

IEE Symposium

3. & 4. September, 2026

u^b

^b
UNIVERSITÄT
BERN



Natural History Museum Bern

CONTENT

(Clicking the headings will take you to the corresponding section)

IEE DIVISIONS & GROUPS	3
ORGANISING COMMITTEE	3
PROGRAMME	4
ABSTRACTS	8
VOLZ PRIZE NOMINEES	20
POSTERS	23

Code of conduct:

Aligned with the IEE's values, we are prioritizing inclusivity and respect at the IEE Symposium. This gathering aims to foster connection and goodwill among all members of our institute (and significant others), promoting a healthy and fruitful social environment where everyone feels welcomed and valued. If you experience or witness any behavior that detracts from this atmosphere, please take steps to intervene and raise awareness, seeking further assistance from the organizing committee if careful actions are needed.



IEE DIVISIONS & GROUPS

Abbreviation	Division/group	Head
AQUA	Aquatic Ecology & Evolution	Ole Seehausen
BEHAV	Behavioural Ecology	Eva Ringler
CB	Conservation Biology	Raphaël Arlettaz
PopGen	Population Genetics	Gerald Heckel
EVOL	Evolutionary Ecology	Katie Peichel
EvoMorph	Evolutionary Functional Morphology	Anne-Claire Fabre
ELVIA	Evolving Interactions	Xiang-Yi Richter
IBCS	Integrative Biodiversity Conservation Science	Margaret Owour
TERR	Terrestrial Ecology	Maddy Thakur
THEE	Theoretical Ecology & Evolution	Claudia Bank

ORGANISING COMMITTEE

Bárbara Freitas
Ben Sulser
Daniel Lee Jeffries
Dario Josi
Franziska A. Brenninger
Jean-Yves Humbert
Laura Bashor
Loraine Hablützel
Maddy Thakur (Chair)

Emma Ohsner (Booklet-Design)

PROGRAMME

Thursday 3rd September

Registration starts at 12:30

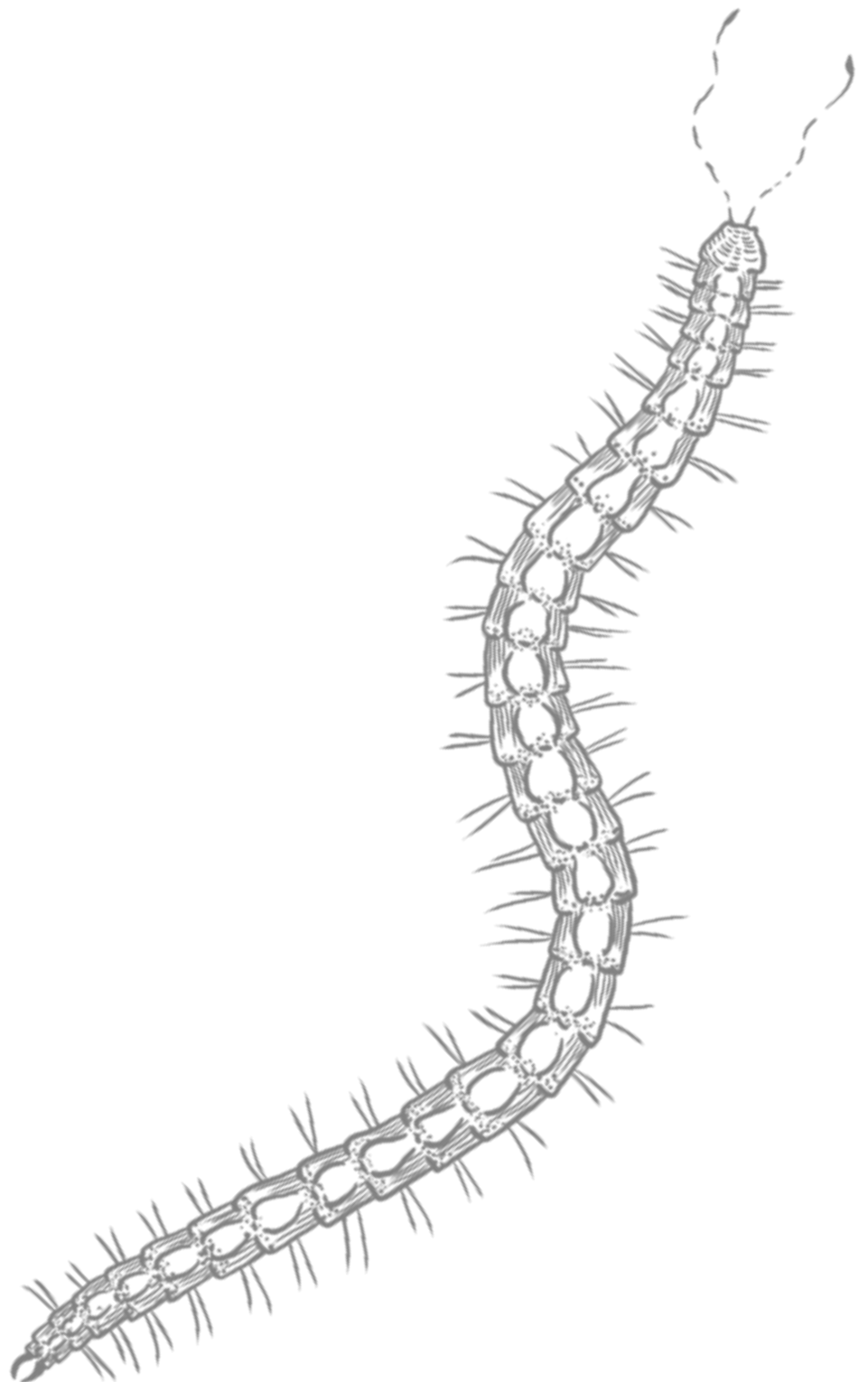
13:00	Maddy Thakur (& committee) Welcome			
Session 1 (Chair: Franziska A. Brenninger)				
13:30	Nicholas Ofiti	TERR	Postdoc	Climate extremes reorganise microbial controls on soil carbon cycling
13:45	Laura Bashor	PopGen	Postdoc	Diversity and structure of the canine gut virome in Uganda and Switzerland
14:00	Morgane Fournier	EvoMorph	PhD	How intraspecific life cycle variation shapes the morphology of two European species of Caudata
14:15	Amo Ikiror	THEE	MSc	Genomic insights into persistent antimicrobial resistance in <i>E. coli</i> from antimicrobial-free Swiss dairy heifers
14:30	Isabelle Arnold	CB	PhD	VOLZ: Relaxation of management intensity promotes butterfly communities in mountain grasslands
15:00 – 15:30	Coffee break			
Session 2 (Chair: Loraine Hablützel)				
15:30	John Bosu Mensah	BEHAV	PhD	Close range assessment of tadpole deposition sites and control of offspring release in a tadpole transporting Neotropical poison frog
15:45	Katie Peichel	EVOL	PI	Experimental evidence for selection on chromosomal inversions
16:00	Eugenio de Melo Filho	IBCS	Msc	Communication, knowledge-sharing and environmental literacy in biodiversity conservation initiatives: preliminary insights from Brazil and Kenya
16:15	Xiaoqing Zhang	ELVIA	PhD	Spatiotemporal interactions between biocontrol bacteria and pathogenic oomycetes
16:30	Bruno Camargo dos Santos	BEHAV	PhD	VOLZ: Sibling number and early interactions shape social competence for life
17:00 - 19:00	Poster session			

Friday 4th September

Coffee starts at 8:30

Session 3 (Chair: Bárbara Freitas)				
9:00	Jia Zheng	ELVIA	Postdoc	Simulation analysis of ibis conservation: Inbreeding and demography interact to influence recovery of bottlenecked populations
9:15	Julio Ayala-López	THEE	PhD	The effect of hybrid incompatibilities on a cline
9:30	Felix Rentschler	TERR	MSc	How do consumer diversity and patch connectivity explain trophic regulation after heat waves?
9:45	Gilliane Borel	BEHAV	MSc	Drought effects on parental care behaviour in poison frogs
10:00	Laura Forgione	CB	PhD	VOLZ: Restoring plant diversity in lowland grasslands: Efficacy of different seed addition and soil preparation methods
10:30 – 11:00 Coffee break				
Session 4 (Chair: Laura Bashor)				
11:00	Jingjing Shi	TERR	PhD	Fungal-bacterial interactions asymmetrically influence fungal and bacterial stability under climate extremes
11:15	Ben Sulser	EVOL	Postdoc	Is morphological evolution predictable? Insights from an evolutionary experiment in nature
11:30	Colin Guignet	CB	MSc	Effect of passive restoration on soil microbiome in mountain grasslands
11:45	Qingqing Chen	CB	Postdoc	Field-scale restoration experiments reveal drivers of dark diversity across trophic levels in grasslands
12:00	Lorraine Hablützel	THEE	PhD	VOLZ: Studying the genetic basis of ecological interactions with intergenomic epistasis
12:30 David Marques - an obituary Ole Seehausen				
12:45 - 14:00 Lunch break				

Session 5 (Chair: Ben Sulser)				
14:00	Isabelle Toussaint	Evo-Morph	PhD	Testing the impact of metamorphosis and size on the aquatic feeding kinematics of the Iberian ribbed newt (<i>Pleurodeles waltl</i> Michahelles, 1830)
14:15	Ella Rees-Baylis	ELVIA	PhD	Mating system, sexual selection, and the evolution of sex differences in ageing
14:30	Ianis Vilela	THEE	PhD	Automated machine learning to identify drivers of microbial community composition
14:45	Anna Mahulu	AQUA	Postdoc	Mechanisms of species coexistence in a hyperdiverse and incredibly young adaptive radiation
15:00	Hiranya Sudasinghe	EVOL	PhD	VOLZ: Convergent genome streamlining accompanies independent miniaturization in the world's smallest fishes
15:30 – 16:00	Coffee break			
Session 6 (Jean-Yves Humbert)				
16:00	Diogo F. Antunes	BEHAV	Postdoc	Mechanisms of parental care
16:15	Luiz Jardim de Queiroz	AQUA	Postdoc	Lakes as islands: a fresh(water) perspective on island biology
16:30	Lynn Wedekind	EVOL	MSc	The role of chromosomal inversions in phenotypic divergence
16:45	Nicolas Stettler	CB	MSc	A semi-automated method to study family size and age structure of the Eurasian Beaver <i>Castor fiber</i>
17:00	Marion Zohra Noëmi Talbi	AQUA	PhD	VOLZ: Rapid evolution of recombination landscapes during the divergence of cichlid ecotypes in Lake Masoko
17:30	Director's round table with Claudia Bank & Ole Seehausen Moderated by Maddy Thakur			
19:00	Dinner & Volz Prize Ceremony Moderated by Ben Sulser & Franziska A. Brenninger			



ABSTRACTS

SESSION 1

Climate extremes reorganise microbial controls on soil carbon cycling

Nicholas O.E. Ofiti, Itzel Lopez-Montoya, Zachary Bailey, Adrien Mestrot, Daniel B. Nelson, Ansgar Kahmen, Ludovico Formenti, Madhav P. Thakur

Abstract: Increasing climatic extremes are expected to reshape terrestrial ecosystems, but whether warming alone explains microbial responses during droughts and heatwaves remains uncertain. We used a multifactorial outdoor mesocosm experiment to test how warming, recurrent heatwaves and drought restructure grassland soil microbial communities during drought resistance and recovery. These drivers interacted in ways not captured by warming alone. Drought amplified realised warming, and microbial responses peaked during resistance, when stress-tolerant taxa increased and bacterial and fungal communities diverged. Bacterial communities were structured mainly by the resistance-recovery sequence, whereas fungal communities responded directly to warming and drought. Compound extremes also altered microbial thermal physiology. Hydrolytic enzyme activity and growth were suppressed during drought, growth declined more than respiration, and rewetting did not fully restore pre-drought temperature responses. Despite pronounced compositional turnover, community-level carbon processing remained stable through compensatory shifts in microbial biomass, turnover and enzyme investment. Microbial controls over soil carbon therefore depend on interacting thermal and hydrological extremes rather than warming alone. Accounting for non-additive and legacy effects will be critical for predicting soil carbon-climate feedback in a warmer, more variable climate.

Diversity and structure of the canine gut virome in Uganda and Switzerland

Laura Bashor, Gerald Heckel

Abstract: Most domestic dogs worldwide live in close proximity to humans but roam freely, which in turn moves the microbial communities that they host. Despite this, little is known about how the spatial and genetic structuring of free-roaming dog populations and their associated viruses relates to the spread of infectious diseases. In this pilot study, we compared two methods to characterize viral metagenomes from domestic dog feces collected in Switzerland and Uganda: (1) bulk paired DNA and RNA extraction and (2) viral particle enrichment followed by extraction and reverse transcription (N = 6 individuals, 2 pools of five). The initial results provide a basis for selecting an approach to maximize information and minimize bias for the larger study. Ultimately, our work will inform strategies to minimize canine-mediated spread of infectious diseases and answer basic questions about virus diversity and evolution across time and space.

How intraspecific life cycle variation shapes the morphology of two European species of Caudata.

Morgane Fournier, Vivien Louppe, Isabelle Toussaint, Julien Clavel and Anne-Claire Fabre

Abstract: Intraspecific variation in life cycle is well-known in Caudata. It has evolved independently in several species with complex life cycles involving multiple ecologically distinct developmental stages associated with metamorphosis. This variation can result in simplified pathways, lacking intermediate stages and/or completing development within a single ecological niche. The associated changes in growth rates and developmental processes may constrain the range of phenotypes produced, influencing body size, allometric trajectories, and morphology. Here, we investigate how intraspecific life cycle variation influences morphological patterns in adults of two Caudata species, the Alpine newt (*Ichthyosaura alpestris*) and the fire salamander (*Salamandra salamandra*). Using linear measurements and geometric morphometrics, we quantify the effects of alternative life cycles and associated functional constraints related to feeding and locomotion on body size and morphology. We test whether alternative life cycles lead to distinct allometric trajectories and differences in morphological patterns.

Genomic insights into persistent antimicrobial resistance in *E. coli* from antimicrobial-free Swiss dairy heifers

Amo Ikiror, Adamantia Kapopoulou, Stephan Peischl

Abstract: This thesis investigates the persistence of antimicrobial resistance (AMR) in *Escherichia coli* from Swiss dairy heifers, building on the Schmid et al. 2026 dataset (n=966 isolates, n=19 WGS isolates). Antimicrobial use in this population is very low overall, and was absent on the two farms where clonal persistence of resistant isolates was observed and whose isolates were sequenced. The primary question is why some isolates show AMR without detectable resistance genes, and why some have antimicrobial resistance genes (ARGs) without the corresponding AMR phenotype. Given the small sample size, especially of sequenced isolates, the analyses are framed as exploratory. The approaches include: analysis of phenotypic resistance profiles and turnover over sampling periods, exploration of genotype-phenotype association, population genomics analyses, compilation of ARG presence/absence and of methylation status at ARG promoters. These approaches aim to better understanding the genetics of AMR by identifying genomic regions or epigenetic marks that vary with resistance, and to propose candidate mechanisms or hypotheses on what enables the maintenance of AMR in environments with low AMU. The guiding question is, in the absence of selection pressure, what supports the maintenance of resistance?



Close range assessment of tadpole deposition sites and control of offspring release in a tadpole-transporting Neotropical poison frog

John Bosu Mensah, Rosanna Mangione, Max Ringler, Eva Ringler

Abstract: Parental care is a key component of many animal reproductive biology. Offspring survival depends on the intensity of care received in the form of time, energy, and nutritional investment, but also on decisions made by parents regarding the best habitat for offspring. However, how parents assess habitats in order to make decisions that ensure offspring survival is understudied in many animals, especially in anurans. Using the brilliant-thighed poison frog, we investigated how the presence and chemical cues of conspecific tadpoles, heterospecific anuran, and insect predators influence site preferences at tadpole deposition. We conducted artificial pool choice experiments during two breeding seasons in 'Les Nouragues', French Guiana. Depositing frogs significantly avoided artificial pools containing dragonfly predators but not tadpoles of dyeing poison dart frog during close range assessment of habitat suitability. The presence of conspecific tadpoles yielded mixed results as frogs preferred them in one year, but avoided them in the other, possibly due to differences in the number of tadpoles used. The number of tadpoles released at a time was significantly influenced by the amount of time spent inside a given pool, suggesting a time-based mechanism on how transporting frogs can regulate the number of tadpoles released during tadpole deposition.

Empirical evidence for selection on a chromosomal inversion in stickleback

Katie Peichel, Nicole Nesvadba, Anna Raess, Juliana Rodriguez Fuentes, Marius Roesti, and Dolph Schluter

Abstract: Chromosome inversions are hypothesized to play a special role in adaptation to divergent environments. Because there is no recombination within the inversion in heterozygous individuals, inversions can harbor genetic differences that contribute to local adaptation, even if the rest of the genome experiences gene flow. Although inversions are common between populations adapted to divergent habitats, studies directly demonstrating selection on inversions are rare. We conducted such a test in the threespine stickleback (*Gasterosteus aculeatus*), which has three chromosomal inversions that are highly differentiated between marine and freshwater stickleback populations. In 2022, I placed marine sticklebacks heterozygous for the marine and freshwater orientation of either the chromosome 11 or the chromosome 21 inversion into each of three freshwater ponds at the University of British Columbia, Canada. Hence, the marine and freshwater inversion orientations were present on a consistent marine genomic background and started at an equal frequency in each pond. Between 2023 and 2026, we tracked inversion orientation frequencies across four stickleback generations. Surprisingly, the freshwater orientation of the chromosome 21 inversion has not increased in frequency. However, the freshwater orientation of the chromosome 11 inversion has increased in all three replicate ponds, suggesting it provides a selective advantage in freshwater.

Communication, knowledge-sharing and environmental literacy in biodiversity conservation initiatives: preliminary insights from Brazil and Kenya

Eugenio de Melo Filho, Margaret Owuor

Abstract: Environmental literacy has been recognised as an important component of biodiversity conservation, yet relatively little is known about how communication, knowledge-sharing and participation are organised in conservation initiatives. This MSc research investigates these processes through a comparative qualitative study of biodiversity conservation initiatives in the Brazilian Cerrado and Laikipia County, Kenya. The study combines document analysis with semi-structured interviews and focus group discussions involving conservation practitioners, community organisations and local participants. Preliminary findings suggest that communication and knowledge-sharing are organised through different mechanisms across the two contexts. Brazilian initiatives emphasise communication adapted to local realities and the integration of local and scientific knowledge. In Kenya, preliminary interviews indicate that communication is commonly mediated through community governance structures and trusted representatives. Participants also describe scientific research as contributing to capacity-building, complementing local knowledge and strengthening communities' ability to participate in conservation and local decision-making. These findings provide empirical insights into how communication, participation and knowledge-sharing operate in biodiversity conservation initiatives.

Effective biocontrol emerges from stimulus-responsive spatial redistribution rather than antagonistic activity alone

Xiaoqing Zhang, Chujin Ruan, Dan Xiao, Xiang-Yi Li Richter, David R. Johnson

Abstract: Metabolites and Motility are both thought to govern bacterial biocontrol, yet their relative roles remain unclear. We show that biocontrol bacteria suppress oomycete growth by actively tracking hyphae. Surprisingly, metabolite-deficient mutants retain or even enhance efficacy through faster hyphal interception. Early response timing and spatial colonization determine suppression outcomes, revealing that motility-driven behaviour can override reduced antagonistic activity.

Simulation analysis of ibis conservation: Inbreeding and demography interact to influence recovery of bottlenecked populations

Jia Zheng, Ella Rees-Baylis, Thijs Janzen, Daiping Wang, Zhengwang Zhang, Xiangjiang Zhan, Xiang-Yi Li
Richter

Abstract: Biodiversity loss driven by climate change and human activities poses a critical global challenge. Population restoration and reintroduction programs are essential for mitigating this threat to endangered species, yet their outcomes often remain unpredictable due to poorly understood success factors, such as the inevitable inbreeding during bottleneck events. The conservation programme of the crested ibis (*Nipponia nippon*) marks a successful example where the population rose from just seven individuals to over 9000 in the past four decades. By developing an individual-based model that simulates the restoration process and incorporates species-specific demography and inbreeding data, we conclude that this successful restoration is largely deterministic, as our results closely mirror empirical recovery time and population level inbreeding coefficients. To establish general guidelines for reintroduction programs, we compare how inbreeding depression influences the recovery success of two reintroduction strategies involving small founder populations. Our simulations reveal that the ‘firework’ approach (one-source translocations) outperforms the ‘sequential’ (serial translocations) approach in restoration effectiveness. Furthermore, by expanding analyses over a broad demographic space, we demonstrate that the net effect of inbreeding varies with species-specific demography and highlight the importance of considering their interaction when interpreting conservation outcomes and designing future reintroduction programs.

The Effect of hybrid incompatibilities on a cline

Julio A. Ayala-López, Stephan Peischl, Claudia Bank

Abstract: Hybrid zones form where populations with diverged backgrounds come into secondary contact. Along an environmental gradient, a cline of allele frequencies can emerge, shaped by selection, dispersal, and recombination. Theory has shown that linkage disequilibrium, a product of selection on locally adapted alleles, can steepen clines, strengthening barriers to gene flow. Moreover, intrinsic —environment-independent— selection can interact with local adaptation dynamics in the cline, adding complexity to the population dynamics. For example, (Bateson-)Dobzhansky-Muller incompatibilities (BDMIs) can sharpen clines and strengthen reproductive barriers. Here, we investigate a model of evolution in continuous space in which two locally adapted loci interact epistatically via a BDMI. We characterise cline width and stability across different environmental geometries. We compare steep and gradual environmental transitions to examine how geometry modulates the interplay between local adaptation, DMIs, and recombination. We also examine how heterosis can alter cline shape, asking if hybrid advantage can counteract the barrier to gene flow imposed by BDMIs. Our analysis reveals that the long-term outcome depends critically on the relative strength of selection and recombination, where steep environmental change and strong BDMIs strengthen a reproductive barrier, whereas overdominance can facilitate gene flow if it is stronger than extrinsic selection.

How do consumer diversity and patch connectivity explain trophic regulation after heat waves?

Felix S. Rentschler, Gerard Martínez-De León, Jingjing Shi, Ludovico Formenti, Jan Tscheulin, Armelle Valat, Pilar Junier, Martin Holmstrup, Madhav P. Thakur

Abstract: Extreme heat events increasingly threaten ecosystem stability, leading to potential collapses. Therefore, communities need to resist and then recover from them, processes which can be facilitated by factors such as connectivity and diversity. This talk presents the findings from my master's thesis on the effects of connectivity and consumer (Collembola) diversity on the resistance and recovery of a soil community containing bacteria, fungi, and Collembolans. I will present two experiments. The first being a small feeding trial and the second being our main experiment where we use microcosms with different connectivity levels and levels of consumer diversity. We found that consumer diversity significantly increases the overall recovery of the community while differences in connectivity have no significant effect in both resistance and recovery. Our results demonstrate the importance of consumer diversity as a main driver of community recovery even within highly connected landscapes. These findings could be extrapolated to more complex communities making them interesting for conservation efforts.

Drought effects on parental care behaviour in poison frogs

Gilliane Borel, Lauriane Bégué, Eva Ringler

Abstract: Extreme weather such as droughts, fires, and floods, are becoming more frequent due to climate change, threatening species' survival and fitness. Animals have different possibilities to react to these challenges like moving, adapting, acclimating, or mortality, which can be achieved through behavioural plasticity. Because amphibians are very susceptible to changes in environmental conditions, they are excellent candidates to study behavioural shifts in response to drought events. Poison frogs are particularly interesting since they display different parental care behaviours, directly impacting the survival of their offspring. In our project, we aimed to investigate paternal care in *Allobates femoralis* during clutch development under drought conditions. We asked if fathers adjust their parental behaviour in response to drought, and if this leads to differences in offspring survival. We predict that males will try to compensate for the lack of water availability by increasing the care they provide to their clutch (e.g. hydration events, clutch visits). Additionally, we also examine possible effects of the drought on the clutch survival, and larval development. Our study will provide insight into how behavioural plasticity may help poison frogs to cope with future climate change.



Interactions asymmetrically influence fungal and bacterial stability under simulated climate extremes

Jingjing Shi, Pilar Junier, Madhav P. Thakur

Abstract: Soil fungi and bacteria drive nutrient cycling and plant productivity, yet their responses to climate extremes are rarely studied as interacting partners rather than in isolation. We paired a bacterium (*Pseudomonas putida* KT2440) with one of four *Trichoderma* species that differed in growth rate, then exposed these fungal-bacterial pairs to an extreme heat event followed by recovery under two soil moisture levels. We find that these interactions asymmetrically shape resistance and recovery: *Trichoderma* facilitated bacterial persistence through heat stress, while *P. putida* constrained fungal biomass recovery, regardless of soil moisture. Faster-growing *Trichoderma* species conferred stronger facilitation of bacterial resistance and recovery, and bacterial density showed a positive covariance with fungal biomass during heat stress, indicating net fungal facilitation of bacterial persistence. Together, these results show that fungal-bacterial interactions can simultaneously buffer and constrain microbial responses to climate extremes, with consequences for soil microbial stability as climate variability increases.

Is morphological evolution predictable? Insights from an evolutionary experiment in nature

Benjamin R. Sulser, Thomas Schiller, Sheila Christen, Lucas Eckert, Åsa Lind, Catherine Peichel

Abstract: Is it possible to predict evolution in nature? To test this question, we have established an experiment in nature where populations of threespine stickleback (*Gasterosteus aculeatus*) have been reintroduced to eight fishless lakes in the Alaskan Kenai peninsula; four lakes are benthic (with macroinvertebrate prey), and the other four are limnetic (with zooplanktonic prey). To test whether stickleback evolve predictable phenotypes associated with these niches, we have collected photographic data from each fish used for the introductions in 2019 and specimens collected over the subsequent seven years from these lakes. We have designed and applied machine-learning (ML) based pipelines to filter and landmark data of over 15,000 specimens accurately and efficiently. We present our findings based on data from the last six years of sampling on this project. In addition, we indicate the value of natural experimental studies for understanding whether the direction, tempo, and mode of evolution is predictable.

Effect of passive restoration on soil microbiome in mountain grasslands

Colin Guignet, Isabelle Arnold, Madhav Thakur and Jean-Yves Humbert

Abstract: Mountain grasslands are threatened by land-use intensification, yet the effects of passive restoration on soil bacterial communities remain poorly understood. Here we compared bacterial diversity and community composition across three management intensities (high-intensive, low-intensive, and extensive) in 32 meadows across 11 sites in Valais, Switzerland, using full-length 16S rRNA amplicon sequencing. After six years of extensification, plant species richness increased significantly, with forb and legume richness approximately 25% and 43% higher under extensive compared to intensive management, respectively. Soil nutrient availability declined, with available phosphorus and nitrogen decreasing by up to 54% and 12%, respectively. Despite these above-ground changes, bacterial alpha diversity and community composition did not differ significantly across management practices, with site identity explaining around 70% of community variation. Soil pH, moisture, and legume richness were identified as significant predictors of bacterial community structure. These results suggest that local environmental conditions are stronger drivers of soil bacterial communities than management intensity, and that six years of passive restoration may be insufficient to significantly restructure the soil microbiome.

Field-scale restoration experiments reveal drivers of dark diversity across trophic levels in grasslands

Qingqing Chen, Laura Forgone, Raphaël Arlettaz and Jean-Yves Humbert

Abstract: Grassland restoration is widely used to reverse plant diversity loss in agricultural landscapes, but its effects on higher trophic levels remain poorly understood. We established a field-scale restoration experiment across twelve Swiss lowland grasslands, manipulating seed addition (hay transfer, directly harvested seeds, or multiplied seed mixtures) and soil disturbance (shallow or deep tillage). Five to seven years after restoration, we quantified species richness change (lost, persisting, and gained species) and dark diversity in plants, Auchenorrhyncha, and Orthoptera. Species persistence was high across taxa, but invertebrates showed greater turnover than plants, with more species losses and gains from surroundings and fewer species originating from donor. Restoration treatments strongly influenced plant community assembly but had weaker effects on invertebrates. Initial species richness in receiver and donor meadows was a key predictor of restoration outcomes. Across taxa, 41–46% of absent donor species belonged to the dark diversity pool. Restoration treatments affected dark diversity differently across taxa, highlighting contrasting assembly processes and restoration limitations.

The impact of metamorphosis and size on the aquatic feeding kinematics of the Iberian ribbed newt (*Pleurodeles waltl* Michahelles, 1830)

Isabelle Toussaint-Lardé, Merlin Hugon-Daune-Fäs, Anthony Herrel, Anne-Claire Fabre

Abstract: Metamorphosis involves abrupt morphological changes separating larval and adult stages. The adaptive decoupling hypothesis proposes that metamorphosis breaks the correlations among the phenotypes expressed at the different life stages, enabling their independent evolution. This should be reflected in differences in functional performance linked to the body parts remodelled during metamorphosis. Moreover, changes in body size throughout ontogeny, can also influence functional performance. We investigated the influence of metamorphosis and size on suction feeding kinematics in larvae and metamorphs of *Pleurodeles waltl* analysing high-speed videos. Most duration variables increased with size in larvae, while decreasing with size in metamorphs. This may reflect greater cranial ossification after metamorphosis, enabling more direct muscle force transmission and consequently, faster movements relative to size. Finally, larvae may enhance suction and prey retention through labial lobes and gill slits, whereas metamorphs may compensate the loss of these larval structures through faster movements enabled by cranial ossification.

Mating system, sexual selection, and the evolution of sex differences in ageing

Ella Rees-Baylis, Charlotte de Vries, Xiang-Yi Li Richter

Abstract: Sex differences in ageing and lifespan are often associated with mating system: females typically outlive males in polygynous species, whereas differences are weaker under monogamy and may even favour longer male lifespans. However, mating system is a multifaceted concept that covaries with other life-history traits, making causal explanations difficult to infer from comparative data alone. Sexual selection is thought to be a key driver, yet includes diverse processes with potentially contrasting effects on ageing and survival. Here we develop an evolutionary individual-based model to examine how alternative mating system assumptions and consequences of sexual selection shape the evolution of sex differences in ageing and longevity. The model incorporates reproductive competition, mating costs, and trade-offs between reproductive effort and somatic maintenance. We use this framework to identify conditions under which mating system generates, weakens, or reverses sex biases in lifespan, helping to clarify the processes underlying observed empirical associations.



Automated machine learning to identify drivers of microbial community composition

Ianis Vilela, Adamantia Kapopoulou, Claudia Bank, Stephan Peischl

Abstract: Microbial communities play critical roles across diverse biological systems, yet identifying the environmental factors that shape their composition remains challenging. Advances in sequencing technologies have increased data availability, intensifying the need for analytical approaches capable of handling high-dimensional, compositional microbiome data. While there is strong interest in uncovering multi-factor environmental drivers, conventional methods such as PERMANOVA, redundancy analysis (RDA) often fail to capture threshold-like patterns and complex interactions common in ecological systems. We propose an automated, machine learning based framework to identify environmental drivers of microbial community structure in a user-friendly and generalizable manner. By relaxing model assumptions, this approach enables detection of complex, non-linear relationships between environmental variables and community composition. Simulation studies using synthetic microbial communities demonstrate that the proposed machine learning framework outperforms traditional methods in models with cluster-like threshold influence patterns and complex interactions between environmental variables and community composition. These results highlight the potential of the proposed machine learning framework. An R package currently in development shall facilitate its application to complex datasets.

Mechanisms of species coexistence in a hyperdiverse and incredibly young adaptive radiation

Anna Mahulu, Alexis Roberts-Hughes, Pooja Singh, Clement Mlay, Ole Seehausen

Abstracts: Hyperdiverse species communities challenge ecological theory, particularly when hundreds of endemic species coexist in a closed ecosystem despite evolving from a common ancestor only a few thousand years ago. This scenario characterizes the cichlid fish communities of East Africa's Lake Victoria. Using standardized surveys conducted between 1993 and 2025 across multiple islands and two distinct macrohabitats, we investigate the ecological and spatial dynamics that maintain this extraordinary diversity. We combine analyses of community structure, trophic ecology, depth-related turnover, geographical turnover, and temporal dynamics. Within a given macrohabitat, species richness varies along environmental gradients, with substantial turnover across both reef (more dispersal-limited) and open-water habitats (weakly dispersal-limited). Surprisingly, turnover is only weakly related to geographical distance, indicating that dispersal limitation alone cannot explain community structure. Instead, communities are shaped by ecological differentiation, resource heterogeneity, and metacommunity dynamics involving local colonization and extinction. These findings provide new insights into how hyperdiverse communities evolve, assemble, and persist.

Mechanisms of parental care

Diogo F. Antunes, Eva Ringler

Abstract: Parental care has evolved independently multiple times across vertebrates and it's thought to have facilitated the transition from aquatic to terrestrial reproduction. Despite its evolutionary relevance, the neuronal mechanisms underlying parental investment remain poorly understood. Due to the energetic costs associated with caregiving, animals must evaluate social and environmental cues to decide whether to care or to abandon offspring. Past research focused on the ecological drivers regulating parental care decisions, assuming that due to the phenotypic gambit selection optimizes behaviour, and thus overlooked proximate mechanisms. However, this preconception undermines the role of environmental context in shaping behavioural responses. Thus, to comprehend how environmental context influences parental decisions, we must identify how context is perceived in the brain and builds behavioural responses. In my talk I will focus on the poison frog *Allobates femoralis*, a species with obligatory paternal care, where males decide to either care or to cannibalize clutches present in their territory. By comparing neuronal activation patterns between caregiving and cannibalistic males, I will show that these distinct behavioural states are regulated by distinct brain regions. These results suggest existence of regulatory networks which are based on the behaviour's function, highlighting the importance of function over generalist neurobehavioural models.

Lakes as islands: a fresh(water) perspective on island biology

Luiz Jardim de Queiroz, Sarah Zimmermann, Tim Alexander, Daniela Achleitner, Martin Luger, Hubert Gassner, Carmela Doenz, Soraya Villalba, Lukas Rüber, Rampal Etienne, Luis Valente, Ole Seehausen

Abstract: Island biology traditionally focuses on oceanic archipelagos, leaving „inverted islands“ largely unexplored. Using a natural experiment of 79 postglacial peri-Alpine lakes (<15,000 years), we examined island-biology patterns at regional (γ -diversity) and between-lake (β -diversity) scales. Regionally, the lacustrine Island Species-Area Relationship (ISAR) assembled rapidly, contrasting with the millions of years required by oceanic islands. Instead of a traditional power law, the ISAR follows an asymptotic rational function, likely due to a limited regional species pool. At the between-lake scale, β -diversity patterns are shaped by dispersal limitation and environmental filtering, governed mostly by geographical distance, elevation, and depth dissimilarity among lakes. Mechanistically, a 20-meter depth threshold acts as a key filter: shallow zones promote community overlap among lakes, while deep, cold waters isolate specialists, unlocking opportunities for adaptive radiations. Thus, peri-Alpine lake dynamics mirror classic island biodiversity assembly but are compressed in time and dictated by three-dimensional environmental complexity.

The role of chromosomal inversions in phenotypic divergence

Lynn Wedekind, Juliana Rodriguez-Fuentes, Nicole Nesvadba, Verena Saladin, Marius Rösti, Catherine Peichel

Abstract: Chromosomal inversions suppress recombination and allow co-adapted alleles to be inherited together, making them an important mechanism for maintaining adaptive variation in the face of gene flow. While inversions have been associated with genomic divergence between populations across many systems, the phenotypic consequences and the selective forces driving their spread and maintenance remain poorly understood. Using the threespine stickleback as a system, we investigated the direct phenotypic consequences of a chromosomal inversion that consistently differs between marine and freshwater populations worldwide. Using controlled F2 laboratory crosses from a stream population of the Lake Constance basin, inversion genotype was associated with variation in sensory and external morphological traits. These associations were compared across three datasets differing in population background and experimental design, allowing robust inversion effects to be disentangled from population-specific or environmentally driven variation, pointing to selective forces that may maintain this inversion in nature.

A semi-automated method to study family size and age structure of the Eurasian Beaver *Castor fiber*

Nicolas Stettler, Raphaël Arlettaz, Stefano Canessa

Abstract: After being nearly driven to extinction in the early 19th century, the Eurasian beaver (*Castor fiber* Linnaeus, 1758) has flourished since its reintroduction across Central Europe beginning in 1922. Much of our knowledge of the species was therefore gained during marked population growth well below carrying capacity. As populations now approach capacity, we ask how the beaver's life history and ecology change. Here we focus on family size and age structure at high territory densities. Using three camera traps per territory, we identified and aged beavers by tail traits, developing machine-learning methods to reduce the considerable manual work this requires. Across 30 territories in Switzerland's densest beaver area, we found an average of 6.6 individuals per territory—larger than expected—with up to 16 in some, strong intercolony overlap, a high adult ratio, and floaters visiting up to five territories. These factors, linked to density dependence, may benefit population stability at carrying capacity.

VOLZ PRIZE NOMINEES

Isabelle Arnold
(Session 1)



Title of the paper:
Relaxation of management intensity promotes butterfly communities in mountain grasslands

[Link to the paper](#)

Abstract

Semi-natural mountain grasslands are currently threatened by either land abandonment or management intensification, which calls for evidence-based recommendations for sustainable and biodiversity-friendly farming of these valuable biodiversity hotspots in the long run. We investigated the effects of the relaxation of the management intensity on their plant and butterfly communities, via an experimental reduction of fertiliser inputs. In 2019, 13 study sites were selected in the SW Swiss Alps, each including three meadows that had been intensively managed for at least the previous 20 years. Adopting a randomised block design, two out of three meadows per study site were restored by shifting their mode of exploitation towards low-intensity (1/3 of the fertiliser dose applied beforehand) or extensive management (cessation of fertilisation), respectively, while the third continued to be managed intensively, serving as control. After four years (2023), plant species richness had increased by 9.3 % in extensively managed meadows compared to baseline. Yet, butterfly abundance was more than twice greater (112 %) and species richness 81 % higher in extensively managed meadows compared to controls. A higher butterfly abundance and species richness following management relaxation was mostly driven by a decrease in vegetation density and an increase in forb cover. Extensively managed meadows also exhibited higher conservation values, harbouring comparatively more threatened butterfly species, whilst no change was observed in low-intensity meadows. Altogether these results indicate that the butterfly communities of mountain hay meadow respond rapidly and massively to a relaxation of management intensity.

Bruno Camargo dos Santos
(Session 2)



Title of the paper:
Sibling number and early interactions shape social competence for life

[Link to the paper](#)

Abstract

The social environment experienced during development plays a crucial role in shaping social competence—the ability to respond appropriately to social challenges. Sibling number and the social interactions between them are key components of the early lives in many animals. While these components are well known to influence social development in humans, their role in nonhuman animals remains unclear. Here, we show that both the number of siblings and opportunities for social interaction are essential for developing social competence in the highly social cichlid *Neolamprologus pulcher*. Fish reared in large broods (LB) displayed more affiliative and fewer aggressive or submissive behaviors during early life compared to those reared in small broods (SB) or in large broods with restricted opportunities for interactions (4 × 8). Later in life, LB fish were more socially competent. Thus, social competence arises not from the number of individuals or interactions alone, but from the combination of both.

Laura Forgione
(Session 3)



Title of the paper:
Restoring plant diversity in lowland grasslands: Efficacy of different seed addition and soil preparation methods

[Link to the paper](#)

Abstract

The biodiversity of semi-natural grasslands has dramatically declined over the past century. We experimentally tested, at field scale, the efficacy of different assisted (active) restoration methods to enhance plant biodiversity in species-poor, extensively managed lowland meadows. Four restoration treatments, plus one control were randomly allocated to five meadows at 12 spatially-replicated study sites in the Swiss lowlands in 2019: 1) hay transfer from a species-rich donor meadow on a harrowed meadow; 2) the same as 1 but on a ploughed meadow; 3) sowing a directly harvested native seed mixture originating from a species-rich donor meadow on a ploughed meadow; 4) sowing a multiplied native seed mixture on a ploughed meadow; 5) control, i.e. with no soil disturbance and no reseeding. Vegetation surveys were performed before (2018) and after the restoration actions (2021 and 2023). After a pronounced biodiversity rise in 2021, plant species richness had stabilized by 2023 across most treatments with, on average, 29% more species compared to 2018 and 16% more species in restored compared to control meadows in 2023. Moreover, 90% of the restored meadows qualified for the result-based payment scheme in 2023. Harrowing before seeding was as effective as ploughing. While the multiplied seed mixture initially showed a stronger increase, this effect had decreased by 2023, reaching levels comparable to the other treatments. Beta diversity was higher in hay transfer treatments than in the control and other restoration treatments, indicating greater heterogeneity in community composition. Findings provide evidence-based guidance for cost-effective and practically feasible grassland restoration.

Loraine Hablützel
(Session 4)



Title of the paper:
Studying the genetic basis of ecological interactions with intergenomic epistasis

[Link to the paper](#)

Abstract

In a community, the phenotype or fitness of genotypes of a focal species can depend on the genotypes of other species. Such between-species genetic interactions are increasingly referred to as intergenomic epistasis, analogous to the classical definition of (intragenomic) epistasis in genetics. Here, we propose the first mathematical definition of intergenomic epistasis, which formalises the minimal conditions for the existence of inter-species genetic interactions. By discussing empirical studies of interacting species from the literature, we argue that intergenomic epistasis is a useful umbrella concept that engulfs multiple co-evolutionary relationships of interacting species, such as genotype-specific or gene-for-gene interactions. Consequently, intergenomic epistasis can be asserted in a study system when 1) the specific ecological interactions are unknown, 2) the genetic basis of between-species interactions is unidentified, or 3) the underlying genetic architecture is complex and involves genetic interactions within and between genomes. Moreover, the term itself highlights the importance of genetic factors in the study of ecological interactions, thus encouraging links between research in genetics and ecology. Finally, we argue how models incorporating intergenomic epistasis may facilitate the study of co-evolution.

Hiranya Sudasinghe
(Session 5)



Title of the paper:

Convergent genome streamlining accompanies independent miniaturization in the world's smallest fishes

[Link to the paper](#)

Abstract

Miniaturization, the reduction of adult body size to an extreme degree, has evolved repeatedly across vertebrates. Yet its genomic underpinnings remain poorly understood. Cypriniformes, the most species-rich order of freshwater fishes, contains multiple miniaturized lineages that have evolved contrasting developmental processes. Proportioned dwarfs are tiny-bodied but otherwise morphologically similar to larger relatives, while progenetic miniatures exhibit developmental truncation thus retaining larval-like anatomical features into adulthood. Using a new time-calibrated phylogeny of 309 cypriniform species and comparative genomic analyses of 33 high-quality genome assemblies, we investigated the evolutionary history and genomic correlates of miniaturization across this order. Ancestral state reconstruction revealed multiple independent origins of both miniature types, with reversals to the non-miniature state rarely recovered and miniature origins non-randomly distributed across the phylogeny. The origins of the two types of miniatures differed in their timing. Progenetic miniatures arose predominantly in the Eocene whereas proportioned dwarfs arose mainly within the Miocene period. Genome size variation across Cypriniformes has been overwhelmingly driven by polyploidy. However, progenetic miniatures but not proportioned dwarfs showed a directionally consistent, though non-significant, trend toward genome size reduction. Comparative genomic analyses revealed that all three independently-evolved progenetic miniature lineages share convergent signatures of repeat loss alongside genome-wide intron shortening, patterns absent in proportioned dwarfs. Our study provides the broadest evidence to date that progenetic miniaturization, despite independent origins, is underpinned by predictable structural genomic changes, revealing a fundamental link between developmental truncation and genome architecture in vertebrates.

Marion Zohra
Noëmi Talbi
(Session 6)



Title of the Paper:

Rapid evolution of recombination landscapes during the divergence of cichlid ecotypes in Lake Masoko

[Link to the paper](#)

Abstract

Variation of recombination rate along the genome is of crucial importance to rapid adaptation and organismal diversification. Many unknowns remain regarding how and why recombination landscapes evolve in nature. Here, we reconstruct recombination maps based on linkage disequilibrium and use subsampling and simulations to derive a new measure of recombination landscape evolution: the Population Recombination Divergence Index (PRDI). Using PRDI, we show that fine-scale recombination landscapes differ substantially between two cichlid fish ecotypes of *Astatotilapia calliptera* that diverged only ~2,500 generations ago. Perhaps surprisingly, recombination landscape differences are not driven by divergence in terms of allele frequency (F_{ST}) and nucleotide diversity ($\Delta(\pi)$): although there is some association, we observe positive PRDI in regions where F_{ST} and $\Delta(\pi)$ are zero. We found a stronger association between the evolution of recombination and 47 large haplotype blocks that are polymorphic in Lake Masoko, cover 21% of the genome, and appear to include multiple inversions. Among haplotype blocks, there is a strong and clear association between the degree of recombination divergence and differences between ecotypes in heterozygosity, consistent with recombination suppression in heterozygotes. Overall, our work provides a holistic view of changes in population recombination landscapes during the early stages of speciation with gene flow.

POSTERS

Chunyan Lu & Maddy Thakur (TERR)

Resistance-recovery relationships under climate extremes

Abstract: Ecological resistance (the immediate response once an extreme event ends) and recovery (the response some time afterwards) jointly determine the long-term stability of ecological systems under climate extremes. The relationship between them further indicates whether a system accumulates ecological debt: recovery that remains incomplete despite extended time since the event. In a global meta-analysis spanning >5,000 effect sizes, we show that such debts are widespread in plants and microorganisms, and most pronounced under heat extremes.

Dhanya Bharath (THEE)

From Hunters to Hunted: Predator-prey role reversal catalyses fishing-driven regime shifts

Abstract: Catastrophic population collapses of top predators often trigger trophic cascades leading to mesopredator release and predator-prey role reversal. Using a physiologically-structured food-web model, we show that mesopredator predation on juvenile top predators can drive regime shifts under fishing pressure, highlighting the crucial role of ontogenetic processes in ecological resilience.

Emma Ochnser (THEE & CB)

Modelling different management strategies for an extinct-in-the-wild species – the sihek (*Todiramphus cinnamominus*)

Abstract: Extinct-in-the-wild species carry an elevated extinction risk due to reduced genetic diversity in small founding populations. Using SLiM simulations, the sihek's (Guam kingfisher) future population dynamics and heterozygosity were modeled under three mating strategies: random, highest-relatedness, and lowest-relatedness. Random mating best preserved heterozygosity, suggesting reintroductions should prioritize maximizing genetic diversity over minimizing relatedness.

Franziska A. Brenninger (ELVIA)

Transmission mode impacts the spread of a parasite in a spatially structured host population

Abstract: How parasites transmit from one host to the next is an essential part of host-parasite dynamics. Although transmission modes are known to shape infection dynamics within single populations, their effects across spatially structured environments remain poorly understood. We explore how spatial structure changes the impact of different parasite transmission strategies.

Gustavo Akira Tomam (EVOL)

From Karyotype to Genome: A Chromosome-Scale View of Sex Chromosome Evolution in the Neotropical Fish *Hoplias malabaricus* (Teleostei; Characiformes)

Abstract: *Hoplias malabaricus* species complex exhibits remarkable sex chromosome diversity across seven karyomorphs. We present a chromosome-scale genome assembly of karyomorph D, harboring a multiple X₁X₂Y sex chromosomes. Using this resource, we characterized sexual strata, Y degeneration, and sex-linked genes, providing genomic insights into multiple sex chromosome evolution in Neotropical fishes.

Hang Zhao (TERR)

Recurring extreme droughts promote acquisitive plant strategies and simplify grassland communities under warming

Abstract: In a 4-year mesocosm experiment, we tested how recurring extreme drought affect plant community strategy under different warming regimes in grasslands. From the third year, repeated drought reduced biomass and shifted leaf traits toward acquisitiveness, even though slow-growing species dominated community. Species richness declined in the third year, with the strongest decrease under heatwaves. These results demonstrate that compound and recurring climatic extremes can simplify grassland communities by eroding species richness and altering community functional composition

Iris Bontekoe (CB)

Obstacle avoidance in large soaring birds during good versus poor visibility

Abstract: To investigate whether raptors avoid obstacles during poor visibility, we use high-resolution GPS data from bearded vultures and golden eagles, combined with weather and obstacle data. Analyses reveal species-specific differences in flight distance to obstacles under good versus poor visibility. Results provide insights into the behavioural responses of raptors to human-made obstacles under suboptimal visibility.

Jennifer Nunes Pompeo (EVOL)

Satellite DNA highlights karyotype diversity and sex chromosome differentiation in a frog species complex

Abstract: The Edentulus clade of *Engystomops* comprises *E. pustulosus* and the Amazonian *E. freibergi*–*E. petersi* species complex, which exhibits high karyotype diversity. Here, we mapped satDNAs by FISH in all species and found conserved satDNA sequences with variable accumulation patterns, while sex chromosomes showed distinct compositions in the Amazonian complex.

Joey Felsch (BEHAV)

Acoustic self-recognition in a Neotropical poison frog?

Abstract: Reaction time of the territorial response during playback experiments using foreign and own calls was measured in 63 *Allobates femoralis* males in French Guiana. If males have acoustic self-recognition, we expected that territorial males would respond less aggressively to their own call than to a foreign call.

Matilda Angeloni (CB & PopGen)

Population genetic structure and connectivity of stoats in Switzerland using genome-wide sequencing

Abstract: The stoat is an elusive small mustelid with a poorly understood population ecology. Using genome-wide SNP data from over 50 tissue samples across Switzerland, this study assesses population structure, isolation by distance, and demographic history. This research aims to improve our understanding of the species' status and population trends, thereby supporting conservation management in human-dominated landscapes.

Mia Steinke (TERR)

Plant phenology and reproduction under climate extremes

Abstract; In an outdoor mesocosm experiment, we measured flowering phenology and reproductive traits across nine plant species exposed to climate extremes. Warming and drought shifted flowering phenology in opposite directions in several species, whereas drought dominated the response of seed traits. Phenological and reproductive responses to climate extremes are likely decoupled, with consequences for reproductive output under compound warming–drought events.

Rüya Arslan (THEE)

Journey to the peak: which fitness landscape metric predicts evolutionary success better?

Abstract: Fitness landscapes map the genotypes to their fitness. The basins of attraction of fitness peaks are metrics for predicting evolutionary outcomes. This study compares three basin size measures (absolute, overlap-adjusted and gradient) against reachability in theoretical and empirical fitness data. Gradient basin measure predicts the reachability the best compared to other basin measures.

Simon Rérat (BEHAV)

Mechanisms of cross-modal recognition with unfamiliar individuals in the princess of Zambia

Abstract: In a cross-modal recognition experiment setup, the highly social fish *Neolamprologus pulcher* is able to detect incongruence of visual and olfactory cues. The extent of this ability remains unknown. Here, we test its ability to detect incongruence of sensory cues provided by a single unfamiliar individual in different social statuses.

Xiaoqing Zhang (ELVIA)

Effective biocontrol emerges from stimulus-responsive spatial redistribution rather than antagonistic activity alone

Abstract: Metabolites and Motility are both thought to govern bacterial biocontrol, yet their relative roles remain unclear. We show that biocontrol bacteria suppress oomycete growth by actively tracking hyphae. Surprisingly, metabolite-deficient mutants retain or even enhance efficacy through faster hyphal interception. Early response timing and spatial colonization determine suppression outcomes, revealing that motility-driven behaviour can override reduced antagonistic activity.

