exposure of populations to its main underlying processes - dispersal, selection and drift.

How Reliable are Morphological Criteria for Species Identification: a case study using ants of the *Lasius* genus

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The species concept defines a species as a group of potentially interbreeding populations. However, many species are described only by their morphological characteristics. This can make identification time intensive and cause inconsistencies with indistinguishable or intermediate phenotypes. Now, molecular methods of identification have begun to be used in conjunction with morphological methods as sequencing techniques become more accessible. These can be used to evaluate the consistency of morphologically identified species and true reproductively isolated populations. However, molecular methods can pose their own challenges, such as contamination from non-target species during the DNA extraction process, making the contaminated sequence data unusable for most analyses. Here, we use a dataset of over 1,000 RAD-seq and COI-gene sequenced individuals that were morphologically identified in the *Lasius* ant genus to investigate the congruence between genetic and morphological species identification and identify interspecific hybrid individuals. We developed a method based on minor allele-depth and competitive mapping to detect and remove sequence contamination from non-target species. We were able to find consistent agreement between the morphological and genetic identifications, as only 1.9% of individuals were incongruous. We could also identify 49 likely hybrid individuals across 6 species. Therefore, using genetic marker analysis of *Lasius* individuals within the surveyed geographic range can be a reliable method to quickly and accurately identify them to the species level. Perfecting these techniques of species identification is imperative for accurate analysis across the fields of ecology, evolution, and conservation biology.

Accidental biocontrol: human-mediated dispersal of insect parasitoids and predators

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Globalization of human activities has increasingly facilitated the spread of alien species. Insects are among the most numerous and damaging aliens, with widespread impacts on biodiversity, agriculture, and human health. Classical biological control of alien species involves introducing 'natural enemies' from their native range to control their population. Current selection processes for biocontrol agents are rigorous, and generally based on host-specificity. However, parasitoid and predatory species are also increasingly introduced accidentally through human-mediated dispersal. Such random introductions may favour generalists that establish more easily due to their broad host range, which could have considerable impacts for both alien and native species. We used a large dataset of border interception records in the United States of America from 1913 to 2019 to assess the human-mediated transport of parasitoid and predatory insects. 94 families of 'natural enemies' were detected, with 193 species identified. The insects largely arrived with various plant products, but commodity associations differed between taxa. 12 parasitoid species that are not yet established in the USA either have hosts established there, or also detected at the border. 90 % of intercepted predator species are generalists, making it likely that suitable prey is available. Furthermore, ten of the 'natural enemy' species arriving in the USA are listed as invasive species. The surprisingly extensive transport of 'natural enemy' species calls into question the rigorous and protracted processes for classical biological control. The insects detected could have significant impacts, both positive and negative, if they eventually become established.

Genomics of plant toxin resistance in entomopathogenic nematodes

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Some specialist insect herbivores have evolved the ability to sequester specialized metabolites from their host plant. The sequestered compounds can be deterrent or toxic for the herbivore natural enemies. The western corn rootworm (WCR), *Diabrotica virgifera*, stabilizes and sequesters a maize benzoxazinoid, which can be reactivated upon attack. Additionally, the WCR constantly exude a benzoxazinoid detoxification product. Both compounds can considerably limit for the success of entomopathogenic nematodes (EPNs) in infecting a WCR larva. EPN strains that have co-evolved with the WCR in their natural range (North America) are able to tolerate the presence of benzoxazinoids in their hosts but strains that originate from areas where WCR has been present for less than 50 years do not have this ability and suffer from the chemicals. In this study, we de novo assembled and annotated a chromosome-scale assembly of the EPN *H. bacteriophora* and conducted whole genome sequencing of 35 strains within this and other closely related *Heterorhabditis* species from different locations across the globe. These data not only increased the resolution of nematode phylogeny, but further provided indirect evidence linking the evolutionary history of the EPN strains to benzoxazinoid tolerance. We discuss the relevance of these findings for the development of efficient and sustainable pest-management strategies.

Context-dependence of pre- and postcopulatory sexual selection in *Drosophila prolongata*

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The strength of sexual selection is thought to be driven by population density and the operational sex ratio due to their influence on the absolute and relative encounter rates between sexual competitors and potential mates. Both population parameters may themselves be influenced by the abundance and distribution of important resources and the degree to which they can be monopolized by certain individuals of the population. However, empirical studies on the relative contributions of these factors to the strength of, and covariation between, pre- and postcopulatory sexual selection are currently lacking. Here, we experimentally manipulated the density and composition of populations of individually marked *Drosophila prolongata* that were allowed to interact freely in artificial arenas with uneven distributions of dietary and oviposition substrate. Across five days, we monitored the context-dependent distributions of flies (e.g. monopolization of resources), social interactions, and individual mating frequencies and combinations. We then assigned parentage to the offspring to disentangle the effects of these social dynamics on both pre- and postcopulatory fitness outcomes. *Drosophila prolongata* is unusual among drosophilid flies, in that males are larger than females and exhibit exaggerated forelegs that they use in male-male competition and elaborate courtship displays, and they can employ alternative reproductive strategies to gain matings. Further, females vary substantially in their mating frequency, thereby causing considerable variation in the level of postcopulatory sexual selection.

Asynchronous migration of plants and butterflies: will butterflies choose new host plants from higher elevations?

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The world is currently facing rising temperature, forcing species to track their optimal climatic niche, such as by migrating towards higher elevations. However, asynchronous range shifts of species like sessile plants and flying insects could alter current biotic interactions, leading to yet unpredicted population and community dynamics.

Along elevation gradients, during warming, migrating insects are expected encounter novel host plants, leading to two potential scenarios: i) insects can develop on closely related host plant species, leading to unexpected increased herbivore pressure on alpine plants, ii) insects cannot survive on alpine species, and are therefore constrained to track the slow upward movement of their host plants.

Using field common gardens and climate-controlled laboratory experiments, we studied the preference and performance of two low-elevation butterflies, *Melitaea celadussa* and *Zygaena filipendulae*, on their current host plants, *Plantago lanceolata* and *Lotus corniculatus*, and their potential novel alpine host species, *Lotus alpinus* and *Plantago atrata*, respectively.

We found that both butterfly species preferred to oviposit and feed on their current host plants, while the performance of caterpillar did not differ between host plants. Moreover, wing area and the ability to produce a second generation within a year were reduced when caterpillars developed on alpine plants.

While our results indicate that butterflies are able to oviposit and grow on alpine plants, their preferences are still directed toward the low-elevation plant. Furthermore, by altering both the life cycle and the phenotype of butterflies, novel host plants can potentially drive novel adaptative responses of butterflies during climate warming.

A biosystematic revision of the family Cribrariaceae

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Cribrariaceae systematics has largely been neglected in recent studies on Myxomycetes. The generic and species boundaries, as well as the evolution of phenotypic traits, have never been analyzed in detail, especially not in a phylogenetic context with modern techniques.

Since less than 20% of the accepted species have been sequenced up to date, we will first test the monophyly of the family using multilocus DNA-based phylogenetic analyses and fair taxonomic sampling. We will also evaluate the taxonomic boundaries of the three genera (*Cribraria*, *Lindbladia*, and *Licaethalium*) currently included in Cribrariaceae since preliminary data indicate that the generic circumscriptions may disagree with the phylogenetic relationships among species in these genera. We will further explore the evolution of some phenotypic traits and their significance for the taxonomy and diversification of the group. Finally, we will address the species-level taxonomy, trying to identify new species, cryptic taxa, and address synonymies. With all this information, we expect to propose a revised classification and an updated monograph of the family, to further accumulate knowledge in this group.

The ultimate goal would be to address the conservation status of the recognized species, in order to detect potentially threatened species or to identify habitats of special interest that may require protection.

Family matters: Early social complexity and development of social behaviour

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Social competence, i.e the ability of an individual to optimally adjust its social behaviour to the prevailing social information, is influenced by the early social environment in a wide range of vertebrates. Early life also influences other life-history traits like the propensities to provide alloparental care, to disperse or to reproduce. We investigated how rearing group size influences different components of social behaviour and life-history strategies in the cooperatively-breeding cichlid *Neolamprologus pulcher*. We raised the fish in large social groups of ten individuals or in small groups of three individuals. After 60 days of social experience, fish were kept under identical conditions in sibling groups. At the age of 120 days, we tested two individuals per experimental brood for social competence; we recorded the social behaviours expressed by a focal fish in response to a gradient of conspecific aggression in two tests: (i) towards video recordings of conspecifics and (ii) towards a larger live conspecific intruder. At one year of age, we tested the explorative, helping and dispersal behaviour of the same fish. Rearing group size did not affect aggressive behaviour in the video test, nor exploration, helping and dispersal behaviour later in life. Fish raised in large groups showed more submission per received aggression from a larger conspecific, they showed submission earlier and exhibited more flexibility in the expression of submissive behaviour compared to fish raised in small groups. Our results emphasize the importance of early-life social complexity for the expression of social behaviour.

Ecological niche modeling for *Ptilostemon greuteri* (Asteraceae): implications for in situ conservation and future translocation

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Ptilostemon greuteri, a woody thistle endemic to north-western Sicily (Italy), is one of the most threatened vascular plants of the Mediterranean Basin. Two subpopulations only, each with an estimated number of a little more than 250 individuals, are currently known. Only a few studies have been conducted to assess the current conservation status of the species. Despite reports on the stable size of its two subpopulations, wildfires are causing a decline in habitat quality and population range. Protecting the habitat has been recommended for the long-term conservation of the species, but no monitoring plan has been formulated so far to highlight the threats and the dynamics of its subpopulations.

To improve the safeguarding of this species, an international research project was started in 2021. The main aims are (1) to assess the ecological requirements of the species to develop an action plan and implement in situ conservation measures, and (2) to model its ecological niche to find new suitable areas for translocation to increase the number of subpopulations and ensure its long-term protection and conservation.

This poster illustrates the field sampling method used for data collection. We also show the latest results at the community level concerning the environmental drivers of the species composition patterns issued from the analysis of vegetation plots. Additionally, we will present the life forms of the plants co-occurring with *P. greuteri*. The plant traits of the communities where *P. greuteri* lives highlight the unique conditions that the species requires to survive and the challenges that this implies for conservation efforts.

Intraspecific trait variation, local adaptation, and environmental conditions as drivers of host disease risk along an elevation gradient

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Host functional traits are a promising tool to predict infectious disease risk in the face of global change, but three major challenges remain. First, studies commonly assume fixed trait values for individuals of the same species, neglecting potential influences of within-species trait variation. Second, host adaptation to local pathogens is not necessarily reflected in commonly measured functional traits. Third, environmental gradients can modify trait-disease patterns which questions the idea of general and rigid “disease-traits” in hosts. In the present study, we aim to capture the roles of intraspecific trait variation, local adaptation and environmental conditions in driving disease risk using a reciprocal transplant experiment along a 1100m altitudinal gradient. We factorially crossed seed source elevation, soil source elevation and recipient elevation for four common alpine grassland species (*Dactylis glomerata*, *Phleum pratense*, *Plantago lanceolata*, *Plantago media*) on a low, intermediate, and high elevation site. At four timepoints within two growing seasons, we measured plant survival, height, specific leaf area, phenological status and foliar disease infection severity. Preliminary results show that plants that adapted to high elevation environments had more disease overall, indicating increased resistance in populations from low elevation origin. However, this effect weakened when plants were grown in soils from high elevations. We found trait-disease relationships, but they depended on the species and on the recipient elevation. Our results highlight the importance to further explore how host traits in different environments mediate pathogen infections, to understand how global change will shape future disease landscapes.

Maize benzoxazinoid exudation in soil follows a diurnal rhythm

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Root exudation of specialized metabolites is a dynamic process that shapes soil properties, plant nutrition, and plant interactions with soil organisms and other plants. While the pivotal roles of root exudates are increasingly acknowledged, the factors that modulate their release remain poorly understood. Here, we characterized the diurnal exudation of the maize specialized metabolites, benzoxazinoids (BXs). BX exudation increased over daytime and decreased during nighttime. The release of DIMBOA-Glc and of DIM2BOA-Glc respectively reached at 6.2 and 2 ug/cm 14 hours after sunrise and decreased to levels below 1.2 ug/cm at night. HDMBOA-Glc exudation rapidly increased to 1.5 ug/cm after sunrise and remained rather constant over daytime, before dropping 15-fold at night. To investigate whether these patterns were modulated by light or by the plant circadian rhythm, we exposed the plants to extended darkness for 12 hours. Preliminary data suggest that BX exudation is mostly modulated by light but should be further confirmed. Understanding exudate patterns and their regulation is critical to better grasp plant-environment interactions at the root-soil interface.

How changes in life cycle and associated environment foster functional diversity: A comparative analysis of prey capture kinematic in *Caudata*

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There have been several transitions between terrestrial and aquatic environments throughout tetrapod history. These environments induce distinct selective pressures due to their radically different physical properties. To better understand these transitions, amphibians are a model of choice because, depending on their life cycle strategy, they can undergo metamorphosis implying drastic changes from one environment to another during their lifetime. The aim of our study was to test whether the environment (water vs. land), developmental stage (adult vs. larva), life history type (biphasic vs. paedomorphic), and prey capture success impacted the kinematics of prey capture in salamanders. To do so, we gathered kinematic data on feeding (changes in the position of key structures during feeding) using high-speed video recordings. We contrasted the feeding kinematics of nine species of *Caudata* belonging to three families. Our analyses revealed that the feeding environment had the greatest influence on feeding kinematics while the life cycle had no significant effect. The observed differences in kinematics are due to differences in optimal feeding strategies (suction in water vs. tongue prehension in air) resulting in faster hyoid and jaw movements in water compared to on land.

Do pollen nutrients constrain the diet of wild bees in urban areas?

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Wild bees are crucial for biodiversity and ecosystem services such as pollination. However, wild bees are declining and continuously facing various challenges including habitat changes such as urbanization. Urban ecosystems with a mixture of native and exotic floral resources may threaten the dietary and nutritional requirement of wild bees. A previous study (Casanelles-Abella et al. 2021) on four common European wild bee species and their diet requirement in five urban areas (Antwerp, Paris, Poznan, Tartu, and Zurich) suggested that wild bees with generalized host plants were predicted to be less sensitive to urban intensity due to their broader diets. However, host-plant generalization does not necessarily reflect nutrient generalization. In fact, generalized host-plant feeding bees can be nutrient-limited if they targeted on some uncommon nutrient shared within these host plants. Here, we will further explore the nutrient requirement based on Casanelles-Abella et al. (2021)'s study to get a deeper understanding on nutrient limitation for wild bees in urban ecosystems. Specifically, we will focus on a group of lipid nutrient, namely sterols, that cannot be synthesized by bees but are crucial for their growth, development, and reproduction. By analyzing sterol composition and amount in bees and in pollen they collected and stored in their nests, we ask: 1) do sterol profiles in bee's body match that in their pollen diet? 2) How consistent are the pollen sterol nutrient landscape for these four wild bees in different urban areas? 3) Are more generalized wild bees also more sterol generalists? This is a new study that we hope to get some preliminary results before the conference.

Comparative and experimental evidence that sticklebacks cause benthic trophic cascades in Southern Greenland ponds

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Trophic cascades occur when predators indirectly affect primary producers via effects on the abundance and trait distribution of prey. Obtaining evidence for trophic cascades in natural populations is challenging due to multiple confounding factors that can influence food web structure. Here, we describe efforts to obtain both comparative and experimental evidence for the cascading effects of three-spined sticklebacks (*Gasterosteus aculeatus*) on freshwater pond ecosystems in Southern Greenland. We use both a survey of 24 ponds with different food web configurations and a manipulative experiment of 6 ponds to investigate the effect of a stickleback-mediated trophic cascade. Specifically, our work focuses on the direct predation effect of sticklebacks on the local benthic macroinvertebrates, and how to obtain evidence for trophic cascades in natural populations.

Learning accelerates the evolution of slower aging, but constrains the evolution of negligible senescence

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The risk of dying tends to increase with age, but this trend is far from universal. For example, human mortality is comparatively high at a young age, declines during juvenile development and increases again during adulthood. For other species, mortality never increases, or even continuously declines with age, which has been interpreted as absent- or reverse-aging. We developed a mathematical model that suggests an alternative interpretation. The model describes the age-dependence of mortality as the sum of two opposite processes. The mortality risk due to physiological decline increases monotonously with age. But old individuals gain survival benefits through processes like growth and learning. This simple model fits mortality dynamics for all human age classes and for species across the tree of life. Simulations revealed an unexpected complexity by which learning impacts the evolution of aging. An ability to learn initially accelerated the evolution of slower aging but constrained the slowest possible rate of aging that can evolve. This constraint occurs when, despite a remaining aging rate, learning reduces mortality during the reproductive period to near negligible levels and thereby eliminates selection for a further slow-down of aging. In conclusion, learning accelerates the evolution of slower aging, but species with strong learning-associated survival benefits cannot evolve negligible senescence.

New Ways to Gain More Reliable Insights Into Adaptive Radiations - A Case in Anoles

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Adaptive radiations and their causes have long fascinated evolutionary biologists, and trait-dependent diversification models were a popular means to analyse them. However, the field has been grappling with various reliability issues in SSE models in the past years, and their correlative nature limits one's ability to make confident conclusions. Here, we first test the adequacy of SSE models for the data using posterior predictive simulations and calculation of a number of summary statistics on those simulations. This allows to identify whether the inference of trait-dependence was misled by the signature of other processes. Such adequacy tests go beyond a mere check of appropriateness of the model. The summary statistics capture properties of the data which can also inform us of how the model fails to adequately describe the data. Thus, we secondly further leverage this by formulating a number of competing causal scenarios, implementing them in an SSE model framework, and using the summary statistics from the adequacy test to further characterise any differences in the signatures the competing causal scenarios may have left on the data. We use *Anolis* lizards as an example, in which viviparity has often been linked to increased rates of lineage diversification. However, this result seems biologically questionable. Using the approach outlined above, we formulate a series of alternative causal scenarios and explore our ability to distinguish how plausible they are for this data. While no absolute proof for a particular scenario is possible, certain scenarios can be ruled out like this.

The genetic architecture of populations where females, males and hermaphrodites stably coexist

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The co-existence of females, males and hermaphrodites, also known as trioecy, is rare in both plants and animals and not predicted by theory. However, puzzling cases of trioecious populations do exist in nature and are still poorly understood. Here, we presented data on sex ratios and geographical distribution of 109 *Mercurialis annua* populations in southern Spain, among which 36 populations are trioecious. We further showed crossing experiments between males, females and hermaphrodites of the trioecious populations. We fitted the sex ratios of the crosses and showed that maleness is determined by a Y chromosome while femaleness may arise from one to two recessive loci. We used simulation to address the population equilibrium and compared the results with the field sex ratios to show a possible cytotype variation. We discuss the stability and evolution of these trioecious populations based on their distribution and the history of *Mercurialis annua*.

Investigating cognitive flexibility using a full custom-made behavioural set-up

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Cognitive flexibility is an executive brain function that refers to the ability of a subject to switch between thinking about two different or multiple concepts and to shift attention between task sets, attributes of a stimulus, responses, perspectives, or strategies. Many animal species, including humans, succeed in various cognitive flexibility test paradigms. Nevertheless, evaluating animal performance in a given task can vary greatly depending on the experimental set-up used. Here, we designed and built a touch screen operant chamber, controlled by the one-board computer RaspberryPi TM (RPIs), that we used to investigate cognitive flexibility abilities in rodents (mice) on a set-shifting task. The set-up allowed us to record behavioural parameters fundamental to understand the degree of cognitive flexibility in mice. Moreover, we used Python language programming to adjust specifically our task to the animal performances. Although preliminary, with our work we further confirmed the possibility to build an efficient custom-made set-up for animal cognitive testing that is considerably low-cost than other options available on the market. The main advantages are certainly the cost reduction and the opportunity to easily adjust the set-up based on the researcher's needs. Finally, our behavioural set-up is also compatible for in vivo electrophysiological recordings, hence both behavioural and neural physiological measurements can be acquired.

Can herbivorous insects in Switzerland provide insights into the biological control of *Robinia pseudoacacia* in South Africa?

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Robinia pseudoacacia (Fabaceae) is a deciduous tree native to the Appalachian Mountains of North America but has been introduced throughout the world, including Europe and southern Africa. Since its introduction in the 17th Century it was quickly distributed over much of Europe based on its beneficial uses and still today, it is a highly valued tree in some parts. However, outside of its native range including Europe and South Africa, it is considered an invasive species with negative ecological and economic impacts. Mechanical and chemical control of invasive populations of *R. pseudoacacia* is extremely challenging, labour intensive and expensive. In this case, biological control may offer a safe and sustainable option. In Switzerland, several native North American herbivores have been inadvertently introduced and have established populations. This offers a unique opportunity to study the biology of three species of interest; the leaf curling midge, *Obolodiplosis robiniae* and two lepidopteran leaf miners, *Parectopa robiniella* and *Phyllonorycter robiniella*, to determine if they could be safely introduced into South Africa for the biological control of *R. pseudoacacia*. The study aims to determine the host specificity by exposing closely related plant species to *R. pseudoacacia* under natural and semi natural conditions over a two-year study period (2023-2024). The results from this study will guide researchers in determining if any of these species would be suitable biological control agents for eventual release in South Africa.

Soil community responses to climate extremes at different elevations across seasons

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Extreme heat events are getting more frequent and severe due to climate change, with the potential to induce large ecological responses. The magnitude of ecological responses may depend on the spatial and temporal interactions between the climatic event and natural communities. For instance, it is likely to observe variable responses to heat events at different elevations due to their distinct biological and climatic features. Since phenological patterns vary across elevational gradients, the timing of heat events could exert distinct ecological effects at high and low elevations. Yet, the ecological significance of the timing of heat events at different elevations has been rarely assessed. To this end, we tested how soil communities at high- and low-elevation sites respond to extreme heat events in different seasons (spring, summer and autumn). In a laboratory experiment using field-collected intact soil cores, we simulated heat events characterized by statistical extremity (i.e., a week at the 99th percentile of the site-specific daily average temperature) to generate similarly unusual climatic conditions across seasons and elevations. We measured the responses of soil invertebrates (Collembola), fungi and plants at the end of the extreme event and after a 5-week recovery period. Our preliminary results show that collembolan abundances were most sensitive to extreme heat from the low elevation sites during spring. However, this immediate decline was followed by compensatory population dynamics allowing them to a full recovery. We further aim to provide insights into soil community responses by linking collembolan responses to fungal and plant responses to extreme heat.

Effect of larval nutritional stress on wing morphology in *Culex pipiens*

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Culex pipiens complex plays an important role in the transmission of numerous pathogens, such as avian malaria parasites (*Plasmodium* spp.). The transmission potential of mosquito-borne pathogens is influenced by mosquito life-history traits, such as survival, size, and fecundity. Previous studies have shown that some life-history traits depend on environmental conditions, such as nutritional status of the adults and larvae. Here, we evaluated the effect of food deprivation at larval stage on mosquito wing morphology, using morphometric techniques. We compared the geometric patterns of wing venation of adults whose larvae were reared under five concentrations of ad libitum (ADL) food (commonly used in our colony maintenance): 100%, 50%, 25%, 10%, and 5% ADL. Nineteen-landmarks were digitalized on wings of 201 females and 145 males. Wing size decreased significantly with the reduction of the food concentration in both sexes, mosquitoes whose larvae were reared in poor food concentration were smaller. Only the shape of female wings was significantly different among treatments, females of high regimen food have slender wings. Variance of size and shape was larger in mosquitoes from low food regimens. Sexual dimorphism of size and shape occurred in all the nutritional treatments. Males have smaller and slender wings; however, the sex-related differences in size decrease with food reduction. These findings showed how larval conditions influence adult wing morphology (size and shape) and, due to the wing ecological functions in flight and mating communication (buzz of flying), mosquitoes' vectorial capacity and the dynamic of pathogen transmission.

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

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

Engineering blue-green infrastructure for and with biodiversity in cities

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Engineered blue-green infrastructure (BGI) can address numerous urban problems, such as flood risk, increased temperatures, and water pollution. They can also support biodiversity conservation, providing suitable conditions for plants and animals in cities. Yet, BGI are typically designed with engineering objectives in mind, which can reduce their potential for conservation efforts. We contend, however, that it is necessary to address both engineering and ecological objectives before BGI implementation. Through an interdisciplinary review of engineering and ecological literature, we demonstrate that this joint focus will not only strengthen urban biodiversity, but also fulfill engineering expectations of BGI. Here we present how different facets of biodiversity can contribute to increase BGI performance and resilience while decreasing management costs. We then highlight the local and landscape environmental characteristics that shape biodiversity and how adjusting BGI design parameters can improve habitat conditions for species in different BGI elements. Finally, we discuss eventual trade-offs when both engineering and ecological objectives are jointly addressed, and how collaboration between engineers and ecologists can help to reach common solutions.

Hybridization upon secondary contact - the purple-edged copper butterflies (*Lycaena hippothoe*) in the Swiss Alps

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During glacial periods, many species have retracted their ranges into one or multiple glacial refugia where they diverged over time. Zones of secondary contact between closely related lineages or species that arose in such geographically isolated refugia provide the outstanding opportunity to study speciation because often reproductive isolation is not yet complete. Here, I study a zone of secondary contact between two subspecies of the purple-edged copper *Lycaena hippothoe*, i.e. *eurydame* and *euridice* in central Switzerland combining a machine-learning approach to capture phenotypic variation with ecological and whole-genome data. Unlike for other butterflies that form secondary contact zones, I found substantial gene flow between the two subspecies over an extensive range. Importantly, my results implicate that while non-admixed *euridice* still exist at high elevations, no pure *eurydame* individuals occur anymore at low elevation in this region. The increased genetic admixture is moreover associated with increased phenotypic variation, likely swamping potential prezygotic barriers. Consequently, the contact zone populations show little reproductive isolation given the amount gene flow and resulting hybrids.

The genetics of sex allocation evolution in a herbaceous plant: a sex chromosome introgression project

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The evolution of dioecy from hermaphroditism is not rare in plants. However, recent evidence shows that this transition is reversible, as was shown in the herb *Mercurialis annua* by the mean of evolution experiment. This herbaceous species exhibits a XY sex determination system. But the ability of its females to produce few male flowers can lead, in the absence of XY males, to the selection of a larger male allocation in XX females, leading to hermaphroditism. To investigate the genetic basis of this process, we will conduct an introgression experiment. We will introduce the Y chromosome into all-XX hermaphroditic population to examine its effects on sex determination in a genetic background that has evolved without it for more than 10 years. I will present the method we will use and the theoretical results we expect using verbal and computational models. When available, our results will provide insight into the genetic mechanisms underlying sex allocation in *M. annua* and on the genetic basis of a system capable of rapid transitions between dioecy and hermaphroditism.

Vertical, horizontal or environmental? Research on symbiont acquisition calls for proper controls

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Symbiotic associations are ubiquitous in nature and can have profound effect on animal diversity and evolution. Symbionts can be transmitted i) vertically, when symbionts are passed directly from mother to offspring during early life; ii) horizontally transmitted symbionts are acquired in later life-stages through feeding on infected corpses, faeces, or through physical contact between conspecifics; and iii) environmentally transmitted symbionts, also acquired later in life, can be obtained through contact with or uptake of surrounding matter such as water or soil. Many animal hosts are also associated with more than one key symbiont, and these communities and their genes that they contain are referred to as microbiomes. Majority of studies describe the microbiome in terms of bacterial diversity without knowing how microbes are acquired and what is the proportion of microbes derived from early-life colonization. We propose a method that allows to control the contribution of early-life microbial colonization in a model organism group, terrestrial isopods (Crustacea: Isopoda) that is characterized by brooding developing embryos inside the female brood pouch i.e., higher chances for mother-offspring symbiont transmission. Our experimental approach involves two steps: obtaining symbiont-naïve offspring from the brooding mother while preventing any source of horizontal and environmental transmission; and subsequently simulating alternative transmission modes through feeding manipulation and quantifying the host fitness. Our method exemplifies what is required to disrupt a vertical transmission in animal model systems with a parental brooding, and in the host organism that entail significant benefits from the acquired microbes.

Host Specialization in Bat Parasites: Host Choice Experiment and Genetic Comparison of *Cimex lectularius*

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Host specialization is a phenomenon that is visible in the Cimicidae family. The bug *Cimex lectularius* is known to have two lineages associated with human and with bat, its primary host. It is a competent vector of the *Trypanosoma cruzi*, responsible for the Chagas disease in humans. Therefore, host specialization in *C. lectularius* is important to study to understand the risk of pathogens transmission between hosts. We first tested if the original host influenced the host choice using an olfactometer experiment. Then, we did a genetic comparison between and among human and bat associated bugs from Western Switzerland using three markers: COI and 16S rRNA mitochondrial genes, 12 microsatellites markers and knock-down resistance gene variants. The host choice experiment is supporting evidence of behavioural differences with the bugs that are more active during the minimal activity period of their host and the human associated bugs that prefer the human odour and recognize the bat odour. The genetic comparison suggests patterns of genetic differentiation between the two hosts associated populations of bugs. A median-joining analysis exhibits a clear separation of haplotypes that are not shared between hosts. The analysis of genetic structure reveals two genetic clusters associated with bats and humans. This clear separation between the two hosts is also supported by the knock-down resistance analysis. Our results are consistent with previous studies supporting differences in response according to the host. The risk of pathogen transmission is unlikely to occur between the two hosts.

From a supergene to social polymorphism in fire ants

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The integration of biological units into higher organizational level is a central theme in evolutionary biology. Supergenes underlie social polymorphism in several ant species. However, the mechanisms by which supergenes regulate colony social organization are yet to be discovered. Here, we outline prospective experiments aiming at identifying how a supergene regulates social organization in the fire ant *Solenopsis invicta*. In this species, workers bearing the Sb polygyne haplotype induce non-bearing nestmates to accept multiple queens, but only those with a Sb haplotype. It has been hypothesized that Sb-bearing individuals share some specific cuticular chemical signals. Non-bearing workers would become tolerant of Sb queens through their exposure to Sb-bearing nestmate workers. We will first use behavioural experiments to assess whether chemical signalling underlies acceptance of multiple queens by non-bearing workers. Next, we will compare cuticular chemical profiles of Sb-bearing workers and queens to identify shared chemical signals. Finally, to identify the neuronal mechanism underlying this change in social behaviour, we will perform single-nuclei transcriptomic analysis of the peripheral and central nervous system of non-bearing workers. Deciphering the mechanisms by which the Sb haplotype leads to polygyny would improve our understanding of how genotypes interact to form phenotypes at a higher level of organization.

Investigation of the host finding behavior of *Phytobius vestitus* for the biological control of the invasive weed *Myriophyllum aquaticum*

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Native to South America, parrot's feather (*Myriophyllum aquaticum*) is a macrophyte that has rapidly invaded other regions, including Europe. Outside its native range and in the absence of natural enemies, this plant forms dense mats in aquatic ecosystems, negatively impacting the environment and human activities. Given the invasion into sensitive habitats, biological control may offer a safer and more suitable solution for its management. The weevil *Phytobius vestitus* is reported to use parrot's feather as its main host in North America, and therefore this weevil could be used as biocontrol agent in the invaded range, if it does not spill over to other native species. To this end, using custom-made olfactometers, we studied the attraction of *P. vestitus* toward *M. aquaticum* and related plant species. Using both no-choice and choice tests, we show that suggest *P. vestitus* is indeed more attracted to parrot's feather over the other, non-target, plant species, and that this weevil can discriminate odor blends emitted by the host and non-target plant. Therefore, this first evidence indicates that *P. vestitus* is host specific, however, further studies testing for performance on different plant species are required before releasing this weevil into new regions for parrot's feather management.

Harvestmen communities of three vegetation stages in a revitalised pre-alpine riparian forest (Arachnida, Opiliones)

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Influenced by fluvial dynamics, the riparian forest is one of the most biodiverse ecosystems in the northern hemisphere. These forests provide important ecosystem services. Human activities have mostly destroyed this environment over the last 200 years. Almost all the remaining forests at lower altitudes have lost their characteristic habitat and vegetation heterogeneity. During the current biodiversity crisis, efforts are made to revitalize the remaining areas. However, the effects of such processes on species communities are widely unknown. In this study we looked for differences in harvestmen (Opiliones) species richness, activity density and species composition across three vegetation stages in a newly restored (2014 – 2016) pre-alpine riparian forest near Bern, Switzerland. All harvestmen were captured by using pitfall traps. We also used a plant community-based indicator value system to look for correlations between species composition and environmental parameters. We found significant differences in species richness between the vegetation stages, and the highest abundance in the oldest vegetation stage. No differences were found in activity density and species composition. Furthermore, the importance of microclimatic conditions for harvestmen is demonstrated: Each species showed at least two distinct (i.e. only slightly varying) indicator values. We conclude that harvestmen are good ecological indicator species, and that all the found harvestmen species were most likely present already prior to the revitalisation process.

The role of life cycle variation on morphological diversity in European populations of salamanders and newts

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Several European species of salamanders and newts display an exceptionally wide geographic distribution and a variety of life cycle types ranging from an obligate to facultative metamorphosis and from simple to complex life cycles depending on the population. As species with a complex life cycle change their environment from the larval to the adult stage, they provide an excellent model to test the capacity of an organism to adapt to environmental change by producing morphological variation in response to this challenge (evolvability). To do so, we have chosen to focus on four species: the Alpine newt (*Ichthyosaura alpestris*, populations can be paedomorphic or biphasic), the fire salamander (*Salamandra salamandra*, populations can be pueriparous or larviparous), the palmate newt (*Lissotriton helveticus*, populations can be paedomorphic or biphasic) and the crested newt (*Triturus cristatus*, populations can be paedomorphic or biphasic). We will quantify the morphological variation in several populations (larval and adult stages) using linear measurement and geometric morphometrics using collection specimens from several European museums. We will determine whether populations with a complex life cycle (biphasic and larviparous) have a higher morphological variability than populations with a simple life cycle (paedomorphic, and pueriparous) using disparity analyses. Finally, we will test whether European salamander and newt populations with complex life cycles are more modular than populations with a simple life cycle, and we will assess the pattern and magnitude of phenotypic modularity and integration for each data set depending on developmental strategy.

Evolutionary constraints at low-latitude range edges under climate change

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Warm edges of species distribution have been shown to be under particular threat by climate warming as range retractions are commonly observed. It is unclear why many populations cannot adapt to and long-term persist under warmer, dryer, or hot-drier conditions. Theory suggests that changes in the selection regime and genetic limitations can play an important role in setting range limits: Selection regimes may contribute if environmental gradients become too steep or are multivariate. Genetic limitations may include low genetic variation for environmental tolerances, or genetic correlations antagonistic to the direction of selection. In a greenhouse experiment, manipulating temperature and watering, we investigated how genotypic variation for growth and performance changed from no stress to univariate to combined stress, and the presence of trade-offs among stress tolerances. We raised full-sib plants of 120 families of a genetically diverse central population of *Arabidopsis lyrata* under average southern edge conditions, as well as under heat or drought as can sometimes occur, or combined heat and drought. By tracking growth, development, and allocation strategies we produced genetic variance-covariance matrices (G-matrix) within and across experimental environments. We will present results that shed light on the role of stress on evolutionary potential in multi-trait space, the presence of trade-offs in coping under multiple stressors, and their effect on adaptation at warm range limits.

Darwin wasps (Hymenoptera: Ichneumonidae) – little (known) fellows in nature conservation

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Darwin wasps are one of the most diverse groups in the tree of life constituting nearly 10% of the expected insect species in Switzerland. However, the species record is still far from complete and information about their ecology and conservation status remain sparse. Due to their high trophic level and specialization as parasitoids, it is likely that Darwin wasps react rather sensitive to habitat changes and thus many species are potentially threatened. Empirical studies investigating the conservation status or the effect of conservation efforts on Darwin wasps are still lacking. In a novel study, we investigate whether conservation measures with a focus on vertebrate diversity have a positive co-effect on the species richness of Darwin wasps. This conservation project is carried out in a lowland meadow in the canton Aargau. The project aims to improve the habitat diversity by the construction of new ponds, hedges, deadwood and stone piles, and the change to an extensive land use. The goal of this study is to investigate whether the species richness in Darwin wasps changes with the planned conservation measures. A survey documenting the status before the measures was conducted in May–September 2022 yielding about 1300 specimens of Darwin wasps collected with a Malaise trap. A comparative survey will be conducted in 2024, one year after the conservation measures are completed. We present here the hypotheses and preliminary results based on the partial identification of the material.

Effects of local and landscape factors on pollinator genetic diversity and differentiation

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Of the many alterations to natural ecosystems brought on by human impacts, land-use change is among the strongest drivers of biodiversity change. With a growing population size, maintaining stable ecosystem services while ensuring global food production is proving to be a major challenge. Despite the importance of natural and semi-natural habitats to insect pollinators (and biodiversity as a whole), in agricultural landscapes, these remaining areas are often highly fragmented and degraded. With an increasing number of studies revealing negative impacts of habitat fragmentation and isolation on pollinators, there is an urgent need for the proper identification of risk indicators to ensure effective implementation of conservation and restoration efforts. However, critical knowledge gaps remain regarding the relative importance of various local and landscape factors, and their interactions with protected habitats. Here, we use a systemic approach considering independent gradients in local (e.g., patch size) and landscape factors (e.g., composition, configuration, connectivity) to examine their effects on genetic diversity and population structure in wild bees. We sampled wild bees in 30 protected dry calcareous grasslands embedded in agricultural landscapes in Switzerland. Next, we will use Double digest Restriction-site Associated DNA sequencing (ddRADseq) to measure genetic diversity and population structure in select wild bee species, and will assess the influence of the factors driving pollinator genetics. Data on flowering plant and pollinator communities (bees, hoverflies, butterflies), and their interaction networks will additionally be analysed to improve our understanding habitat dynamics in protected calcareous grasslands, as a prerequisite for effective conservation management and policy.

Characterization of maize plants response to entomopathogenic nematodes

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Multitrophic interactions between plants, herbivores, and the enemies of the herbivores are key drivers of ecosystem functioning and biodiversity. While many of these interactions have been well described, whether plants can perceive and respond directly to herbivore enemies remains unclear. Here, we investigated how maize plants respond locally and systemically to the presence of entomopathogenic nematodes (EPNs) in soil. By combining metabolomics and transcriptomic analyses, we demonstrate that maize plants can detect EPNs, resulting in a shift in the primary metabolism in leaves and roots. In particular, soluble sugar profiles show drastic changes in plants exposed to EPNs. We discuss why plants may have evolved the ability to perceive the enemies of its enemies and its relevance for fundamental and applied biology.

Host-parasite communities along a gradient of environmental disturbances preserve their structure but differ in driving factors

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Host-parasite communities are biased toward high degrees of intervality. It is expected that as new host-parasite interactions emerge co-evolutionary dynamics saturate the communities. This implies that a host-parasite matrix of interactions can be ordered so that the host ranges of parasite species are contiguous segments. Although, intervality may not be complete as in some segments gaps appear because of constraints imposed by other parasites' host ranges. However, we do not know if the intervalstructure is preserved when host and parasite diversities are affected. We assessed the degree of intervality [0,1] of helminth-rodent communities in a gradient of environmental disturbance. We evaluated what factors explain the interval ordinations: phylogeny, overlap in ecological interactions, or their combination. Communities along the gradient of environmental disturbance had a high degree of intervality: 0.75-0.87 for parasites and 0.86-0.93 for hosts. These results suggest that all hostparasite communities are saturated regardless of the environmental disturbances. From parasites' perspective, both host phylogeny and host overlap in their parasite community explained intervality. From hosts' perspective, none of the considered factors significantly explained intervality, although their relative importance differed between habitats. In climax or less disturbed habitats the combined information was the most relevant factor in explaining intervality. Whereas in disturbed habitats, the overlap in ecological interactions was the first factor to explain intervality. Our study suggests that, despite the structure of the network is preserved, different factors must be considered when predicting host-parasite interactions in habitats differing by disturbance.

Comparing the use of three different anesthetics on the freshwater snail *Radix balthica*

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An effective method for anesthesia is important to reduce discomfort for research organisms and is often unavoidable for experiments such as in vivo imaging, as they require the subject to be still during image acquisition. Additionally, some experiments have a timeline that requires the snails to stay alive during and after the procedure. Criteria such as affordability, easy to acquire and low health impact should also be considered, narrowing down the already small list of known gastropods anesthetics. We examined for the first time the effects of Listerine (commercial mouthwash with 5% ethanol and 10% ethanol/menthol), clove oil and menthol crystals as anesthetics on the freshwater snail *Radix balthica*. Three replicates of three individuals each were put into three different concentrations of each agent. Anesthesia was assessed by gently scraping the foot of the animal with a paintbrush to test its reaction. Time to recovery was recorded until the moment they would react again to the strokes. We recorded the time to full recovery from the reaction to the brush until they were out of their shell and in motion. Our results demonstrate that the Listerine had the shortest time to anesthesia and the longest time to recovery between the different anesthetics. Its also a very cheap, easy, and nonhazardous solution to use. Although the results were slightly worse for the menthol crystals and the clove oil, they successfully anesthetize the snails and could still be interesting solutions to investigate.

Biodiversity promotion areas improve diversity and richness of wild bee pollinators in nearby cherry orchards

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Human wellbeing is directly linked to agricultural systems yielding enough and stable amounts of food every year. To ensure this, ecosystem services providing a diversity of animals such as bees pollinating wild plants and crops are needed (Oerke 2005; Gallai et al. 2009; Garibaldi et al. 2013).

We measured the diversity and abundance of bee pollinators in cherry orchards. Former studies have found that cherry yield was reduced by 10%, mainly caused by a decreased fruit set due to suboptimal pollination. “Thermal resilience” (Kühnel and Blüthgen, 2015) of the pollinator community was the strongest predictor of this decrease (Sutter et al. 2019). The key question remains, however, how a farmer could enhance this thermal resilience closely linked to wild bee pollinator diversity to ensure stable pollination services and food production on his farmland. Therefore, cherry orchards along a gradient of extensively used meadows and hedges in their environments were chosen. The higher proportion of usable habitats in the proximity of the cherry orchards should positively influence wild bee diversity and abundance, enhance cherry pollinator community niches and thermal resilience, and thereby stabilize pollination services and yield. The results show that especially hedges are increasing the shannon diversity, richness and the niche complementarity of pollinators. No positive relationships were found between the fruit yield and the presence of pollinators. This might be explained by the fact that many farmers introduced honeybee hives and these compensate for the absence of suitable habitats for wild bees. Further studies are needed to disentangle the effects of introduced managed bees and the natural occurrence of wild bees on cherry yields.

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Contrasting plant community-mediated effects of herbivore grazing on plant diseases with different life history

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Herbivore grazing is the most extensive management form of grassland worldwide. The effects of large herbivore grazing on plant community structure and ecosystem functioning have been widely studied, whereas the impacts of grazing on plant diseases, especially under various herbivore species and for diseases caused by different pathogens, remain poorly understood. Here, we integrated a grazing experiment, and a removal experiment manipulating plant density and litter biomass, to evaluate how large vertebrate herbivores (i.e., cattle and sheep) affect foliar fungal diseases with different life history (i.e., biotroph and necrotroph), and to identify potential mechanisms underlying such grazing effects in a temperate grassland in northeast China. By measuring plant population and community-level variables, plant disease severity and microclimatic conditions, we found that cattle grazing significantly reduced pathogen load, either for biotroph or necrotroph. While sheep grazing had a positive effect on biotrophic pathogen load, but not on necrotrophic pathogen load. The SEM analysis showed that indirect pathways, including plant community characteristics, played predominant roles in our systems, overwhelming the direct effects of grazing (e.g., consumption of spores). Moreover, litter biomass play an important role in modulating necrotrophic pathogen load, while this mechanism has not received much attention. Overall, our results demonstrate cattle and sheep grazing exert contrasting impacts on pathogen load, particularly via indirect pathways of changes in plant community, and that these effects vary across pathogen life history. This finding has important implications for leading to more effective disease management and rational grazing regimes in grassland systems.

Effects of population size on fitness traits in four common and four rare congeneric alpine plant species

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While for lowland species it is known that small populations have a reduced individual fitness and therefore increased risk of local extinction, alpine species are not sufficiently studied in this regard. Also, it is not clear how species rarity can mediate the direction and strength of the relationships between population size and fitness. We assessed how population size and rarity affect seed mass, seed number, germination, germination initiation time, seedling survival and seedling height in 90 natural populations of four congeneric alpine plant species pairs in the Swiss Alps (*Androsace chamaejasme*, *A. puberula*, *Gentiana acaulis*, *G. alpina*, *Potentilla crantzii*, *P. nivea*, *Viola calcarata* and *V. lutea*). We observed significantly larger seed numbers in larger populations across all species. At the same time, the number of germinated seeds and surviving seedlings was marginally significantly lower in larger populations, indicating a trade-off between seed quantity and quality. While there was no difference in fitness traits and population size between common and rare species, significant positive relationships between fitness and population size were more prevalent in rare than in common species. Our results indicate that population size affects individual plant fitness also in alpine species. Especially rare species might suffer from a reduced fitness in small populations, which could make them even more susceptible to environmental changes. Future studies should therefore address also long-term fitness traits such as adaptive trait plasticity when studying the relationships between fitness and population size.

Life history trade-offs and genetic constraints at elevational range limits in *Cardamine hirsuta* (Brassicaceae)

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Species are limited in their spatial distribution. There are several potential causes of range limits, ranging from ecological ones such as dispersal limitation to evolutionary ones such as limited genetic variation at range margins, small population sizes and accumulation of deleterious alleles due to genetic drift. While there is good support for their relevance in some species and for some range limits, there are also many cases where none of them seem to be at play. One neglected and likely cause of range margins is the multivariate nature of selection and the genetic integration of traits, which can constrain adaptation at range margins. Here, we used three populations of the montane annual crucifer *Cardamine hirsuta*, collected at low, mid, and high elevation sites of its elevational distribution. We reared plants in the greenhouse, subjecting them to two growth treatments (heat and control), and measured plant growth and leaf functional traits. We found the consistent trade-off between growth rate and plant size – fast growing plants end up being smaller. Next, we found that plants with higher acquisition capacity (specific leaf area) had lower dry mass in their leaves, they were less robust. There was considerable variation among populations in their response to heat, e.g., low-elevation plants were smaller than high-elevation plants in the control treatment, but the opposite was observed under heat. Our results indicate that such trade-offs can limit species ranges, effectively constraining the evolution of important traits due to their tight genetic integration.

Unraveling the genomic origin of species in large white-headed gulls

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Two approaches to better understand speciation have been to study hybrid zones and species pairs with varying levels of reproductive isolation across the speciation continuum. But rarely have they been applied in a single evolutionary lineage. Here, I introduce our research program on the genomic basis and architecture of speciation in large white-headed gulls (*Larus* spp.), one of the fastest radiating lineages in birds that produced 16 species and 35 subspecies in less than 1 million years. With chromosome resolved reference genomes for nine large white-headed gull species and three outgroups, we will test comparative genomic hypotheses about the role of genome structure evolution in rapid speciation. Building on earlier study of two hybrid zones between four large white-headed gull species in Eastern Europe and North America, we will quantify the genomic architecture of reproductive isolation across each hybrid zone and uncover the genetic basis of traits under sexual or natural selection showing parallel phenotypic divergence between species. In addition, pairwise species comparisons among twelve gull species will allow us to densely sample the speciation continuum in this clade and test hypotheses about how genomes diverge, genomic architecture of species differences evolves and contributions of neutral process, sexual and natural selection change across the speciation continuum. We will complement this dataset with multiple genomes of all described white-headed gull taxa to reconstruct the evolutionary history of this radiation and reassess the biogeographic context, timing and the role of vicariance and gene flow in this rapid species radiation.

Reference panel phasing for low-coverage sequencing imputation on non-model species barn owl (*Tyto alba*)

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High sequencing costs have limited research on non-model species. However, sequencing many individuals at low read depth (low coverage Whole Genome Sequencing lcWGS), thus reducing costs, is a new approach that has proven robust in model and non-model species. LcWGS read depth is too low to confidently call individual genotypes and, thus, delivers genotype likelihoods only. To obtain genotypes rather than their likelihood, an alternative is to use imputation from a reference panel of individuals sequenced at high coverage. Here we describe different strategies to create such a reference panel for the barn owl (*Tyto alba*), combining information from Illumina reads and pedigree. Specifically, we phased sequencing reads into longer inserts using either reads information only or reads and pedigree at different depths (if pedigree information was available) and then polished the results with statistical phasing. In line with previous research, we expect phasing using pedigree information having a higher accuracy than with reads only. However, the difference in accuracy achieved after statistical phasing is to be determined. Eventually, this work will help establish a high-accuracy lcWGS workflow for a non-model species.

A New Species of *Haematoloechus* Looss, 1899 (Digenea: Plagiorchioidea) Infecting The Lung of Crab-Eating Frog *Fejervarya cancrivora* from Indonesia

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Haematoloechus Looss 1899 is a species-rich genus with 70 described species of lung flukes of anurans with a worldwide distribution. Distinguishing among the species morphologically is problematic due to their high intraspecific variability, and molecular methods are still rarely used. Here we proposed a new species of the genus *Haematoloechus*, parasitic of the common rice frog *Fejervarya cancrivora* from Indonesia. The new species resembles morphologically more closely to *H. singaporensis* in most morphometric features, as well as in having the same extension of longitudinal extracaecal uterine loops that reach almost midlevel of body. However, the new species is distinguished notably by (1) the presence of an esophagus, which is absent in *H. singaporensis*; (2) the smooth oval shape of ovary, versus an ovary with four unequal lobes in *H. singaporensis*; (3) the number and distribution of clusters of vitelline follicles in the forebody, which is limited to four clusters of follicles lateral to each cecum in *H. singaporensis* versus 2-4 extracaecal and 1-6 intracaecal clusters in the new species. In addition, phylogenetic analysis of the 28S rRNA gene and the Internal Transcribed Spacers (ITS) and mitochondrial COI gene demonstrate that Indonesian specimens form a species-level lineage in the phylogeny of *Haematoloechus*. However, the lack of molecular data for *H. singaporensis* prevents us from confirming the validity of our species at the molecular level.

Effects of artificial light at night (ALAN) on the expression of floral traits in wildflower strips

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Artificial light illuminates the nights and with it many organisms. Apart from some positive effects like human safety, disturbed dark periods can alter species behavior, physiology or morphology. In natural communities, not only individual species are affected, but also species interactions. It is known that nocturnal and diurnal plant-pollinator interactions are altered under artificial light at night (ALAN), but knowledge about the mechanism of how ALAN impacts these interactions is restricted. In this field experiment, we tested the impact of ALAN on eleven Swiss native wildflowers and analyzed how the expression of three morphological floral traits (flower height, floral display size and flower number) was altered by the light. Six out of 12 study sites were artificially illuminated with commercial LED streetlamps. Moreover, we quantified how the light had an impact on diurnal insect visitation and the resulting seeds set for four target species. We found that floral traits were altered by ALAN, while seeds set were reduced for all species by the light. For the number of insect visitations at day, we found no effect of ALAN. We concluded that ALAN altered the expression of some floral traits, but different species reacted in different directions. Consequently, reduced seeds set could be a direct result of the changed morphology of the plants. But there are also other potential mechanisms. Future research should focus on testing the effect of ALAN on a larger selection of floral trait to get a clearer understanding of the mechanisms that are altering plant-pollinator interactions.

Identifying how life cycle variation drives biodiversity in changing environments over space and time

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Almost all successful lineages of animals have a complex life cycle, implying a change in morphology and ecology during the lifetime of an individual, transforming it from a larva into an adult. Yet, the origin and evolution of different life-history stages and their impact on species diversification remain poorly understood. At the time of the sixth mass extinction, it is crucial to identify whether life cycle complexity may allow organisms to cope with environmental change by producing significant morphological variation during their life span. We will combine different methodologies to disentangle the factors driving diversity at different ontogenetic stages across space and time. We will use Caudata as a model group, as they are diverse and show a large variation in life cycle types. We aim to identify how developmental strategies foster patterns of morphological and functional variation throughout ontogeny. We will: 1) study the role of life cycle complexity in the evolution of phenotypic diversity at both a fine-grained scale using populations displaying a wide geographic distribution and differing in life cycle type and globally at the interspecific level across broader evolutionary timescales; 2) link morphological change in time and space to environmental change using historical and spatially explicit data; 3) test whether life cycle variation has played a major role in shaping biodiversity by linking the evolution of phenotypic and developmental diversity to climate variation; 4) simulate future diversity using different climate change scenarios that can be used to prioritize species and areas for conservation actions.

Brooding modulates the call of a glass frog with male parental care

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In most animals, the costs of reproduction are higher for females than for males. Therefore, females should be the choosy sex and select males with preferred traits. In anurans, females are known to select males based on their body condition and body size. Moreover, as male parental care is quite common in frogs, females are also suggested to assess male parental performance and care quality. Whereas traits like body condition and body size can be reflected in call parameters, we don't know how females assess the parental state of a male. In certain glass frogs, males are the only caregivers and stay with the clutches until the tadpoles hatch. More importantly, females prefer caring males over males without clutches. Here, we investigated whether information on the care state is encoded in the call. To that end, we recorded 27 males with different care states and analysed their calls for differences in temporal and spectral call components. We found that males have significantly shorter calls and longer intervals between the calls when sitting and calling on top of the clutch (brooding) compared to males calling from next to the clutch and males without clutches. Therefore, only when a male that has clutches is simultaneously brooding and calling, then the call is modulated such that females could possibly deduce the parental state of this male. These results do not only give insights into female mate choice in species with male-only care, but more generally into mechanisms of acoustic intersexual selection in anurans.

Assessing the impact of glacier retreat on biodiversity and plant–insect interaction dynamics

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The retreat and extinction of glaciers worldwide is followed by the loss of plant and insect species from ecological networks and local communities. Furthermore, due to glacier retreat, new plant and insect species are moving up to higher altitude, causing changes in species diversity, species composition and also in plant-insect interactions. An integrative understanding of network dynamics and ecosystem functions following glacier retreat is therefore of major importance to biodiversity maintenance and environmental health. At Mont Miné glacier, Swiss Alps, we reconstructed the retreat of glacier during the last two centuries using geochronology and addressed four main stages of deglaciation ranging from recently ice-free terrains to late stages of development since the end of the Little Ice Age (c 1864). Following this glacier retreat gradient, we surveyed plants and pollinator insects to investigate the structure and dynamic of pollination networks and unveil their assembly by means of network analysis. We observed sharp changes in biodiversity of both plants and pollinators following glacier retreat. Communities close to the glacier are characterized by pioneer plant species characteristic of glacier environments but pollinator species from lowland. We found an increase in the abundance and richness of interactions shortly after glacier retreat. Yet, the complexity of pollination network decreased in late stages a century after the retreat of glacier. These results indicate that, in the long-term, glacier retreat can decrease the diversity and stability of ecological networks.

Effects of varying niche width on eco-evolutionary dynamics and community properties

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How species diversify to fully occupy available niches has been the object of much ecological investigation throughout the years. However, with a few exceptions, traditional works on niche packing and diversification dynamics have mostly focused on the position of species along a resource axis, while assuming constant niche widths. Yet we know that in nature species and populations fall along a specialist-generalist continuum, be it in habitat preference, resource use, or seasonal activity. How allowing for such differences affect niche packing and species coexistence is largely unknown.

We first derive a Lotka-Volterra model from an explicit resource-consumer model. We then consider coevolution in a community governed by these dynamics, under the framework of adaptive dynamics, where both niche position and niche width are evolving traits. We observe that even under perfectly symmetric resource scenarios, eco-evolutionary dynamics can lead to differentiation of niche widths so that we observe emergence of generalist and specialist phenotypes. Then we explore the effect of resource width and trade-off shape on the evolutionary outcomes, and how these impact community coexistence and structure. Finally, we discuss implications of our model when applied to phenology distributions and their variation in different growing season regimes, and whether this approach may contribute to a more mechanistic understanding of latitudinal patterns of species interactions.

Resolution of phylogenetic relationships within the fern genus *Botrychium* s.s. (Ophioglossaceae) using target enrichment sequencing

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The representatives of the fern genus *Botrychium* s.s. (Ophioglossaceae; eusporangiate ferns) are widely distributed around the world. Many species are circumtemperate to circumboreal, and the presumed centre of diversity is considered to be located in the Western North America. There are currently more than 30 species of *Botrychium* s.s. recognized. Despite several taxonomic and systematic revisions in the last years, it is clear that more reevaluations are needed. Some of the species traditionally assigned to *Botrychium* are now placed into distinct genera *Botrypus* and *Sceptridium* (and together with *Botrychium* s.s. they are denominated as *Botrychium* s.l.). From the systematics point of view, the *Botrychium* group is very complex. The species are usually small and morphologically simple, and the whole diversity is certainly underestimated as many populations have not been sampled yet. Moreover, more than half of the species are polyploids which further challenges the comprehension of the phylogenetics and evolutionary history of the group. Molecular studies detected many cryptic species in certain *Botrychium* clades and possibility of the existence of many more was indicated recently. In our study, we examined 84 selected *Botrychium* s.s. taxa from Northern America, Europe and Asia with the use of about 400 nuclear exons and flanking regions obtained by targeted enrichment sequencing. We use these newly obtained data to investigate the phylogenetic relationships in the group, estimate the parental lineages of certain hybrids and to detect potential cryptic species.

Petrochromis sp. "kipili brown" a chocolate-coloured beauty from Lake Tanganyika

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Cichlid fishes received a lot of attention in evolutionary research over the last decades. Despite the improvements in reconstructing their evolutionary history, their taxonomy received considerably less attention.

In our study system, the cichlids of Lake Tanganyika, many species still await their formal description while several genera need taxonomic revisions and re-evaluation of their classification. In this taxonomic study we focused on the Tropheini, one of the most species rich tribes within the cichlid radiation of Lake Tanganyika. The Tropheini currently consist of 24 valid species which are assigned to nine different genera. One genus, *Petrochromis*, is polyphyletic consisting of three clades of which its species are specialized algae grazers dwelling on rocks at the shore of the lake. Three species occur at deeper water levels than the other *Petrochromis* species.

One of those three species, *P. horii*, is formally described whereas the other two remain undescribed: *P. sp. "kipili brown"* and *P. sp. "red"*. In order to be able to identify diagnostic characters for a proper species description for *P. sp. "kipili brown"*, we compiled a morphological dataset including 30 meristic characters as well as 23 morphometric measurements of all currently recognized taxa of the Tropheini. Principal component analyses enabled us to test for morphological discreteness of the different taxa on species level and to identify potential diagnostic character states and combinations to distinguish the different species. In addition, our dataset provides further information about the three clades of *Petrochromis* and their discreteness.

Why stick insects are perfect just the way they are: optimal sex ratios under facultative parthenogenesis

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In obligately sexual organisms, Fisherian sex ratio theory predicts equal parental investment into sons and daughters. This is because each individual has one mother and one father, and hence the total reproductive success of all males of a population is equal to the total reproductive success of all females of that population. Conversely, in facultatively parthenogenetic animals, such as stick insects, some individuals only have a mother, and no father. As a result, the total population-wide reproductive success of females is higher than that of males, and hence female-biased sex allocation is favored. The degree of the female-bias is directly related to the rate of parthenogenesis: if parthenogenesis is more common, optimal sex ratios become more female-bias. In stick insects, asexually produced offspring are always female, while sexually produced offspring have unbiased sex ratios. Using a mathematical model, we show that this system achieves optimal sex ratios in stable environments, but not in unstable or cyclic environments. We further compare stick insects to other facultatively sexual animals such as aphids and *Daphnia* and argue that the ability to produce males asexually enhances adaptation to unstable environments in facultatively sexual organisms.

Genomic consequences of miniaturization in zebrafish relatives

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Miniaturization is the evolution of extreme reduction of adult body size in animal taxa. Among vertebrates, miniaturization has evolved repeatedly in teleost fishes and is often accompanied by morphological, ecological, or physiological novelty. In cypriniforms, miniatures are especially frequent in zebrafish relatives (danionines). Two extreme types of different phenotypes can be identified in danionines as proportioned dwarves and progenetic miniatures. Proportioned dwarves are tiny but resemble almost identical copies of their larger relatives whereas progenetic miniatures are developmentally truncated and characterized by larval appearance resembling an early developmental stage in their larger relatives. A previous study identified extensive genome miniaturization and developmental gene loss in the danionine progenetic miniature *Paedocypris*. The repeated evolution of both progenetic miniatures and proportioned dwarves among danionines offers a system to identify the genetic and genomic changes responsible for the loss of characters and the evolution of morphological novelties in a comparative framework. Based on a broad taxonomic sampling of cypriniforms, using available genomic resources and newly generated genomic data during this project, we will provide a comprehensive phylogeny of Cypriniformes, place the rogue miniature taxa *Paedocypris*, *Danionella*, and *Sundadanio*, and test previously published competing hypotheses on cypriniform phylogeny. We will then reconstruct the evolutionary history of miniaturization. Based on our phylogenetic framework, we will then explore comparative genomics of miniaturization in danionines to reveal general trends in genome evolution linked to miniaturization.

Fertility signaling games: should males obey the signal?

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Game theory has made researchers realizing that two sexes may have conflicting interests. Males may benefit from a higher mating rate than females do. A temporal component of this conflict has been rarely modelled: females' interest in mating may depend on when females become fertile. This sets conditions for male-female coevolution, where females may develop fertility signals, and males might benefit discriminating them, i.e., obeying the signal targeting signalling females only. Modelling this temporal aspect to sexual conflict yields two equilibria: (i) a trivial equilibrium without signals and males targeting all females, and (ii) a signalling equilibrium where all females signal before ovulation, and where either some, or all, males obey the signal. The 'all males obey the signal' equilibrium is more likely if we assume that discriminating males have an advantage in postcopulatory sperm competition. While in the absence of this benefit, we find the 'some males obey the signal' equilibrium. Also, equilibria can be stated to have one sex as a 'winner' and the opposite sex as a 'loser'. From early models emphasizing 'battle of the sexes' style terminology, we recommend moving on to describe the situation as non-signalling equilibria having stronger unresolved sexual conflict than signalling equilibria.

Effects of artificial light at night and the differences between day and night on insect abundance

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With increasing urbanisation worldwide, artificial light at night (ALAN) is also on the rise. Light fundamentally determines and influences the natural rhythm and behaviour of insects and plants. However little is known about how ALAN influences herbivory on a global scale, with subsequent indirect potential consequences on other ecological mechanisms, such as pollination. Therefore, we investigated the effects of ALAN on the abundance and species diversity of herbivores, plant-herbivore interactions as well as the herbivory intensity on wild flowers commonly found in the Swiss agricultural landscape. In order to investigate this, we conducted a field experiment, where we measured the effects of ALAN on diurnal and nocturnal herbivores on 12 different wild flower stripes, of which six were illuminated with commercial LED street lamps. We tested whether there was a difference between dark and artificially illuminated sites in their abundance as well as in their feeding behaviour, measured by the initial damage to the plants, such as to the flower heads and to the leaves.

In a further step, we sampled insects in the three different structures, including forest edges, extensive meadows and wild flower stripes, at day and night to test whether there was an effect of the habitat on the circadian activity of herbivores. We regularly sampled insects in six fields per habitat by swipe netting the vegetation during the day and at night and subsequently sorted the insects at the orders levels to analyse how habitat influence daily and nocturnal herbivore communities.

One or Three: Empirical data facilitates conservation of musk deer suggesting only one species of musk deer in Western Himalayas

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Musk deer species are poorly studied throughout their distribution range due to their elusive nature and occurrence in inhospitable habitats of high-altitude Himalayas (>2500m). Past distribution records based on ecological studies with few photographic and indirect evidence, provide inadequate information on species distribution which leads to uncertainty in defining the presence of specific taxonomic units of musk deer in Western Himalayas. Consequently, species-oriented conservation is hampered due to lack of species-specific investments in monitoring, protecting and tracking illegal poaching of musk deer for Musk pod (“a preputial gland in a sac under the abdominal skin of male musk deer, used for making perfumes, medicines and for religious purposes as well”). The present study was conducted in Lahaul–Pangi landscape of Himachal Pradesh and Uttarkashi district of Uttarakhand. We used camera trapping (255 cameras), transect surveys (220 trails), non-invasive DNA sampling (40 samples) and geospatial modelling (279 occurrence records) to verify the geographic presence and map suitable habitat of Kashmir musk deer. All captured images confirmed a new record of Kashmir musk deer (*Moschus cupreus*) followed by genetic based identification in Uttarakhand and Himachal Pradesh with predicted suitable habitats in Western Himalayas. Surprisingly, other species of musk deer (e.g., Himalayan musk deer and Alpine musk deer supposed to occur in the landscape) were not captured in any of the studied sites. Since the population of KMD is declining at an alarming rate, future conservation plans and management needs to be evaluated accordingly. The identified suitable habitats should be prioritized for conservation and management planning.

Switch off the light! Artificial light at night reshape floral traits of wild plants, with consequences for reproductive success

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Among drivers of environmental change, artificial light at night (ALAN) is poorly understood, yet is increasing on a global scale and affects biodiversity in multiple ways. Plant-pollinator networks, as an example, are impacted and disruptive effects of ALAN have been quantified on diurnal pollination, leading to negative consequences for plants reproductive success. We investigated the mechanisms driving the indirect effects of ALAN on the interactions between plants and day-active pollinators. As ALAN may impact plants' development and growth, we hypothesized that ALAN may also alter the expression of several floral traits involved in plant-pollinators interactions, leading to a reduced attractiveness for the pollinators. This question was investigated by means of garden experiments as well as a large field study, in which six out of a total of 12 Swiss wild flowers stripes were illuminated using commercial LED streetlamps. The expression of three morphological floral traits were measured on seven native wild flowers grown with and without light treatment. Attractiveness of these plants were quantified by the means of choice experiments, where the number of insects visiting potted plots displayed in a neutral surrounding were quantified and the number of seeds produced at the end of the season were counted. Our results only showed an effect of ALAN on the expression of one trait (number of flowers), but an overall negative impact on the number of flower visitors and seeds sets. These results suggest that other mechanisms are involved in the alteration of diurnal pollinators visitors due to ALAN.

Small structures for mustelids

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The intensification and homogenization of agricultural practices have led to a dramatic decline in biodiversity in Swiss agroecosystems. The loss of natural and semi-natural habitats is one of the main causes of this decline. The establishment of new small structures, specifically branch and stone piles, is encouraged by many experts and nature conservation agencies to improve habitat conditions for farmland species such as stoats (*Mustela erminea*) and weasels (*Mustela nivalis*). However, so far, no scientific study has investigated the conservation success of such small structures. Here, we used scat detection dogs and camera trap boxes as complementary passive sampling methods to monitor the occurrence of stoats and weasels in the landscape in relation to the presence or absence of small structures. While mustelids occurred at sites with small structures (16 out of 128), species densities were too low to statistically assess habitat preferences. Furthermore, camera trapping data allows for the investigation of habitat preferences of small mammal species occurring on the same small structures. First results have revealed a positive effect of roads and a negative effect of buildings on Arvicolinae, shedding further light on the effect of anthropogenic activity on farmland biodiversity. The project will continue in 2023, doubling the sampling size. Ultimately, the project shall deliver recommendations on where and how to place small structures in the agricultural landscape.

Predator sensing by plants: Consequences for tri-trophic interactions

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Tri-trophic interactions between plants, herbivores, and herbivore natural enemies are key drivers of ecosystem functions and determine yield in agriculture. Evidence is accumulating that plants perceive the presence of herbivore natural enemies and respond to it. Yet, it remains unknown how relevant the response is for multitrophic interactions. In this study, we investigated how the maize response to the presence of entomopathogenic nematodes (EPNs), predators of root herbivores, affect the performance and behaviour of root and leaf herbivores under laboratory and field conditions. Upon exposure to EPNs, maize plants exhibited changes in the metabolomic profiles of root exudates, root-, and leaf tissues. Additionally, a prior exposure of maize plants to EPNs altered the distribution of the stem borer *Ostrinia nubilalis* in the field. Preliminary assays suggest that these shift in herbivore population dynamic relies on changes in female oviposition site selection, but not on larval performance. We discuss the potential adaptive value of the plant response and how the interplay between plants and natural enemies of herbivores and may help to increase the efficiency of EPNs as a biocontrol agent.

The moulding of intra-specific diversity by selection under ecological inheritance

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Organisms continuously modify their environment, often impacting the fitness of future conspecifics via ecological inheritance. When this inheritance is biased towards kin, selection favours modifications that increase the fitness of downstream individuals. How such selection shapes trait variation within populations, however, remains poorly understood. Using mathematical modelling, we investigate the coevolution of multiple traits in a group-structured population when these traits affect the group environment, which is then bequeathed to future generations. We examine when such coevolution favours polymorphism as well as the associations among traits that emerge. We find in particular that two traits become associated when one trait affects the environment while the other influences the likelihood that future kin experience this environment. To illustrate this, we track the coevolution of (a) the attack rate on a renewable resource, which deteriorates environmental conditions, with (b) dispersal between groups, which reduces the likelihood that kin suffers from such deterioration. We show this often leads to the emergence of two highly-differentiated morphs: one that readily disperses and depletes local resources; and another that maintains these resources and tends to remain philopatric. More broadly, we suggest that ecological inheritance can contribute to phenotypic variation and lead to complex ecological polymorphism.

Functional Approach Using Soil Protists as a Taxon-free Tool for Environmental Quality Assessment

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Soil organisms are useful as bioindicators to assess the impact of ongoing climate change on ecosystem functioning. Peatlands, which represent a major reservoir of soil organic carbon, are threatened by anthropogenic influence. Water table depth (WTD) is a key factor controlling the carbon balance in peatlands. Testate amoebae are routinely used as WTD indicators using predictive models. These transfer functions require taxonomic identification based on shell morphology, but some taxa are commonly misidentified. An alternative approach is to use functional traits. Our aim was to assess the extent of taxonomic bias and to compare the performances of species-based and traits-based models.

A set of light microscopy images of testate amoeba was compiled using samples collected across European peatlands. Species identifications with degree of confidence for each picture were analysed by researchers with contrasted expertise. We compared diversity metrics derived by each observer. For our second aim, we developed a trait-based transfer function with a trait database for the most commonly identified species morphotypes.

The degree of identification bias differed among taxa leading to strong variation in diversity metrics. The functional traits model performed equally well compared to the morpho-taxa-based one.

As ecological information is being routinely lost due to species misidentifications and taxonomic uncertainty, taxon-free approaches potentially offer safe and robust alternatives for rapid and accurate ecological assessments. We conclude that functional traits models overcome limitations of taxonomy-based ones for WTD inference, and may also prove to be better-adapted for inferences of ecosystem functioning.

Molecular role of a *C. elegans* germline-specific RNA helicase

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N6-methyladenosine (m6A) is catalysed by RNA methyltransferase “writers”, while the functional consequences are mediated by “readers” that specifically recognize the modification. The YTH reader proteins recognize m6A via the YTH domain to modulate splicing, translation, or stability of mRNAs. One of five mammalian YTH proteins, YTHDC2 is a germline-specific RNA helicase that is essential for mouse fertility. Importantly, YTHDC2 is the only YTH protein conserved in nematodes.

In mammals, deletion of YTHDC2 leads to misregulation of the germline transcriptome and prevents proper progression through meiosis. This function is independent of m6A-binding but requires YTHDC2 RNA helicase activity. The molecular mechanism by which it regulates germline transcripts is currently unknown. We are studying the nematode ortholog, F52B5.3 (wYTHDC2), to investigate how this conserved RNA helicase targets and regulates germline transcripts. Consistent with a lack of the m6A writer-reader system in *C. elegans*, wYTHDC2 lacks a recognizable YTH domain.

Here, we show that deletion of wYTHDC2 leads to temperature sensitive post-embryonic developmental arrest via a classic stress response pathway induced by environmental conditions like reduced food availability. We have identified wYTHDC2 as a component of germline P-granules, evolutionarily conserved RNA-rich condensates that ensure proper germline gene expression. P granules also contain factors important for small RNA production, and heritable small RNAs have recently been implicated in inherited response to environmental changes. This suggests a potential role for wYTHDC2 in recruitment of RNA targets to P-granules, where they serve as substrates for small RNA generation, which may be maternally deposited to influence development.

Are resistance and post-drought performance of temperate grassland species related to specific leaf area and drought length?

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Intensification of grasslands has favoured fast-growing, resource-acquisitive species with high specific leaf area (SLA) at the cost of slow-growing, resource-conservative species with low SLA. At the same time, droughts are becoming more frequent and more severe in Europe. According to the leaf economic trade-off, resource-conservative traits are expected to be favourable during droughts, whereas resource-acquisitive traits can favour regrowth post-drought. If SLA is determining plant responses to drought, it is thus likely, that the combination of land-use intensification and climate change will have marked impacts on the stability of temperate grassland ecosystems.

To investigate the role of SLA for the stability of grassland ecosystems in response to drought, we established a common garden experiment. We included 48 species, that are most abundant in four temperate grassland types, covering a gradient from very low to high land-use intensity. We let all plants establish under ambient conditions for one season before exposing them to simulated droughts of four different lengths and one control treatment. In the year of the experimental drought and in the spring to early summer post-drought, we repeatedly recorded the frequency and measured the biomass of each species in each plot.

With my poster, I will present the results of this study, namely how plant drought resistance and post-drought performance is related to SLA and drought length.

Genetics of the *Calamagrostis stricta* (Poaceae) species complex in Europe, with special focus on the newly described *C. lonae*

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Discovery and description of *Calamagrostis lonae* Eggenberg & Leibundgut (Poaceae) as a new endemic species from the Pennine Alps in Switzerland is without a doubt one of the most extraordinary findings of the last decades. The taxon was discovered 2018 near Pas de Lona, close to the village of Grimontz. *Calamagrostis lonae* is an herbaceous plant. Morphologically and ecologically, the taxon shows similarities with the glacial relict *C. stricta* and especially with its Arctic subspecies *C. stricta* subsp. *groenlandica*. *Calamagrostis stricta* species complex is a circumpolar, boreo-arctic and montane element, well spread in the Arctic and Subarctic regions but much rarer the closer you get to Western and Central Europe. The phylogeny, biogeography and taxonomic division of this species complex is not fully understood.

The present research project is the first to investigate the genetics of the *C. stricta* species complex on a broad geographic scale, with special focus on the newly discovered *C. lonae*. The main topics of our study are (1) assessing *C. lonae* species status compared to European *C. stricta* populations, (2) understanding the origin of the taxon, (3) offering a guideline for conservation.

The poster will briefly introduce the newly discovered taxon and population in Switzerland. Key findings on the distribution and genetic structure of the *C. stricta* species complex across Europe will be presented and explained using maps and plots. The poster will end with a brief discussion about its recent evolutionary history, its dispersal across the European continent, and its conservation status.

Benzoxazinoid metabolism by entomopathogenic nematodes

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Benzoxazinoids are plant specialized metabolites produced by cereals, like maize and wheat. The Western corn rootworm (WCR, *Diabrotica virgifera virgifera*), a specialist root herbivore, sequesters benzoxazinoids and uses them against its natural enemies, entomopathogenic nematodes (EPNs). Yet, how EPNs cope with the sequestered benzoxazinoids remains unknown. Here we investigated whether and how EPNs metabolize HDMBOA-Glc. We found that different strains of EPNs, originating from Europe and the US, have evolved metabolism strategy to cope with the chemical. All 12 strains deglycosylated the compound, resulting in the accumulation of the toxic MBOA aglucone. Surprisingly, the metabolism path employed by the different strains did not correlate with their survival and infectivity success. We discuss possible nematode adaptations to benzoxazinoid sequestration by their host and the relevance for developing EPN breeding programs for sustainable agriculture.

Testing the influence of masking factors on activity patterns of cichlids

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Cichlid fish from the Rift Valley Lakes of Africa represent an outstanding model for the study of explosive diversification, exhibiting exceptionally fast diversification rates and differences in morphological, ecological, and behavioural phenotypes allowing them to inhabit a vast number of different ecological niches.

One possible way that cichlids could partition their habitat and ecology is by introducing variability in their circadian activity periods, which is also known as temporal niche differentiation. However, it is unclear which aspects of the environment are responsible for shaping their circadian behaviour.

Previous experiments that measure and document diel activity patterns of >60 endemic Lake Tanganyikan cichlid species have shown that activity patterns are exceedingly variable in length and timing including diurnal, crepuscular and nocturnal activity (Nichols, Shafer et al. unpublished). However, some shell dwelling species, which anecdotal observation would indicate to be diurnal, display strong nocturnal activity when they are individually assayed in a reductionist setup without shells. This drastic change in phase could originate from the absence of a shell or conspecifics as a masking factor, altering the output of the underlying endogenous circadian rhythm. This study will record the circadian activities of individuals of *N. multifasciatus*, *N. brevis*, and *L. ocellatus* on site in Lake Tanganyika and in a controlled laboratory setting, to investigate the influence of environmental cues on daily behavioural rhythms. Ultimately, we aim to identify the evolutionary history of these behaviours and the neural circuitry responsible for these drastic shifts in circadian behaviour.

The rust fungi collection in herbarium G: from unknown to becoming a world reference

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Biological collections play an essential and central role in a plethora of studies dealing with fundamental biology, ecology, conservation, taxonomy, phylogeny, biochemistry, pharmacy, ethnobotany, etc., both in basic and applied fields. These subjects of research are traditionally preserved in museums and herbaria, representing part of the biological, historical, and cultural heritage. Despite its importance, the value of natural collections is often underestimated, especially in the era of molecular research and informatics. However, these collections are an almost never-ending source of unique data about biodiversity and the environment, provide important insights into our history, and form a foundation for education and taxonomic knowledge, all of which can now be extracted with different analytical techniques (NGS/museomics, CT-scan tomography, isotope analyses, etc.).

The mycological section of herbarium G holds the second largest fungal collection in Switzerland, including specimens of all major groups of fungi from all parts of the world. As part of a SwissCollNet project (financed by the SCNAT), in collaboration with the herbarium Z+ZT, we aim at making publicly available and searchable an important part of the rust fungi specimens (Pucciniomycotina), none of which have been databased prior to this study. A detailed survey revealed over 4000 species names in more than 100 genera, of which an impressive 30 % have associated type material. All potential type specimens were extracted and several nomenclatural issues were solved. At the end of the project, the nomenclature will be updated, specimens properly classified, and types both databased and macro- and microscopically imaged. This will serve to pave the way for future research in systematics, biodiversity, and conservation, with important implications in other disciplines, such as molecular biology, morphology, etc.