Abstract booklet

biology17, 2-3 February 2017, University of Bern

The abstracts of the contributed talks, flash talks and posters are arranged alphabetically according to the last name of the submitting author.

We wish everybody a successful and enjoyable conference!

The organizing committee

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Feeding the world without costing the earth

Keynote lecture on Friday, 3 February, at 9.00h

Andrew Balmford, University of Cambridge, UK

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Andrew Balmford is a dedicated restoration and conservation biologist. His research focuses on the costs and benefits of conservation, how best to reconcile biodiversity conservation and farming, the reasons why nature is being lost, and examining what works in conservation. He tackles these issues through fieldwork, analyses of large databases, and modeling, and by working wherever possible with colleagues in other disciplines and with conservation practitioners. He co-founded the Cambridge Conservation Forum and he is closely involved in the Cambridge Conservation Initiative.

Island time and the interplay between ecology & evolution in species diversification

Keynote lecture on Friday, 3 February, at 14.15h

Rosemary G. Gillespie, University Of California Berkeley, USA

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Research on the dynamics of biodiversity has progressed tremendously over recent years, though in two separate directions – ecological, to determine change over space at a given time, and evolutionary, to understand change over time. Integration of these approaches has remained elusive. Archipelagoes with a known geological chronology provide an opportunity to study ecological interactions over evolutionary time. In this presentation I will focus on the Hawaiian archipelago and summarize the development of ecological, and evolutionary research; I emphasize spiders because they have attributes allowing analysis of ecological affinities in concert with diversification. Within this framework, I highlight recent insights from the island chronosequence, in particular the importance of (1) fusion and fission in fostering diversification; (2) variability upon which selection can act; and (3) selection and genetic drift in generating diversity. Insights into biodiversity dynamics at the nexus of ecology and evolution are now achievable by integrating new tools, in particular ecological metrics (interaction networks, species abundance distributions) across the chronosequence to uncover community dynamics; and genomic tools to understand contemporaneous microevolutionary change. This work promises key insights into biodiversity dynamics by showing not only how diversity has been shaped in the past, but also how it will be expected to accommodate change in the future.

The structure and origins of austral plant diversity: insights from the danthonioid grasses

Keynote lecture on Thursday, 2 February, at 14.15h

H.P. Linder, Department of Systematic and Evolutionary Botany, University of Zurich

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Linneaus saw himself as the man who organized and described what God had created. Evolutionary systematists have a much more difficult task: to organize and describe what an apparently random process, evolution, generated, and then also to look for repetitive patterns in this process. We do this by setting up hypotheses, testing them, finally assembling those hypotheses that survived into a scenario. I illustrate this interaction using the globally distributed, austro-temperate grass subfamily Danthonioideae. I use a molecular, rate corrected, dated phylogenetic hypothesis to reject vicariance as a possible explanation. I explore the correlates of long distance dispersal, testing whether the West Wind Drift, ocean width, and / intrinsic attributes correlate with dispersal distance. I also explore whether species diversity on each continent is the result of time or available habitats (diversity-dependent diversification). Finally, I explore the possible effects of late-Neogene global climatic change. These process-hypotheses can then be readily linked to the extant diversity in the subfamily, suggesting processes that might have operated for many other austral clades.

Genetic and molecular basis of phenotypic diversity in sticklebacks

Keynote lecture on Thursday, 2 February, at 9.00h

Catherine Peichel, University of Bern, Switzerland
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Catherine Peichel is a geneticist with interests in the genetic and genomic changes that underlie phenotypic evolution, including adaptation, sex chromosome evolution, behaviour and speciation. Her primary model is the threespine stickleback (*Gasterosteus aculeatus*), which displays astonishing natural variation in courtship, parental care, social aggregation, aggression, predator avoidance and spatial learning. Her current work focuses on identifying the genetic and neural mechanisms that underlie the evolution of such behaviors.

The evolution of conflict and cooperation: from insects to human societies and beyond

Darwin Talk on Thursday, 2 February, at 21.00h

Tom Wenseleers, University Leuven, Belgium
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Tom Wenseleers combines theory with empirical research to study the fundamental factors that drive cooperative social behaviour and other complex traits in nature. His research involves (epi)genetic and genomic approaches, as well as advanced chemical communication analysis in a diversity of organisms, including social insects (ants, bees and wasps), microorganisms and humans to better understand the so-called “major transitions in evolution”. He also tackles more applied questions related to honeybee diseases, swarm intelligence, and evolutionary robotics.

Maternal mRNA is able to transmit temperature information across generations in wild fish

Oral presentation

Adrian-Kalchhauser Irene, Walser Jean-Claude, Michaela Schwaiger and Burkhardt-Holm Patricia, University of Basel

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In response to recent changes in environmental conditions, an immediate feedback from parental generation to the offspring that promotes pre-adaptation or priming represents the most promising approach towards fast adaptation and towards optimizing an organism's or a population's fitness. One molecular mechanism that has been proposed to impart life time experiences in a non-genetic yet heritable format on the next generation is parental RNA contribution. In particular, maternally provided mRNAs are a key instrument in many species to govern early and late steps of the offspring development. Our overall objective with this study was to determine whether maternally provided RNA stores have the potential to promote transgenerational inheritance phenomena in wild vertebrate populations. Our results obtained from early cleavage embryos of a wild fish species show that maternal RNA stores indeed reflect the temperature experienced by the mother prior to egglaying. This indicates that maternal RNA may have to be considered a candidate pathway for transgenerational inheritance and fast adaptation phenomena. Our results also substantiate the idea that wild vertebrate populations may rely on non-genetic mechanisms to increase their fitness in the short term much more than we appreciate today.

Fishes match primates in their ability to delay gratification

Oral presentation

Aellen Mélisande and Bshary Redouan, University of Neuchâtel

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Humans are outstanding in their ability to achieve mutual cooperation for direct benefits. One of the proposed reasons is that humans have higher cognitive abilities than other species, enabling us to forsake immediate benefits in favour of delayed gratification. The established experimental paradigm for primates and birds is to give subjects access to a small food reward, which can be exchanged for a larger one or for something better after some waiting time. Here we tested 2 cleaner and 2 non-cleaner wrasses on this paradigm. We considered the cleaner species interesting because of their specific ecology. Cleaner wrasses remove ectoparasites from visiting 'client' reef fish but prefer to eat client mucus. Eating against preference yields delayed gratification due to the client staying longer and returning for its next inspection, thereby yielding higher total amounts of food. As predicted by an ecological approach to cognition, cleaners performed very well in the quantitative task, i.e. like a typical primate. Also, they performed poorly if the delayed reward was of higher quality. Surprisingly, non-cleaner wrasse performed also well in the quantitative task, despite no evidence that they need such ability in nature. In conclusion, delaying gratification is apparently not tightly linked to general cognitive abilities and/or feeding ecology.

Fluvial network structure shapes amphipod communities of Switzerland

Oral presentation

Alther Roman and Altermatt Florian, Eawag & UZH

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Biodiversity patterns and biological communities are strongly influenced by habitat connectivity. The structure of such spatial networks may shape both dispersal of native species but also invasions of non-native species, and can result in characteristic diversity patterns. Fluvial networks offer unique possibilities to study such processes in a spatially explicit manner. Worldwide, rivers are strongly affected by non-native species that often have detrimental effects on natural communities. However, empirical datasets to study spatial dynamics of non-native species are often lacking. We built an extensive database on native and non-native amphipod occurrences in Switzerland, covering over 1,700 sites and 46 species with the underlying dendritic network. We then studied the spatial imprint of the network structure on the community composition of native and non-native amphipod species across river basins. Our analyses revealed distinct patterns of local species richness in the network and specific differences in distribution of native and non-native species. Specifically, non-native species are still mostly restricted to larger and more connected streams whereas small and more isolated headwaters present refugium habitats for native species. Our results improve the understanding of the influence of spatial connectivity on biodiversity and invasion processes in natural systems.

Transmission ratio distortion at a supergene controlling ant social organization

Oral presentation

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Supergenes are clusters of linked genes that control complex adaptive phenotypes, such as Batesian mimicry of *Heliconius* butterflies or color polymorphism and mating strategies in ruffs. Many supergenes have unusual transmission ratio. In the Alpine silver ant Formica selysi, colony social organization is controlled by a large supergene with two haplotypes, Sm and Sp. Ants from single-queen colonies only harbor the Sm haplotype, while ants produced by multiple-queen colonies have at least one Sp haplotype. Here, we examine how the two haplotypes of the supergene are transmitted. We found transmission ratio distortion in the progeny of heterozygous queens. Specifically, the Sp haplotype favors its own transmission over the one of the alternative haplotype, by causing post-segregational developmental arrest of brood that did not inherit Sp. These results contribute to our understanding of the genetic system underlying complex phenotypes.

Song type and syllable repertoire sizes correlate with the annual reproductive success and the extra-pair mating success of song sparrow males (*Melospiza melodia*)

Oral presentation

Andrés Martina L., University of Zurich, Bousquet Christophe A. H., Reid Jane M., Losdat Sylvain, Krippel Jessica, Keller Lukas F., Postma Erik, Nietlisbach Pirmin

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In song bird species, song complexity is an ornamental trait that is thought to be under sexual selection in males via female mate choice. High song complexity may thus increase the reproductive success of males by conveying direct or indirect benefits to females. However, few studies have tested this hypothesis in wild populations. In this study, we investigate the relationship between song complexity and reproductive success in a wild song sparrow (*Melospiza melodia*) population on Mandarte Island, Canada. We used four approaches to measure song complexity: song type and syllable repertoire size, within-male song type diversity, and a network analysis approach that measures so-called small-worldness. Additionally, up to 160 microsatellite markers were used to detect extra-pair reproduction. We found that the song type and the syllable repertoire sizes predict a male's annual reproductive success. Furthermore, males with the largest song type repertoire size among all neighbours of a certain territory were more likely to sire the extra-pair offspring. However, we did not identify any relationship between the diversity index and small-worldness and reproductive success. We concluded that females may gain valuable information about the genetic quality of males based on song type and syllable repertoire sizes and, therefore, these song features are likely under sexual selection.

Geneflow within and among species of *Plecotus* bats in the Alpine range

Poster / FlashTalk

Andriollo Tommy, Natural History Museum of Geneva , Marzia Mattei-Roesli, Centro Protezione Chirotteri Ticino, Raphaël Arlettaz, University of Bern , Manuel Ruedi, Natural History Museum of Geneva

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European species of long-eared bats (genus *Plecotus*) have similar morphologies, karyotypes and echolocation calls, but molecular studies revealed the existence of several cryptic lineages, rendering reliable species identification in the field even more problematic. The presence of morphologically intermediate individuals observed in the Alps poses further challenges to species recognition, and raises the possibility of interspecific hybridization. To address this important question, we used biopsy samples of over 400 individuals living in areas of sympatry and analysed them with both mitochondrial and nuclear DNA markers (23 microsatellite loci). This combination of genetic markers allowed us (1) to estimate rates of current interspecific gene flow, (2) to detect possible events of historical introgression and (3) to test the usefulness of various morphological characters to recognise species. The hypervariable nuclear markers also provided new insights into the genetic diversity and population structure of these bats across the potential barrier represented by the Alpine range.

Decreases in the lowlands, increases at higher elevation – rapid changes in altitudinal distribution of breeding birds

Oral presentation

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Altitudinal gradients represent an attractive system to study the consequences of environmental changes. In a European context, the Alps represent a key region to study these effects; they form an island in the middle of the continent and might serve as a refuge for species that suffer a loss of suitable habitat in lower regions due to climate and other environmental changes. Here, we compare the altitudinal distribution during the breeding season for the entire avian community between the periods 1993-96 and 2013-16. We use the highly standardized territory mapping data of the last two Swiss breeding bird atlases, where over 3% of the territory has been censed. We found a strong relationship between population evolution and altitude. Not just renowned cold-adapted habitat specialists such as the rock ptarmigan, but even common breeding birds show a clear increase in the population`s mean breeding altitude. Besides increases at the higher range margin we found clear decreases at the lower range margin, even for some typical and abundant lowland species. This study reveals striking changes in bird abundance related to climate and environmental change in unprecedented detail. It stresses the key role of the Alpine region that is of major conservation value not only for alpine habitat specialists but for a wide range of subalpine and even lowland species in Europe.

Early social and predator experience affect reproductive performance in a cooperatively breeding fish

Poster

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Developmental plasticity has pervasive effects on phenotypic traits and helps individuals to adapt to changeable conditions. However, in long-lived species plastic early-life effects often vanish already during the juvenile stage. We investigated if early-life experiences can affect the reproductive performance of adults in a long-lived vertebrate, the cooperatively breeding cichlid *Neolamprologus pulcher*. *N. pulcher* live in family groups consisting of a dominant breeder pair and subordinate alloparental brood care helpers. In our experiment we used *N. pulcher*, which had been reared in a 2x2 full factorial design experiencing one of two types of family structure [with guarding parents and siblings (+F) vs. with siblings only (-F)] and one of two predation risk levels [with (+P) or without (-P) predator] for their first two months of life. At an age of 3.5 years, we created 10 pairs from each of the four rearing treatments and monitored their reproductive performance over 4 months. Social and predator experience interactively influenced reproductive performance: Fish raised with parents but without predation risk (F+P-) and fish raised without parents but with predation risk (F-P+) laid more and larger eggs compared to fish of the F+P+ and F-P- treatments. We discuss these results in relation to the reproductive opportunities these fish face in different environments.

The architecture of adaptation: a master mutation or a mass of mutations?

Poster

Archambeault Sophie and Peichel Catherine, University of Washington and University of Bern

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Adaptation can be a major driver of diversity and speciation. The threespine stickleback (*Gasterosteus aculeatus*) is an excellent model for studying adaptive evolution because the marine ecotype has repeatedly invaded and adapted to freshwater environments across the northern hemisphere since the last glacial period. Prior studies have identified genomic regions of divergence between marine and freshwater populations, suggestive of repeated selection on these genomic regions. In addition, quantitative trait loci (QTL) mapping studies have identified several genomic "hotspots" of adaptation, regions which contain QTL for many phenotypic traits. Such clustering is unexpected and could result from tight physical linkage of multiple genetic changes responsible for different traits, or from a single genetic change with pleiotropic effects. In order to disentangle the relationships between genotype and phenotype in these genomic hotspots, we are focusing on a region of chromosome IV where an adaptive hotspot overlaps with a region of strong genomic divergence. We are performing association mapping within this 16 kilobase region in a fully interbreeding, polymorphic, freshwater population of threespine stickleback. Our preliminary data suggest that the clustering of QTL in this region is due at least in part to linkage of multiple causative genetic changes.

When can trait dynamics inform us about population decline?

Oral presentation

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Predicting population decline is an important and an on-going challenge in ecology. Studies have demonstrated trait-demography relationships with recent work suggesting that trait dynamics may be useful in predicting population collapse. However, a mechanistic understanding of when and under what circumstances such traits can be useful in predicting population decline is still unknown. Here, we take a trait-based analytical approach to understand the dynamics of density-regulated population decline in response to various levels of environmental change. Specifically, we take a quantitative genetics approach to investigate whether trait shifts can occur before a population decline. We investigate analytically and with simulations whether there are factors that can promote earlier occurrence of shifts in mean traits before a population decline. We show that under slow environmental change, shifts in mean trait value can precede a population decline, but such a shift is governed by the amount of genetic variation in the trait, plasticity, and reproduction rate. Our above results still hold after relaxing the assumption of constant genetic variation in the trait and other model parameters. Our study highlights the importance of fitness-related traits in informing population decline and has positive implications to include such traits in early warning signals of population collapse.

The evolution of an exaggerated male trait and wing morphology in two closely related Sepsid fly species

Poster / FlashTalk

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The relative importance of sexual selection and reproductive character displacement for morphological divergence during speciation is difficult to unravel. The still interbreeding sister species *Sepsis neocynipsea* and *S. cynipsea* provide a good opportunity to address this issue, as they show a geographic distribution with discrete allopatric and sympatric populations. Applying landmark based morphometrics, an extensive geographic sampling combined with a mating experiment in the laboratory were used to assess patterns of quantitative genetic differentiation and the strength of ongoing sexual selection on the armored foreleg femur and wing morphology. Wing shape differentiation was showing a phylogenetic signal, while male femur shape was divergent according to the geographic origin of the populations. The mating experiment supports ongoing sexual selection in most shape and size aspects but also indicates reproductive character displacement in others. Furthermore we find, that the shape of the foreleg femur is highly condition dependent as well as clinal variation in femur size.

Population genetic pattern and haplotype distribution of European Graylings (Thymallus thymallus) in the river Wiese, a tributary to the Rhine river in Basel

Poster

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We investigated the population structure and a possible upstream migration of European Grayling (*Thymallus thymallus*) from the river Rhine into the river Wiese and connected water systems (Riehen Dike System) in Basel. We applied 8 microsatellite and one mitochondrial DNA (mt DNA) marker to assess the population structure and to reveal their origins (haplotypes). The results showed a high degree of differentiation between the fish from the river Wiese as well as the Riehen Dike System and the Rhine river, as only weak signals of graylings displaying a Rhine genotype were found in the stretch where Rhine and Wiese meet and none more upstream. Three major mt DNA haplotype lineages were identified in both systems (Atlantic 83%, Rhone 6% and Danubian 10% lineage). The Rhone and Danube haplotypes seem to originate mostly from hatchery fish stocked in the river Wiese and the Riehen Dike System between 1990 and 2000.The study shows that also hatchery fish destined for stocking should be genetically analyzed before introduction into a river system.

Feeding ecology in Lake Tanganyika cichlids based on stable isotope analysis

Poster

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The adaptive radiation of cichlid fishes in East African Lake Tanganyika is an ideal model system to study the circumstances and the processes through which a great variety of species arose as a consequence of the adaptation to different ecological niches. Stable isotope analysis, in combination with gut length measurements, allow to estimate the trophic position of a each species and to reconstruct food web structures in an entire community. Here, we analyzed the isotopic signatures of carbon (δ13C), indicating the primary carbon source (benthic-pelagic) and nitrogen (δ15N), commonly used as a proxy for the relative trophic level of 237 Lake Tanganyika cichlid species to characterize their trophic diversification. The obtained data highlight that species-rich tribes cover a broad range of different ecological niches, whereas species from species-poor tribes seem to be more adapted to specific ecologies. In addition, the intestine length measurements for a subset of 100 species support an inverse relationship between gut length and trophic level, with on average longer intestines in primary consumers.

Contemporary evolution against apparent selection and its demographic consequences in a wild rodent population

Poster / FlashTalk

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What happens to a natural population when its environment changes? Does it collapse? Does it evolve? Does adaptation affect the demography? Despite theoretical progresses and lab experiments, these questions remain empirically little explored in the wild and in particular, conclusive evidence for contemporary adaptive evolution remains rare. Applying a quantitative genetic framework to individual-based long-term data for a wild snow vole population, we show that despite a positive association between body mass and fitness, there has been a genetic change towards lower body mass. The latter represents an adaptive response to viability selection favouring juveniles growing up to become relatively small adults, i.e. with a low potential adult mass, which presumably complete their development earlier. This selection is particularly strong towards the end of the snow-free season, and it has intensified in recent years, coinciding with a change in snowfall patterns. Interestingly, the strengthening of selection coincides with a population decline, while the population recovered after genetic adaptation, suggesting a possible case of evolutionary rescue. Building on these results, we now attempt to estimate the respective roles of demographic, genetic and evolutionary rescues in shaping the rebound of the snow vole population.

Frequent and parallel habitat transitions as driver of unbounded radiations: the African Restionaceae

Oral presentation

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The enormous species richness in the Cape Floristic Region (CFR) of Southern Africa is the result of numerous radiations, but the temporal progression and possible mechanisms of these radiations are still poorly understood. Here, we explore the macroevolutionary dynamics of the Restionaceae, as an exemplar Cape clade, using a complete species-level time calibrated phylogeny and models of diversification dynamics. We show that the species diversification is constant through the Cenozoic, showing no evidence of an acceleration with the onset of the modern winter-wet climate or recent density-dependent slowdown. As predicted, diversification is highest in the oldest (montane) and most extensive (well-drained) habitats. Although habitats (montane or coastal; well-drained or wet) are phylogenetically conserved, there are several indications that habitat transitions may drive diversification. Firstly, habitat transitions are associated with speciation rather than with time; and secondly, more than a quarter of all speciation events are associated with habitat transitions. This suggests that the unbounded diversification may have been driven by numerous, parallel habitat transitions. Unbounded diversification may be common in the Cape flora, but the role of habitat shifts has not been explored for any other clade.

Host specificity and vertebrate complement system in the Lyme disease context

Poster

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Closely related pathogen species can be adapted to very different host species but the mechanisms underlying this host-specificity are often unknown. The tick-borne spirochete bacteria belonging to the *Borrelia burgdorferi* sensu lato genospecies complex cause Lyme disease (LD) in humans. In Europe the two most common LD pathogens, *B. afzelii* and *B. garinii*, are associated with rodents and birds, respectively. In vitro studies suggest that this host specificity is mediated by the vertebrate complement system. We will use an experimental infection approach to study host specificity. We will challenge immunocompetent and complement-deficient mice (*Mus musculus*) and immunocompetent canary finches (*Serina canaria*) with *I. ricinus* nymphs that have been experimentally infected with either *B. afzelii* or *B. garinii*. At 30 days post-infection, animals will be infested with xenodiagnostic larval ticks to quantify host-to-tick transmission. We will use qPCR and culture to determine the *Borrelia* spirochete load and spirochete viability in ticks. We predict that the load and viability of each *Borrelia* species in the challenge nymphs will be greatly reduced after feeding on the wrong host (e.g. *B. garinii* spirochetes will be low and non-viable in immunocompetent mice). This study will give further information on how host specificity might be driven by the vertebrate complement system.

Optimising Ensemble of Small Models (ESM) for modelling rare species in conservation practice

Poster

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Ensemble of Small Models (ESM) is a novel strategy built by calibrating simple models, in our case only two predictors at a time, which are averaged to an ensemble weighted by cross-validated AUC scores as a measure of model performance. The ESM strategy is very advantageous in model performance compared to standard models for predicting the distribution of rare species (Breiner et al., 2015. Methods Ecol. Evol). However, this increase in model performance comes along with a high computation effort. We show possibilities how to further improve model performance (1-2) and computation time (3) to increase applicability and efficiency of ESMs:

(1) To find an optimized set of bivariate models by iteratively combining bivariate models to ESMs until the AUC score is maximized or by using thresholds (e.g. AUC = 0.7) to remove weak performing bivariate models.

(2) Including more parameters for bivariate models to calibrate more complex relationships, e.g. interactions.

(3) Using only a reduced set without losing model performance. The subset could be defined by pre-selecting variables according to the variable importance score of standard models.

Including environmental niche information to improve IUCN Red List assessments

Poster

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Information on change in species' environmental preferences is currently not included in IUCN Red List criteria, although such information is key for assessing whether species not only lose geographic range but also lose part of their realized niche. Using niche size quantification and niche-based species distribution models (SDMs), we test if realized niche size and predicted potential range size provide additional information compared with the standard IUCN scores. We simulated extinction events of varying magnitudes (10, 30, and 50% of occurrences). For a set of 148 representative vascular plant species in Switzerland, we tested how accurately the geographic versus niche measures pictured these extinction scenarios respectively. We found that changes in niche size often corresponded to changes in geographic space. However, there was considerable variation and, for many species, changes in geographic and in niche space delivered complementary information. Changes in niche size can thus be used more systematically for Red List assessments. IUCN criteria based on spatial projections of SDMs did not capture extinction events in most cases and often increased the modelled range size, even when up to 50% of the occurrences were removed by simulated extinction events. Change in SDM-predicted range size should be used with caution for IUCN Red List assessments.

Genetic architecture of reproductive isolation and species differences in *Populus alba* and *P. tremula*

Poster / FlashTalk

Bresadola Luisa, University of Fribourg

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Populus alba and *P. tremula* are two widespread tree species, which hybridize despite being strongly divergent from an ecological and a genetic point of view. In this project, we focus on (1) investigating the reproductive barriers between the two species, and (2) unraveling the genetic architecture of ecological differences maintained in the face of gene flow. Towards addressing objective (1), we examined the relationship between genomic ancestry and survivorship in hybrid seedlings growing in a common garden trial. The results indicate higher mortality of genetically intermediate recombinant hybrids compared to first generation hybrids (F1), likely explaining the predominance of F1 among adult trees in natural hybrid zones. This observation suggests that selection is acting to maintain strong postzygotic barriers between the two species and speaks for a role of intragenomic coadaptation in hybrid breakdown. To address objective 2, we used RAD-seq to genotype hybrid seedlings from two common garden locations and measured their phenotypes for ecologically important traits. Local patterns of genomic ancestry revealed the recombinant nature of the majority of the seedlings, thus allowing the use of admixture mapping methodology to link genomic and phenotypic information to infer the chromosomal position of quantitative trait loci responsible for the traits.

FROZENFIRE – A millennium of European fire, vegetation and pollution history from a high alpine ice core in the Swiss Alps

Oral presentation

Brugger Sandra O.[1,2]*, Erika Gobet*[1,2]*, Michael Sigl*[2,3]*, Dimitri Osmont*[2,3,4]*, Margit Schwikowski*[2,3,4]*, and Willy Tinner*[1,2]

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Wild fires are an ecological disturbance agent across ecosystems, driving vegetation dynamics and resulting in disruption of habitats. We analyze pollen as proxies for vegetation composition and agricultural activity, microscopic charcoal as a proxy for fire activity, and framboid organic particles (or soots) as a proxy for fossil fuel combustion which preserve in ice cores over millennia. Our ice core from Colle Gnifetti (4452 m a.s.l) is located in the center of Western Europe, thus allowing to assess vegetation and societal responses to climatic change and wildfire disturbance on a subcontinental scale. The record covers the last millennium with an excellent chronological control particularly over the most recent 150 years - the period that experienced important climatic changes and an increasing globalization of economy. The record reflects large scale impacts such as extreme weather, societal innovations, agricultural crises and pollution of the industrial period in Western Europe and the Mediterranean realm. We aim at disentangling the role of climate, vegetation and human impacts on biomass burning to significantly advance the understanding of the regional role of wildfire events and vegetation responses under future climate change scenarios. To our knowledge we present the first long-term high-resolution palynological record of a high elevation ice core in the Alps.

Healthier or bigger? Trade-off mediating male dimorphism in the black scavenger fly *Sepsis thoracica* (Diptera: Sepsidae)

Oral presentation

Busso Juan Pablo, IEU - UZH, Wolf U. Blanckenhorn, IEU - UZH, Daniel Gonzáles-Tokman, Cátedras CONACYT, Instituto de Ecología A. C.

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Life history trade-offs emerge when limited resources are allocated to multiple functions in an organism. Under highly competitive conditions, trade-offs can result in alternative phenotypes. Such is the case in insects growing under high densities, where resource competition and disease contagion risk are high, prompting important adjustments in immunity, with consequent sacrifices in other fitness-related traits. We evaluated potential trade-offs between immunity, body size and pigmentation in *Sepsis thoracica* flies that show alternative male morphs differing in pigmentation and size. As expected, small/dark (obsidian) males showed higher immunity than larger/orange (amber) males. This negative relationship between immunity and body size, which was also observed in the females, suggests that the costs of growth and immunity result in a trade-off. In contrast, rearing density did not affect immunity, as predicted by the density-dependent prophylaxis hypothesis, which had not been tested in dipterans before. However, density did affect negatively the body size in females and amber but not obsidian males, showing that male morph is largely determined by condition-dependent plasticity rather than genes. Our study provides good evidence that trade-offs between different life-history traits can result in alternative resource allocation strategies, even within one species.

Genetic differentiation in environmental space: a study with two closely related species of lizards

Poster

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The interactions between organisms and their landscape can shape the distribution of spatial genetic variability, resulting in different patterns. Isolation by distance (IBD) occurs when the level of gene flow is influenced by the geographical distances among populations. However, the environment also can affect the spatial distribution of the genetic variation, resulting in patterns of isolation by environment (IBE), independently of the geographic distance. We study two lizard species at local scale through an environmental cline in the Chaco region of Argentina. *Salvator merianae* and *Salvator rufescens* inhabit in different environments but overlap in a narrow ecotone area. We use a highly variable mitochondrial marker to calculate pairwise genetic FST distances between population (FSTP) and between individuals (FSTI) and we performed mantel and partial mantel tests looking for patterns of IBD and IBE. Both species shown genetic differences along the study area, indicating low levels of gene flow. We found IBD in *S. merianae* using FSTI and FSTP and IBE pattern using FSTI but no FSTP. *Salvator rufescens* did not show pattern of IBD nor IBE with both genetic matrixes (FSTP and FSTI). At local scale, the use of FSTP (commonly used) instead FSTI can mask the effect of environment, because FSTP averages genetic distances among the individuals.

Differences in pollinator-plant networks of high and low altitude

Oral presentation

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The pollination of plants by insects is a fundamental ecosystem service. Dramatic ongoing decline of pollinators on a global scale alarmed not only scientists but also governments. To stop this decline researchers try to understand pollinator-plant interactions on a community perspective and how the drivers of pollinator decline affect them. Here we show differences between low and high altitude pollination networks of extensively managed meadows of the central Swiss pre-Alps. Over 3400 interactions from 16 independent low and high altitude sites between 88 plant and 339 pollinator species from all families were analyzed and compared by investigating network parameters. The results show that high altitude communities have higher nestedness and are more robust to drivers of pollinator decline. Moreover pollinator species and families obtain different roles in high and low altitude communities. Whereas wild bees and domesticated *Apis mellifera* show high interaction strength in low altitude networks, their importance decrease dramatically in high altitude networks. Here syrphid flies and *Bombus* are the major pollinator families that the network depend on. Our findings can help to implement more efficient conservation actions and state that they have to be discriminated between different types of habitats and pollinator species and families.

Leaf pathogenic fungi in grassland communities

Oral presentation

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In biodiversity and ecosystem functioning research plant pathogenic fungi have largely been neglected, even though we know that they can have a big impact on ecosystem functioning. Understanding the role of higher trophic levels (such as pathogenic fungi) in ecosystems is crucial when we want to predict how ecosystems react to global change. I investigate how plant leaf pathogenic fungi shape relationships between plant biodiversity and ecosystem functioning in the context of the global change driver nitrogen enrichment and how fungal infection in turn is dependent on plant community properties. I do this in the PaNDiv grassland experiment, where we factorially manipulate plant species richness, plant functional composition, nitrogen fertilization and fungicide addition. My preliminary results show that fungal infection in plant communities is driven by the identity, the functional group and the density of the individual plant species in the community. There is some indication that the fungal community composition on individual plant species varies depending on the plant community the plant species is growing in. Further, our results indicate that fungal infection has the potential to reduce biomass production of the different plant communities.

Adaptive significance of transposable elements in natural populations of *Arabis alpina*

Poster / FlashTalk

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Transposable element (TE) insertions affect phenotypes by either disrupting genes or influencing their expression. Moreover, TE dynamics drive the evolution of structurally divergent, recombinationally inert genome regions. However, to what extent TEs produce evolutionarily significant variation remains debated. Here, we investigate TE variation in the inbred *Arabis alpina* across varying alpine habitats and identified several recently active TEs being significant enrichment in gene-rich regions and representing candidates supporting microevolutionary processes in *Arabis*. We further used resequencing data of 306 individuals from natural populations to comprehensively identify TE variants and produce an alpine pan-genome assisting the genotyping of variant copies inserted in genic or non-genic regions. Analyses associating polymorphic TE loci with environmental factors derived from high-resolution topography is assessing loci enriched near functional genes and their adaptive significance. This is among the first studies addressing how TEs and their arrangements affect local adaptation of plant populations and relate such quantitative estimates with the spatial scale at which TEs generate evolutionary significant variation.

Zelkova in East Asia: a story of demographic expansions and hybridization

Poster

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The Tertiary relict tree genus *Zelkova* comprises six species distributed in Southwest Eurasia and East-Asia. It is a fantastic model to address the effects of geographic barriers on species genetic diversity and structuration. East-Asian species have been poorly studied and are, in many regions, overexploited and threatened by habitat fragmentation. We studied the phylogeography of the three East-Asian species, in comparison with the Eurasian species, with 2 chloroplast loci and 6 microsatellite markers. We furthermore addressed the issue of species delimitations among East-Asian species using Bayesian analyses. In Southwest Eurasia, the effect of Quaternary glaciations on plant distribution was strongly shaped by the presence of many east-west barriers leading to allopatric speciations, consecutive to very good species delimitations and high intraspecific diversities. In East-Asia, the absence of strong barriers south of the Himalayas, allowed for easier and wider recolonization processes and higher opportunities for secondary contacts among species. These features impacted intraspecific diversities as well as species delimitations. Two groups can be recognized within East-Asian species, one represented by Z. serrata and the second one including *Z. schneideriana* and *Z. sinica*. Populations from Taiwan, previously attributed to *Z. serrata*, clearly pertain to the second group.

Fossils and macroevolution: a case study in the Cycadales

Poster / FlashTalk

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In the last decades phylogenies based on DNA sequence data have increasing replaced fossils as primary data for macroevolutionary studies. However, fossils are still pivotal in informing the timing of macroevolutionary events, in offering a unique window into past disparity, for inferring directionality and tempo of character evolution, and for informing the past distribution of organisms. The development of methods that allow the integration of fossil data in a fully phylogenetic framework, such as the fossilized birth-death prior for dated trees, resulted in a new interest in using a much broader array of fossil information in macroevolutionary studies. Nonetheless, there have been surprisingly few applications of this method in macroevolutionary studies of plant groups. Here we show the potential of these methods in a case study on the Cycadales, a group with a rich but poorly understood fossil record. Using a new tree including fossil and extant cycads, we try to gain new insights into their evolution, their biogeographical history and the influence of character evolution and disparification on their evolutionary trajectory. We show that the history of the cycads resulted from both Mesozoic and Recent radiations, influenced by a combination of leaf ecological strategies, climatic change and geological history.

Individual variation in the sickness behavior of coral reef damselfish

Poster

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Sickness behaviour is a set of non-specific behavioural changes that occur when the immune system fights an infection, both in humans and non-human animals. Lethargy, anorexia and fatigue are common behavioural symptoms of sickness, and occur as adaptive responses used to reallocate energy towards fighting the infection. By initiating an immune response, sickness can, therefore, dramatically alter animal behaviour. Here, we investigated whether inter-individual behavioural differences (personality) influence sickness behaviour in the ambon damselfish, *Pomacentrus amboinensis*. We scored the behaviour of 59 individuals twice in each an exploration (novel object) and aggression (mirror) test. We then injected half of the fish with lipopolysaccharide (LPS) to illicit an immune response, and half with a saline control, before retesting their behaviour twice. We examined whether 1) exploration and aggression are correlated behaviours in this species, 2) sickness changes this relationship and 3) individuals differ in their behavioural responses to an immune challenge depending on their personality. Understanding sickness behavior from an individual-level perspective is important to inform possible differences in life-history strategies for dealing with infection.

Trans-lineage polymorphisms in *Daphnia magna*

Poster

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Single Nucleotide Polymorphisms (SNPs) shared between related lineages are rare ancient genetic variants whose origin predates the split of the taxa. Long-term balancing selection is the most likely mechanism that maintains such SNPs at the selected loci, as shown in genes related to immune responses in vertebrates and in plants. We conducted genome-wide analyses in Daphnia magna lineages to identify shared polymorphisms, with the expectation of finding them in proximity of genes related to immunity. The *D. magna* Diversity Panel is a collection of 165 clones from around the world. The whole genome sequence of one clone per population was obtained using Illumina technology. The assemblies of individual mitochondrial genome were used to build a phylogeny, which showed that two major clades of *D. magna* exist: the Western Eurasian and the Eastern Asian groups. These two lineages showed no admixture and a long divergence time, and they might be used as suitable candidates for studying the occurrence of shared polymorphisms between related lineages and the evolutionary mechanisms that maintain them. We found that shared polymorphisms were not randomly distributed across the genome, with some scaffolds showing regions enriched in shared SNPs. Furthermore, shared polymorphisms were found near genes related to immunity and hypothesized to evolve under balancing selection.

The performance of in-solution capture-enrichment experiment for human Y chromosome

Oral presentation

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Uniparental markers (i.e. mitochondrial and Y chromosome DNA) are widely used in population genetics to infer the demographic history of specific lineages. Despite harbouring the largest non-recombining region in the human genome, which allows to trace the patrilineal history of populations, the Y chromosome contains large repetitive and heterochromatic stretches making it difficult to assemble good quality sequence data. This represents a bigger challenge when attempting to analyse ancient samples, where the target DNA comes in low quantities and is highly fragmented. To overcome this challenge, we implemented in-solution capture experiments targeting the non-recombining region of the Y chromosome to improve the quality of the resulting assembly while reducing sequencing costs. We compared enrichment strategies on two samples excavated from a 17th century burial in the Caribbean and investigated the parameters affecting both the quality and the quantity of the data. We then assessed to what extent the enrichment improved the resolution of the haplogroup assignation of the Y chromosome. Preliminary results show that enrichment increased the depth of coverage on the Y chromosome up to 3.7 orders of magnitude, allowing us to sequence informative SNPs and learn about the paternal genetic ancestry of the individuals of interest.

Effects of management intensification on land snail communities in Swiss traditionally managed mountain meadows

Poster

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Traditionally managed subalpine hay meadows are nowadays subject to agricultural intensification, generating drastic changes in the species composition of these habitats of high conservation value. Nevertheless, effects of intensification on land snails remain unclear. Adopting a randomized block design, we experimentally investigated the effects of six levels of management intensification in terms of irrigation and fertilisation on land snail communities in 11 traditionally managed mountain meadows in Valais (Switzerland). After 5 years, no negative effect of intensification was observed, even on xerophilous species, which were expected to be negatively affected. Intensification did not affect species richness but increased abundance. Community analysis suggested the same pattern, that abundances of species were modified by the treatments, but not the species composition. The positive effects of intensification on abundance were potentially due to moisture and pH increases in intensified plots. Treatments remained sufficiently moderate to not negatively impact drought adapted species. According to these results, we recommend that water and fertiliser inputs should not exceed 2/3 of amount necessary to achieve maximum hay yield locally. The absence of effect on red listed and xerophilous species is surprising and call for further investigations.

Fitness costs associated with building and maintaining the burying beetle's carrion nest

Poster / FlashTalk

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It is well-known that features of animal nest architecture can be explained by fitness benefits gained by the offspring housed within. Here we focus on the little-tested suggestion that the fitness costs associated with building and maintaining a nest should additionally account for aspects of its architecture. Burying beetles prepare an edible nest for their young from a small vertebrate carcass, by ripping off any fur or feathers and rolling the flesh into a rounded ball. We found evidence that only larger beetles are able to construct rounder carcass nests, and that rounder carcass nests are associated with lower maintenance costs. Offspring success, however, was not explained by nest roundness. Our experiment thus provides rare support for the suggestion that construction and maintenance costs are key to understanding animal architecture.

The genomic basis of adaptation in the Swiss Alpine whitefish radiation

Poster

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Knowledge about the genetic basis of local adaptation contributes to a better understanding of the role of ecological speciation in creating biodiversity. The recent origins and repeated diversification of fish in post-glacial lakes is an ideal system to study the genomic changes underpinning ecological diversification. During my recently started PhD I plan to investigate the genomic basis of differentiation within the Alpine whitefish (*Coregonus* spp.) species complex, the species of which are found in 17 Swiss lakes. The radiations of six or more sympatric species of whitefish in some lakes are thought to have been facilitated by ecological and reproductive strategy differentiation with sympatric species varying in diet, body length, gill-raker number and spawning depth. The study site for the first part of my project will be lakes Thun and Brienz in which the whitefish have differentiated into five ecologically distinct species, three shared species and two unique to Thun. I plan to use RADseq data collected from each of these species in each lake to investigate population structure of these whitefish at a high resolution. Comparing ecologically distinct species will reveal the number and distribution of genomic regions with exceptional differentiation, reflecting the genetic basis of ecological speciation in this system.

Do cleaner wrasse obey biological market rules when servicing their client fishes?

Poster

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Biological market theory provides a framework for studying the exchange of commodities between partners, and has greatly enhanced our understanding of the evolutionary stability of cooperation. Cleaning mutualisms among cleaner wrasse, *Labroides dimidiatus*, and their "client" reef fishes perfectly illustrate this paradigm. Cleaners are visited by clients regularly visit cleaners to have their ectoparasites removed: both partners benefit because cleaning is exchanged for food. However, cleaners sometimes cheat their clients by eating their mucus instead of their parasites, which is costly for the clients. Since clients can reduce cheating by switching partners, cleaners adjust their cleaning behaviour based on the market conditions (i.e. supply and demand). Recent studies suggest that the abundance of cleaners and competition over access to clients strongly influence service quality. Here, we investigated whether reducing the abundance of cleaners reduces their cooperation levels. We observed natural cleaning interactions on two nearby coral reefs in Australia, and subsequently removed 50% of cleaners from one of these sites. We compared the behaviour of individual cleaners before, two days and one month after the removal, and tested for differences in cleaning service quality (i.e. cheating frequency) across these time periods.

Ontogenetic and environmental influence on inter- and intrapopulation differences in timing of migration

Poster / FlashTalk

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Animals ranging from insects to birds, fish, and mammals follow a migratory life-history strategy, causing wide reaching effects on individuals and ecosystems. Environmental and ontogenetic factors influence the relative profitability of alternative habitats and thereby determine migratory timing, leading to inter- and intrapopulation variation between individuals. Whereas theoretical predictions on such variation are well developed, the lack of replication on population level often limits empirical studies. Furthermore, it can be difficult to determine whether it is the profitability change in the natal- or the migratory habitat that drive differences in migration patterns. Here, we study individual migration patterns of juvenile trout from 14 different populations migrating between natal streams and a shared migratory habitat. We tagged thousands of trout with PIT-tags and recorded migration patterns using stationary antennas. We hypothesized that intrapopulation differences depend on individual traits and environmental conditions in both natal and migratory habitat, while interpopulation variation is driven solely by differences between the natal habitats. We found significant ontogenetic influence on timing, with larger size leading to earlier migration in all populations. Interpopulation differences are mainly determined by the environmental conditions in natal streams.

On the relationship between resilience of growth to drought and future mortality risk in trees

Poster

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Drought events associated with increasing temperatures potentially cause tree mortality, and in turn cause sudden changes in forest ecosystems. The study of the growth resilience, i.e. capacity to reach pre-episode growth levels (resistance x recovery), following drought events will allow us to evaluate the tree ability to survive to future droughts. Our working hypothesis is that trees with lower resistance and recovery to drought events would be more prone to die afterward. For this study, we used 45 tree-ring datasets of 28 species (9 Angiosperms and 19 Gymnosperms) containing tree-ring data for coexisting living and dead trees from 156 sites all over the world (3,857 and 2,346 ring-width series for living and dead trees, respectively) where the cause of death was drought or drought-related effect (bark beetle, competition, etc.). In each site we identified the drought event with the strongest impact, then we computed the indexes of resistance, recovery, resilience based on tree-ring growth, and compared those indices between dead and living trees. Our preliminary results showed that dead trees resisted and recovered less to drought events than living trees, suggesting that lower resilience to previous droughts can be an early signal of tree mortality.

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ecospat: an R package for spatial analysis and modeling species distributions.

Poster

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The aim of the ecospat package is to make available novel tools and methods to support spatial analyses and modeling of species niches and distributions in a coherent workflow. The package is written in the R language (R Development Core Team 2016) and contains several features, unique in their implementation, that are complementary to other existing R packages. Pre-modeling analyses include species niche quantifications and comparisons between distinct ranges or time periods, measures of phylogenetic diversity, and other data exploration functionalities (e.g. extrapolation detection, ExDet). Core modeling brings together the new approach of Ensemble of Small Models (ESM) and various implementations of the spatially-explicit modeling of species assemblages (SESAM) framework. Post-modeling analyses include evaluation of species predictions based on presence-only data (Boyce index) and of community predictions, phylogenetic diversity and environmentally-constrained species co-occurrences analyses. The ecospat package also provides some functions to supplement the biomod2 package (e.g. data preparation, permutation tests and cross-validation of model predictive power). With this novel package, we intend to stimulate the use of comprehensive approaches in spatial modelling of species and community distributions.

Sympatric alpine charr diversity: origin from a hybrid swarm?

Oral presentation

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A wealth of species diversity in a single taxonomic group in one location is among the most intriguing patterns in nature. Such sympatric diversity may arise from multiple allopatrically-derived species coming into contact, from sympatric diversification of one species, or from a mix of these processes. Hybridization between divergent species, often inherent secondary contact and sympatric divergence, may lead to the collapse of species diversity, or may facilitate the generation of unprecedented diversity. However, the evolutionary dynamics at the early stage of contact and hybridization often remain unclear. Here, we explore the evolutionary origins of a morphologically diverse assemblage of charr in pre-alpine Lake Thun. Historical documents on management of charr reveal major introductions from three other lakes into Lake Thun during the last ~100y. Genomic data from RADseq confirm these introductions and indicate high levels of admixture among the different source populations in Lake Thun. Among some of the diverse morphotypes of charr in Lake Thun, we find genomic differentiation and variation in admixture contributions from different source populations. This suggests that we do not simply see a homogenous, but a phenotypically and genetically structured hybrid swarm. We discuss how these results speak to a collapse of species diversity vs. the evolution of new species.

Habitat complementation in a salamander with a complex life cycle

Poster

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Habitat complementation is crucial for species with complex life cycles. For aquatic-breeding amphibians, habitat complementation implies that both suitable aquatic and terrestrial habitat must be available. The relative importance of aquatic and terrestrial habitat characteristics for habitat complementation is often subject of discussions and uncertainty remains. Furthermore, the relative effects of local and landscape-level terrestrial habitat is poorly known. We estimated larval abundances of the fire salamander *Salamandra salamandra* in 50 streams in Northern Switzerland to assess the relative importance of terrestrial and aquatic habitat characteristics. We found strong spatial variation in abundance. We recorded both aquatic and terrestrial habitat variables such as stream structure, forest composition and water quality in the immediate (local) surroundings. We also investigated whether landscape-scale variables (e.g. road density and landscape) influence larvae abundances by using a Geographic Information System (GIS). Our results show that larvae abundances are higher in natural streams with several sections of reduced flow speed. Surprisingly, immediate forest structure and water quality did not show an effect. The results highlight the importance of natural streams as a key factor explaining the vast differences in salamander larvae abundances.

More constant rather than plastic species are the winners of anthropogenic changes: implications for ecosystem functioning

Poster

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Anthropogenic environmental changes reduce local plant diversity. It is hypothesized that plants that can adjust plastically are more likely to survive these changes. There are also assumptions on that more plastic species contribute more to community productivity and its stability due to larger phenotypic variability and smaller population variability, respectively. Theoretically may thus plastic species maintain ecosystem functioning even after extinctions of more constant species. Here we show that more plastic grassland species are less, not more resistant to different anthropogenic changes. We also show that more plastic species display larger, not smaller temporal population variability. Presence of more plastic species in more diverse communities (corresponding to more realistic assembly found in the field) amplified or, in opposite, dampened positive effects of species diversity on community productivity and its stability, as shown by subsetting data from several biodiversity-ecosystem function studies. Our findings suggest that larger phenotypic plasticity in leaf functional traits is an indicator of species sensitivity to environmental changes. As more plastic species are progressively more common in more diverse communities, environmental context may be important determinant of diversity-ecosystem functioning relationships.

Inference of evolutionary jumps in large phylogenies using Levy processes

Oral presentation

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While it is now widely accepted that the rate of phenotypic evolution may not necessarily be constant across large phylogenies, the frequency and phylogenetic position of periods of rapid evolution, also known as evolutionary jumps, remain unclear. In his highly influential view of evolution, G. G. Simpson supposed that such evolutionary jumps occur when organisms transition into so called new adaptive zones, for instance after dispersal into a new geographic area, after rapid climatic changes, or following the appearance of an evolutionary novelty. Only recently, large, accurate and well calibrated phylogenies have become available that allow testing this hypothesis directly, yet inferring evolutionary jumps remains computationally very challenging. Here, we develop a computationally highly efficient algorithm to accurately infer the rate and strength of evolutionary jumps as well as their phylogenetic position. Following previous work we model evolutionary jumps as a compound process, but introduce a novel approach to sample jump configurations that does not require matrix inversions and thus naturally scales to large trees. We then make use of this development to infer evolutionary jumps in *Anolis* lizards and Loriinae parrots where we find strong signal for such jumps at the basis of clades that transitioned into new adaptive zones, just as postulated by Simpson's.

Sex-specific allelic transmission bias suggests sexual conflict at MC1R

Poster

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Autosomal MC1R gene can generate colour variation in sexually dichromatic species, most previous studies have not considered the possibility that MC1R may be subject to sexual conflict. In the barn owl (*Tyto alba*), the allele MC1Rwhite is associated with whitish plumage colouration, typical of males, and the allele MC1Rrufous is associated with dark rufous colouration, typical of females, although each sex can express any phenotype. Because each colour variant is adapted to specific environmental conditions, the allele MC1Rwhite may be more strongly selected in males and the allele MC1Rrufous in females. Our results show an overall deficit of 7.5% in the proportion of heterozygotes in males and of 12.9% in females. In males, inter-annual variation in assortative pairing with respect to MC1R explained the year-specific deviations from Hardy-Weinberg proportions, whereas in females, the deficit was better explained by the inter-annual variation in the probability of inheriting the MC1Rwhite or MC1Rrufous allele. Additionally, we observed that sons inherit the MC1Rrufous allele from their fathers on average slightly less often than expected under the first Mendelian law. Transmission ratio distortion may be adaptive in this sexually dichromatic species if males and females are, respectively, selected to display white and rufous plumages.

Metabolome analysis of flies adapted to chronic juvenile malnutrition

Poster / FlashTalk

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Many organisms have to face periods of nutrient shortage, particularly at young age, and have to grow and develop despite encountering that stress. An interesting question is to study what is the evolutionary potential of organisms to tolerate chronic juvenile malnutrition, and in which trade-offs those adaptations could potentially result. To address this, we have employed an experimental evolution approach on the broadly used model species *Drosophila melanogaster*. Indeed, our lab harbors since more than 200 generations a population of flies submitted to a diluted nutrient content at larval stage. While larvae of those selected populations show a better survival and a shorter developmental time on poor food, adult flies have a lower tolerance to low nutrient content and a small body size compared to control populations. Consequently, it appears that a trade-off exists between adaptation at larval stage and adult performance. To understand better the impact on the adult, we analyzed and compared the metabolome of control and selected populations of adult flies. Significant changes in abundance were observed in a list of 158 different metabolites. An enrichment analysis revealed that lipid metabolism, protein synthesis and purine metabolism are the principal metabolic categories affected in selected flies.

The reinvention of “leaves” in leafless African Restionaceae – the adaptive value of leaf-like organs.

Poster / FlashTalk

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The climatic and topographical heterogeneity of the Cape floristic region (CFR) of South Africa, a diversity hotspot, provides an opportunity to test the significance of environmental adaptations in radiations. The Restionaceae, whose members dominate the CFR vegetation, are leafless graminoid plants. They have fine and branching vegetative shoots in their juvenile stage. About 10 percent of 350 percent of the species have evolved the ability to retain these vegetative shoots during and/or after flowering. We hypothesize that these vegetative shoots are cost efficient organs for photosynthesis, being advantageous in more humid and nutrient rich environments, due to the faster return on investment. Therefore, we expect a link between these environmental conditions and the presence of vegetative shoots. Additionally, we assume that sister species, that differ in the trait would occur in less similar environments. We test these hypotheses by comparing the photosynthetic activity per biomass of vegetative and reproductive shoots; by investigating potential trait-environment relationships, and accessing the similarity of environments between sister species. Preliminary results indicate that these organs may be advantageous for species occurring in climates with higher total precipitation and lower temperature seasonality.

Reduced caterpillar damage benefits *Lygus hesperus* on Bt cotton

Oral presentation

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The wide scale adoption of genetically modified cotton producing insecticidal Cry proteins from *Bacillus thuringiensis* (Bt), has led to area-wide suppression of major lepidopteran pests and a reduction of insecticide applications. However, non-target pests not susceptible to the produced Cry proteins, such as the plant bug *Lygus hesperus*, have increased in Bt cotton fields. In addition to the reduced application of insecticides, *L. hesperus* might also benefit from reduced caterpillar damage on Bt cotton. The latter was found to reduce the induction of insecticidal terpenoids enhancing the crops” susceptibility to other herbivores. The effects of plant induction on *L. hesperus* development was studied by caging nymphs on Bt and non-Bt cotton plants. Plants were either not damaged, previously damaged by Bt tolerant caterpillars (*Spodoptera exigua*), or treated with jasmonic acid (JA), a hormone that induces cotton defense. Caterpillar- and JA induced plant defenses negatively affected *L. hesperus* survival compared to non-damaged plants. Artificial diet feeding assays using purified terpenoids and molecular analyses of potential *L. hesperus* stress gene upregulation are being conducted to better understand mechanisms behind the greenhouse results. This study underpins the importance of plant-mediated, indirect interactions between herbivores for explaining agro-ecological processes.

Proximate mechanisms underlying alternate behavioral strategies in the facultative cleaning goby *Elacatinus prochilos*

Poster

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Cleaner fish are conspicuous members of coral reef communities that remove ectoparasites and dead tissue from larger fishes, referred to as "clients". Caribbean cleaner gobies *Elacatinus prochilos* are facultative cleaners that exhibit alternative behavioral strategies in adulthood, strategies linked to habitat use. Individuals living in coral depend on cooperative cleaning interactions with client fishes for feeding, whereas individuals living in basket sponges feed on micro-organisms living inside the sponges tissue, rarely engaging in cleaning interactions. Here, we aimed to understand the proximate mechanisms underlying this behavioral variation, focusing on the role of cortisol. Results showed that individuals from alternate habitats did not differ in whole body cortisol levels. Behavioral observations also revealed that individuals from both habitats did not differ in latency to interact with either predatory or non-predatory clients or in the proportion of time spent interacting with clients. However, when investigating the effect of sex, we found that male sponge-dwellers abstained almost completely from interacting with clients. Further analyses will reveal whether circulating levels of cortisol differ between individuals from different habitats. Our current understanding suggests that sex, rather than cortisol, correlates more closely with behavioral differences.

No inbreeding avoidance despite reduced offspring survival in cooperative breeders

Poster / FlashTalk

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In cooperatively breeding species, philopatry and low dispersal lead to reduced outbreeding opportunities. The effects of a resulting inbreeding depression and potential avoidance mechanisms are not well understood. In this study we provided individuals of the cooperatively breeding cichlid fish *Neolamprologus pulcher* with the opportunity to spawn either with a related or an unrelated partner. Relatedness did not influence mate choice, despite the ability of this species to recognize kin. Furthermore, neither spawning success nor the latency to egg laying differed between inbred and outbred pairs. In contrast, survival was significantly reduced in offspring obtained by incestuous matings. These findings suggest that limited mating opportunities might overrule the evolution of kin biased mating decisions in cooperative breeders, even if inbreeding reduces individual fitness.

The causes and consequences of parental age effects on offspring survival in humans

Poster

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Parents play an important role in shaping their offspring's fitness: Not only do they pass on their genes, but often they also provide parental care. In several vertebrate species, offspring fitness depends on the age of their parents, which may be the result of the accumulation of deleterious mutations in the gametes, or of a change in the quality or availability of parental care. We expect parental age effects to be particularly important in humans, as they have a long reproductive lifespan, and due to their short inter-birth intervals and extended time of offspring dependence, parents often care for several children simultaneously. Here we use extensive life history data covering multiple centuries for two Swiss villages to quantify parental age effects in humans, and test whether these are driven by age-dependent parental effects. We show that while maternal age has a significantly negative effect on offspring survival, the effect of paternal age is positive but non-significant. We found significant positive effects of the family's socioeconomic status and whether the parents were alive, a negative effect of sib-ship size, and no grandparental effects. Importantly however, neither of these variables accounted for the effects of parental age, suggesting that although they are important, they play a minor role in shaping parental age effects.

Blood fatty acid composition and its influence on bat metabolism

Oral presentation

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Polyunsaturated fatty acids (PUFAs) increase cellular membrane fluidity and improve fat mobilization. Higher ω-6 PUFA concentrations were further related to lower minimum resting metabolic rates and to longer torpor bouts. These characteristics improve heterotherm's survival during harsh environmental conditions. In contrary to ω-6, ω-3 PUFAs may negatively impact torpor, as revealed by recent studies. To fulfill their needs for PUFAs, insectivorous bats can rely on insects which develop in aquatic environments and contain high ω-3 PUFA concentrations. It remains however unknown if these species control the incorporation of ω-3 PUFAs in somatic cell or if they evolved mechanisms allowing efficient torpor behaviors despite high ω-3 PUFA concentrations. To disentangle these two alternative hypotheses, we measured blood ω-6 to ω-3 PUFA ratios of *Myotis daubentonii* and *Nyctalus noctula*, and related them to torpor metabolisms. The blood ω ratios of *M. daubentonii*, which diet is mostly composed of aquatic insects, were lower than of *N. noctula*, which also feed on terrestrial insects. Furthermore, low blood ω-6 to ω-3 PUFA ratios did not affect resting metabolisms in both species. Our results support the hypothesis that insectivorous bat species have evolved torpor physiology, which tolerate high somatic ω-3 PUFAs, in contrast to other mammal species investigated so far.

Genetics of functional novelty in interspecific cichlid hybrids

Poster

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Hybridization often contributes to increased phenotypic variation in hybrids, which may result in extreme trait values not observed in either parental species - termed transgressive segregation. This increased phenotypic variation is the basis upon which natural selection can act and may provide a mechanism by which hybridization could contribute to adaptive evolution. Moreover, hybridization could produce novel trait combinations, generating new phenotypes that may be suited to new ecological conditions.

We use a second generation hybrid-cross between two Lake Malawi cichlid species (a rock-dwelling algae-sucker and a habitat generalist) to investigate signs of transgressive segregation and functional novelty in several traits. F2-hybrids display novel trait combinations in morphology, feeding behaviour, and male breeding colour not found in the two parental species but observed in a large clade of sandsifting species of Lake Malawi. Hence, this could be a case where hybridization reconstructed a phenotype that characterizes part of the radiation in Lake Malawi.

We are quantifying variation in sandsifting behaviour, functional morphology, and breeding colour in males, for both the hybrids and the parental species. Additionally, we are using RAD-sequencing data to identify regions in the genome contributing to variation in these traits.

Measuring the effects of error accumulation on performance metrics of species distribution models and stacked assemblages

Oral presentation

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Knowing the distribution of species and respective assemblages is increasingly important under negative impacts of global changes on biodiversity. Species distribution models are widely used to predict distributions across space and time. However, they can be biased by false presences/absences from various sources, influencing predicted species distributions and assemblages. Using a virtual ecologist approach, we assessed how commonly used evaluation metrics are affected by different types and levels of errors in occurrence data (calibration data). We calibrated models using three sets of presence/absence data with different sample sizes (100, 400, 1600) and added to each set different levels (from 0 to 50%) and types of errors (added to presences, absences or both). A modelling approach was used to predict the distribution of 100 virtual species derived from field observations. The resulting evaluation metrics were: (i) used to determine how errors affect model predictions, (ii) compared with theoretical expectations to see if models can annul randomly distributed errors in the occurrence data. As errors in occurrence data increased, model performance was reduced. However, accurate predictions were possible even with erroneous data. Our results suggest that caution is needed when evaluating models and that error simulation might be useful to help interpret those evaluations.

Riparian conservation under climate change: Predicting colonization of restored areas

Poster

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Alterations of riparian areas by humans resulted in fragmentation of the riverscape. Connectivity is a major issue in conservation of riparian habitat since specialist species are subject to extinction if habitat fragmentation and habitat loss cannot be counteracted. Especially sessile riparian plants underwent massive decreases in population size and distribution, and are therefore target species for river restoration projects. Our study applies a modelling framework to predict the potential future distribution of species of the Salicion elaeagni habitat taking into account climate change and barriers to dispersal. Modelled suitable habitats show dramatic changes, both under moderate and extreme climate change predictions up to the year 2093. Simulations of future distributions reveal that barriers along rivers have a significant effect on the spread of species. Our results suggest that conservation management should focus on connectivity of stepping stone patches along river networks to overcome limitations of habitat fragmentation and dispersal abilities of riparian plant species. This ensures the survival of the plant community of the Salicion elaeagni habitat despite changes in habitat availability due to climate change.

The unexpectedly high diversity of the genus *Occidozyga* on Borneo

Oral presentation

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The biogeographical region Sundaland is a famous biodiversity hotspot. From Borneo, the biggest island of this region, 186 anuran species are currently known, most of them are endemic on this island. However, the number of species will increase significantly, not least due to the application of sophisticated analyzes of molecular data and the resulting identification of so-called cryptic species. In this study we examine the phylogeny of puddle frogs (Dicroglossidae, *Occidozyga*) using maximum likelihood and Bayesian inference analyzes of nuclear and mitochondrial markers of 157 samples from the whole range of this genus. These frogs, which are distributed from mainland Southeast Asia to the Philippines, Sundaland, and the Lesser Sunda Islands, are known for their unique macro-carnivorous tadpoles. Based on external morphology the puddle frogs from Borneo have been assigned to two species: *Occidozyga laevis*, which is also widespread on the Philippines, and *O. baluensis*, endemic on Borneo. In contrast, our results suggest that the range of O. laevis is restricted to the Philippines. Following our obtained phylogenetic hypothesis *Limnonectes rhacodus* must be regarded as a species of *Occidozyga*. Furthermore, our analyzes show that at least seven separate lineages of *Occidozyga* occur on Borneo, that could be considered as valid species.

Non-adaptive origin of evolutionary innovations in interacting networks of digital organisms

Oral presentation

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One of the major questions in evolutionary biology is to what extent adaptive traits have non-adaptive origins. Such non-adaptive traits or exaptations may help bridge gaps between disconnected genotype networks, and thus make more genotypes accessible by populations subject to phenotype-preserving point mutation. This additional connectivity, in turn, could make more novel phenotypes accessible that reside near these genotypes. In spite of this potential importance of exaptations for the origin of evolutionary innovations, we know almost nothing on how pervasive they are in biological systems. This limitation of case studies can be overcome in digital organisms (i.e., self-replicating computer programs that mutate and evolve within a user-defined computational environment), where it is possible to study systematically many genotypes and the phenotypes they form. Here, we will quantify the role of non-adaptive traits in determining the evolution of ecological interactions among digital organisms. Our "in silico" approach will complement current theoretical advances aimed at disentangling the ecological and evolutionary mechanisms shaping species interaction networks.

Effect of soil management on different trophic levels in Swiss vineyards

Poster

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Viticulture is an important agricultural sector in Switzerland that shows intensive practices, leading to homogenous landscapes and reduced biodiversity. The aim of the present study was to show the benefits of less intensive management practices on biodiversity of different trophic levels in vineyards. Within the PromESSinG project (www.promessing.eu), we investigated the effect of soil management on predators (ground beetles), producers (plants) and decomposers (soil microorganisms). Increasing disturbance negatively affected the producer community but neither predator nor decomposer communities. However, since plant diversity was positively correlated to predator and decomposer communities, management might indirectly affect predator and decomposer communities via its effects on producers. Soil microbial communities were mainly driven by soil parameters, mainly soil organic matter content. Overall, our results suggest that a less intensive management is beneficial to producers and in an indirect way to the trophic levels linked to them. Nevertheless, other environmental factors seem to stronger influence decomposer communities than disturbance due to management.

Cooperatively breeding cichlids benefit from anti-predator vigilance

Poster

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Group living can increase protection from predators through enhanced vigilance, often referred to as the “many eyes effect”. Predation risk has been shown to select for sociality and cooperation, partly due to the benefits of task sharing in anti-predator defense. Here we tested whether group members of the cooperatively breeding fish *Neolamprologus pulcher* may benefit from increased predator protection also through enhanced vigilance. We repeatedly exposed single individuals and differently sized groups to computer animated photos of sympatric cichlid fish depicting either a dangerous predator or a harmless herbivore. Individuals in groups generally responded faster to the presentations than single individuals, and this effect increased with group size. Furthermore, groups responded less often inappropriately to the presentation of harmless herbivores. These results reveal potential benefits of increased vigilance behavior in a cooperative breeder, which adds to the accumulating evidence for the importance of predation risk in the evolution of complex social organization.

Biotic interactions and the eco-evolutionary dynamics of range expansions

Oral presentation

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Understanding and predicting the (macro)ecological and evolutionary dynamics of range expansions is of great ecological and economical interest. While theoretical and comparative work has advanced significantly over the last years, experimental evidence for the role of biotic interactions for the eco-evolutionary dynamics of ranges is lacking, which is deeply disturbing as most range expansions will occur in a multispecies context. To understand how different biotic interactions, from positive to negative, impact the eco-evolutionary dynamics of ranges we present theoretical and experimental evidence: We used individual-based models to formalize our hypotheses and test the corresponding prediction using experimental evolution in protist microcosm landscapes. We show that different types of interactions differentially impact ecological and evolutionary dynamics, disrupting eco-evolutionary feedbacks. Specifically, competition restrained range expansions while facilitation and predation led to higher range expansion speeds. The distribution of population densities throughout the range changed from concave to convex depending on the interaction type. The differential evolution of dispersal, reproduction and competitive ability was greatly hampered by any type of interaction.

Recolonization history and selection shape MHC diversity in the European barn owl (*Tyto alba*)

Oral presentation

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Genes of the major histocompatibility complex (MHC) represent excellent candidates to study adaptive genetic diversity due to their direct link with pathogen resistance. One of most intriguing properties of MHC genes is their exceptional levels of functional genetic diversity, which is suggested to be underpinned by pathogen imposed selection. However, it remains unclear whether in natural populations the MHC evolves mainly by (i) stochastic or demographic factors, (ii) local adaptation or (iii) balancing selection. To distinguish between these scenarios, we sequenced MHC-IIβ and MHC-Iα loci using high-throughput sequencing technology in an extensive number of barn owls (*Tyto alba*) sampled throughout Europe (N=400). All samples were also genotyped with 22 neutral microsatellite markers used as a baseline to contrast with MHC diversity and genetic structure. Preliminary results suggest that MHC variation in European barn owls arise through a complex process, involving demographic and probably selective forces. This study provides interesting perspectives for the understanding of evolutionary mechanisms involved in MHC variation.

Detecting selection from linked sites using an F-model

Oral presentation

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A particularly elegant way to describe allele frequency differences among populations is the F-model, which measures differences in allele frequencies by population specific Fst coefficients. It is straightforward to extend this F-model to take into account different evolutionary forces, for instance by partitioning the locus and population specific Fst into a locus specific and a population specific component. The goal is then to identify loci with non-zero components, which are interpreted as being targets of divergent or balancing selection, depending on the sign of their inferred component. Here we present an extension of this model to linked loci by means of a hidden Markov model (HMM). While an HMM implementation of the F-model has previously been proposed to deal with linked loci when inferring admixture proportions, we will used such an HMM to characterize the effect of selection on linked markers by modeling the correlations in the the locus specific component along the genome. Using extensive simulations we then show that our method has increased statistical power as it can benefit from the signal at neighboring sites when inferring selection. We finally present that genome wide association studies from multiple populations can be interpreted as selection inference under our model, which thus offers a natural way to correct for population stratification.

Can wildflower strips positively influence pollinator visits and yield in adjacent pollinator dependent crops?

Poster

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The intensification of agricultural practices has led to a decline of wild bee diversity. Recently, concerns have raised that the ecosystem service pollination may be at risk. Therefore, wildflower strips are commonly used as a measure for counteracting the negative consequences of anthropogenic activity and promoting pollinators. It has been shown that wildflower strips have the potential to enhance wild pollinators in the surrounding, but the efficacy and economic benefit of them remain relatively unknown. We thus asked whether experimentally established wild flower strips enhance a) the abundance and diversity of pollinators on the strawberry fields, b) their pollination success and consequently yield, and c) how far does the expected positive effect of the wildflower strip spill into the strawberry field. To do so, we established wildflower strips adjacent to strawberry crops and recorded the abundance and visitation rates of pollinators, the fruit set and quality of potted strawberry plants in different distances within the crop field and compared it with fields without wildflower strips. We will show preliminary results on fruit set and the quality of strawberry fruits in crops with, and without, adjacent flower strips. We expect that the provision of a forage habitat like a wildflower strips have the potential to higher crop yields in adjacent pollinator dependent crops.

Using polymorphic characters to reconstruct the phylogeny of geoemydid turtles

Oral presentation

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Several attempts to resolve the phylogeny of Geoemydidae (a clade of 70 living turtle species) using morphology have been unsuccessful, when compared to molecular data, largely because of unusually high levels of polymorphism and homoplasy. This situation has hindered the integration of the geoemydid fossil record into a phylogenetic framework. Many methods have been developed to allow incorporating different amounts of frequency information from polymorphic characters in phylogenetic analysis, which has been shown to improve phylogenetic inference. Our goal is to explore the performance of these methods, so that further placement of fossil taxa can be reliably achieved. The methods selected were “majority”, “GFC”, “polymorphic” and “missing”. We compared the result topology of each method with a reference molecular phylogeny, from 4 nuclear and 2 mitochondrial genes. The “polymorphic coding” method was the most accurate and congruent with the reference phylogeny, but with limited resolving power (21%). GFC method yielded the best resolution, but also the worst accuracy (16%). Although we did not find a correlation between the amount of frequency information used by each method and its performance, as expected, this was the first study to assess this amount of polymorphism in Geoemydidae and recover the best accuracy.

Overexpression of the DNA repair factor dPrp19 reduces DNA damage and extends *Drosophila* life span

Oral presentation

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Mechanisms that ensure and maintain the stability of genetic information are fundamentally important for organismal function and can have a large impact on disease, aging and life span. While a multi-layered cellular apparatus exists to detect and respond to DNA damage, various insults from environmental and endogenous sources continuously affect DNA integrity. Over time this can lead to the accumulation of somatic mutations, which is thought to be one of the major causes of aging. We have previously found that overexpression of the essential human DNA repair and splicing factor SNEV, also called PRP19 or hPso4, extends replicative life span of cultured human endothelial cells and impedes accumulation of DNA damage. Here we show that adult-specific overexpression of dPrp19, the *D. melanogaster* ortholog of human SNEV/PRP19/hPso4, robustly extends life span in female fruit flies. This increase in life span is accompanied by reduced levels of DNA damage and improved resistance to oxidative and genotoxic stress. Our findings suggest that dPrp19 plays an evolutionarily conserved role in aging, life span and stress resistance and support the notion that superior DNA maintenance is key to longevity

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Competition between strains of the Lyme disease pathogen in the tick vector

Poster

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Vector-borne pathogens often establish mixed infections inside their vertebrate host as well as in their arthropod vector. Studies on interactions between strains have typically focused on the vertebrate host. Here we used two different strains of the Lyme disease pathogen, the spirochete bacterium *Borrelia afzelii*, to investigate the interactions of mixed strain infections inside the tick vector, *Ixodes ricinus*. Mice were infected with either one strain or co-infected with both strains, and were subsequently infested with ticks. We used qPCR assays to determine the host-to-tick transmission success of each strain and the spirochete load of each strain inside the ticks. The transmission rate of one of the strains was reduced in the co-infection treatment, compared to the single strain infection treatment. For both strains, we found that their spirochete load was reduced by 50% by the presence of the co-infecting strain. The present study therefore demonstrates that *Borrelia* strains compete for limiting resources inside the tick vector. Future studies should investigate whether this competition influences the tick-to-host transmission success of each strain.

Interactions between geomorphology and vegetation in the Vaud Alps: first investigations

Poster

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The plant succession in high altitude areas is controlled by time since deglaciation, debris size, micro-relief and soil development. Furthermore, the influence of earth surface processes can modify the microhabitat conditions and the plant communities. It is therefore important to study how geomorphological activity affects the distribution of plant species to predict future vegetation evolution in a climate change context. To better understand geomorphology-vegetation interactions, three focus sites in the Vaud Alps have been surveyed using different methodologies. Temperature dataloggers have been installed at ground surface in different geomorphological features to investigate the permafrost occurrence, the snow duration and the local micro-climate. Vegetation surveys were also performed in different environments to identify the main aspects of plant communities. In some cases, old surveys were repeated to observe possible changes in the floristic composition. Finally, drone flights were carried out to obtain high resolution images allowing for a detailed analysis of granulometry and geomorphology. In a next step, a semi-automated geomorphological map will be created with geostatistical methods. The map will be used together with DEM, granulometry and other environmental parameters to better understand the geomorphology-vegetation interactions and their spazialization.

Changes of nocturnal plant-pollinator interactions due to artificial light at night

Poster

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In the last century the artificial light at night (ALAN) has dramatically spread around the world but studies on this topic have only recently been addressed. ALAN is known to perturb plant and animal perception of circadian rhythms, insect navigation system and overall physiologic and behavioural activities. However, evidence of how ALAN affects community composition and related ecosystem functioning is still lacking for the terrestrial system. Here, we investigate how the structure of nocturnal plant-pollinator networks are changed due to ALAN. For doing so we selected a total of 14 ruderal and unmanaged meadows in the Bernese pre-Alps which still present low levels of light emission. Half of the sites was illuminated by a LED street lamp that automatically switched on from sunset to dawn, the others were kept in the dark as control. On each site nocturnal plant-flower visitor interactions were sampled between June and September 2015. Our study demonstrates that the structure of nocturnal plant-pollinator networks is altered due to ALAN.

Patterns of postzygotic isolation reveal possible hybridization between two closely related dung fly species in nature with sterile male but fertile female hybrids

Poster

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Characterization of phenotypic differentiation and the genetic basis of traits contributing to reproductive isolation among species are important to understand mechanisms driving speciation, but identifying the relevant traits challenges biological research. The evolution of sexual traits for mating and fertilization is interesting due to their role in the establishment of reproductive barriers to gene flow. We quantified fecundity (i.e. copulation frequency, egg production, hatching success) as indicators of postmating reproductive barriers among four populations each of the sister species *Sepsis cynipsea* and *S. neocynipsea* (Diptera: Sepsidae) occurring in sym-, para-, and allopatry. To understand the role of hybridisation in nature, we examined the resulting F1 hybrid offspring and the corresponding backcrosses with their parental species. Our study documents successful hybridisation with rare copulations in heterospecific pairings but more among F1 hybrids, implying hybrid vigour. Hatching success in F1 offspring was significantly lower, indicating hybrid breakdown. In backcrosses of F1 hybrid offspring with the parental species male hybrids showed sterility while female hybrids were fertile, according to Haldane’s rule. Overall, our study reveals strong hybrid breakdown in fecundity and fertility traits with hybrid males being most strongly affected sex by sterility.

Anthropogenic effects are associated to a lower persistence of marine food webs

Oral presentation

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The dynamics, productivity, persistence, resilience of biological communities, and the services they provide are greatly affected by the way in which species interact. It is therefore necessary to understand how human activities affect those networks of interactions. Both, interactions and impacts, occur in a spatial dimension. However, the vast majority of ecological networks are compiled at specific locations in a non-standard fashion. This has so far precluded the study of how network structural and dynamical properties are distributed across space. We manage to overcome this limitation, and in this paper we study how trophic network structure is distributed in 701 locations across the Caribbean Sea. Moreover, we provide insight on how network persistence correlates with human-driven impacts.

From SSO to NGS in HLA population studies: deciphering the fine nucleotide diversity of full HLA genes in the Mandenka from Senegal

Poster

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In the last few years, high-throughput DNA sequencing (HTS) has catalysed the molecular characterization of HLA genes, leading to a major increase of the number of known alleles and making the study of this polymorphism particularly challenging at the population level. With the aim to understand how HTS improves our assessment of genetic variation within human populations, we reanalysed 8 HLA genes in the Senegalese Mandenka. We compared the results of former PCR-SSO typings from 1992 with those of exon 2 454-pyrosequencing and whole gene MiSeq sequencing to highlight differences and merits of these approaches. We found a high frequency of alleles associated with malaria and onchocercosis. When comparing the 3 typing strategies, the “nucleotidic resolution” appears to be the main advantage of HTS whereas typing ambiguities explain the lower PCR-SSO scores. DPA1 and DPB1 (exon 2 to exon 3) are the only loci with a significant Tajima’s D. We introduce the concept of gene region mutual information to describe the amount of information in a gene region, and its (non-)redundancy with other gene regions. This comparative study shows that HTS refines our appraisal of HLA molecular variation within populations and gives important insights for population genetics studies, but still needs a thorough bioinformatics treatment to provide fully satisfactory results.

Detecting gene networks under selection in biological pathways

Oral presentation

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Understanding the genetic basis of adaptation is a central focus in evolutionary biology. This process is typically viewed as involving selective sweeps that drive beneficial alleles from low to high frequency in a population. By contrast, classical models of selection in the quantitative genetics literature emphasize the importance of modest changes in allele frequencies at many loci. Indeed, adaptive events in natural populations could occur by the evolution of polygenic traits rather than via the fixation of single beneficial mutations. Statistical tests have been developed to detect selection based on a simple selective sweep model, but frequency changes due to polygenic selection may remain below the detection limit of most of these methods. In order to better understand to what extent species adapt by polygenic selection events, we have developed a method to detect this type of selection in natural populations. The general idea is to search for subsets of interacting genes within biological pathways that present unusual features. This search is a combinatorial optimization problem that can be solved using a heuristic approach like simulated annealing. We implemented such an algorithm to search for high-scoring subnetworks of genes in biological pathways data. We applied our methodology to find evidence of polygenic adaptation in human populations.

The mosaic of karyotypes in Swiss house mouse populations: backcrossing restores karyotype and fertility of chromosomal hybrids in one generation

Poster

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How species evolve is one of the central questions of evolutionary biology. One of the possible mechanisms that lead to reproductive isolation between populations is hybrid unfitness due to chromosomal variation. The Swiss Alps harbor a mosaic of populations of house mice (*Mus musculus domesticus*) differing in their diploid chromosome number (2n=22-40) due to Robertsonian fusions. The close proximity of populations varying in karyotype offer the opportunity to study how this mosaic is maintained. We performed laboratory crosses and backcrosses over four generations with mice from two wild Swiss populations with many different fusions. While F1 hybrid males were sterile, females retained a low degree of fertility. Backcrossing of these hybrid females rescued fertility of the half of the offspring whose karyotype was restored to that of the parental population. As hybrid offspring with low fertility are expected be costly for females, we investigated female behaviour in a social test of mate preference. Females were particularly attracted to males of one of the populations, suggesting that reinforcement is unlikely to be contributing to the maintenance of the chromosome mosaic. These results suggest that the population mosaic is maintained by low fertility of hybrid offspring, together with the restoration of parental karyotype and fertility in backcrosses.

Current state of freshwater phytoplankton diversity and ecosystem functioning research

Poster

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Freshwater biodiversity is under major threat by human driven activities such as water contamination and global warming. Despite being one of the most vulnerable ecosystems, we have little knowledge on the consequences of diversity loss in freshwater lotic systems. We performed a review of the existing literature linking phytoplankton diversity to ecosystem functioning in freshwater lakes and ponds. We found 23 studies including a total of 109 experiments that directly manipulated any aspect of phytoplankton diversity and measured its influence on any aspect of ecosystem functioning. Taxonomy based metrics of diversity (e.g., species richness) were by far the dominant facet of up to date phytoplankton diversity manipulations, accounting for 88% of the experiments. Our revision revealed a plethora of ecosystem functions such as chlorophyll-a, biovolume, biomass and resource use efficiency on which the influence of diversity has been tested. Overall, half of the relationships between phytoplankton diversity and ecosystem functioning are linear positive and about another quarter are non-linear positive. Our revision results reveal that while not universal, losing phytoplankton diversity in freshwater lotic systems is detrimental for their overall functioning. More studies based on other aspects of diversity such as functional or genetic diversity are urgently required.

RECHALP A support platform for transdisciplinary research in the Alps of the Canton de Vaud

Poster

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The RECHALP project (von Däniken and al. 2014, 175-178), is the wish of the Faculty of Geosciences and the Environment (FGSE) at the University of Lausanne (UNIL) to create a priority research area in the Alps. The aim is to develop a support platform that encourages and maintains interdisciplinary research in a part of the Alps (Alps of Vaud, ca. 700 km²). This research area in the Alps is becoming one of the most documented and investigated in Europe. The support platform contains an online geo-database storing and retrieving what data and metadata exist on scientific datasets, equipment, projects and activities in the research area. A portal is homed on the UNIL's website at URL: http://rechalp.unil.ch and to date contains > 5000 metadata in the fields of natural and social sciences. This tool is available to everyone everywhere. The promotion and the introduction of the platform are currently in progress. It is now possible using the RECHALP portal to do the inventory of the data linked to the Alps of Vaud and to Lavaux, to identify geographic or environmental gaps in the existing information and to design complementary data sampling strategies. In this regard, RECHALP should open new scientific perspectives for research and teaching, especially in transdisciplinary fields of natural and social sciences.

Scanning the threespine stickleback genome for signatures of adaptation to replicated basic versus acidic habitats

Poster

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Repeated adaptation of populations to the same habitats allows identifying ecologically important genes with high confidence and exploring the history of selected genetic variants. We here take this opportunity by focusing on young stickleback populations residing in replicate basic versus acidic lakes on North Uist Island, Scotland. Basic populations resemble the typical freshwater phenotype with bony plates and spines, while acidic ones have evolved dwarfism and a vast reduction in external bony structures. Stickleback were sampled from 5 basic and 5 acidic lakes. Single nucleotide polymorphisms (SNPs) were detected using a modified RAD approach involving parallel restriction of DNA with multiple enzymes, followed by pooled sequencing. The resulting high-resolution SNP data set was used for mapping the magnitude of parallel basic-acid differentiation across the genome. Divergence mapping revealed several genome regions differentiated with high fidelity between basic and acidic populations, and examining the genes located in these regions produced strong candidate adaptation genes. Our work so far illustrates the power of using parallel evolution at a small spatial scale for detecting adaptation loci. Using genetic data from the ancestor, we will further shed light on the origin of selected variants.

Impact of chronic malaria infection on aerobic performance in migratory birds

Oral presentation

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Infections with avian malaria parasites are common in birds and can drastically reduce the performance of their hosts. Effects of infections might be particularly pronounced in migratory species as they regularly engage in demanding exercise. Although a number of effects of malaria infections have been shown, e.g. slower pace of migration, a reduced reproductive output, etc.; little is known on the mechanisms that lead to these effects. One assumed mechanism is a lower oxygen transport capacity resulting from the malfunction of infected erythrocytes which, however, has not been confirmed yet for birds. We determined the aerobic performance of malaria-infected and non-infected migrants during different stages within the annual cycle. We found that the seasonal variation in metabolic rates predominate the differences found for uninfected compared to chronically infected hosts. Our results estimate the effects of infection on host performance on a physiological level and thus, provide the basis for understanding any cascading effects infections may have on host migration ecology and ultimately, fitness.

Basal cortisol response to food shortage in early life: introduction of an experimental study conducted on captive bats

Poster

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Nutritional conditions during periods of development are of profound importance in determining the subsequent life-history trajectory of an organism. Indeed, a shortage of nutrients during early life is assumed to have long-term consequences notably by impacting the regulation of the main neuroendocrine system, the hypothalamus-pituitary-adrenal axis. We performed an experimental dietary restriction on captive mother-pup bats (*Carollia perspicillata*) hosted in a tropical zoo (Papiliorama, Kerzers). Mothers and their unique unweaned newborn were either restricted by 80% food ad libitum (N=24) or fed ad libidum (N=22). Body hair of both mothers and pups were then collected to assess the hair cortisol concentration (HCC) of each pair. Since animals confronted with reproductive challenges are predicted to increase their cortisol concentration to promote the reallocation of resources to reproduction, we hypothesized that food shortage in lactating mothers generated a prolonged high secretion of cortisol, impacting the maternal behavior thus the juvenile growth. However, we did not find any significant differences across treatments, pairs, and juveniles’ growths. Those surprising results would therefore demonstrate that individuals tend to negatively regulate their cortisol response to decrease their basal level limiting the negative costs of such physiological stress.

How are fish distributed within swiss alpine & prealpine lakes ?

Poster

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How are fish distributed within a lake? Understanding the relationship between fish and habitats is important for effective management of lake ecosystems. Restoring littoral habitats could promote fish diversity by providing additional space for feeding, spawning and as shelter from predators. The national sampling project “Projet Lac” used standardized methods to assess fish biodiversity and its distribution within and among 26 lakes. We used it to identify factors influencing the distribution of fish in the littoral zone, focusing on habitat, competition, predation, productivity and lake morphology. Investigated aspects of the fish community included species presence-absence, abundance, length, species richness and community composition. We explored whether species are associated with habitats by comparing the observed fish occurrence to a random distribution. Most fish species were positively or negatively associated with some habitats. The fish-habitat associations were species-specific and lake-specific. Eg. pike was often caught near vegetation and avoided rocky habitats, while perch was associated with boulders in most lakes, but not all. Variation in fish-habitat associations among lakes is likely driven by differences in the biotic and abiotic context. Our research can be used to guide littoral habitat restoration and implement holistic management of the lake ecosystem

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Using NGS technology to reveal evolutionary dynamics of RNA viruses

Poster

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Reconstructing evolutionary history of RNA viruses is challenging due to small genome sizes and high mutation rates. Tula virus (TULV) is an European hantavirus with a tri-segmented genome mainly associated with the common vole (*Microtus arvalis*). Phylogenetic reconstruction based on partial genomic sequence revealed strong geographic structuring of highly diverged clades. However, their deep evolutionary relationships remain unclear. In this study we aim to produce full genome sequence data using next generation sequencing to reconstruct the deep evolutionary history of TULV strains and their distribution in Europe. It is our goal to establish a method to enrich the virus genomic material compared to host background to obtain comprehensive viral sequencing depth and coverage for a broad sample range. This deep sequencing data may further inform about multiple infection, reassortment and potential recombination between virus strains at local scale. We already found evidence for multiple infection and reassortment in TULV from partial genomic sequence data. It is therefore possible that reassortment played a role earlier in TULV evolutionary history. The knowledge we gain from studying this virus in its natural system could help us to understand basic principles of virus biology and evolution.

The genomic basis of experimental evolution of aging in *Drosophila*: how individual SNPs affect lifespan

Poster

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Both diet and reproduction are known to have a strong influence on lifespan and aging in a wide-range of animal species. In our project we study a unique set of experimentally evolved (EE) *Drosophila melanogaster* lines that have evolved an extended lifespan in response to selection on postponed reproduction and/or developmental over- or undernutrition. Genome analyses have revealed consistent differences in SNP allele frequencies that correlate with the observed variation in lifespan. In order to test how alternative SNP alleles affect lifespan, we used lines from the Drosophila Genetic Reference Panel to reconstitute outbred populations with a diverse genetic background that differ consistently only at the specific SNP position of interest. We used this approach to test 5 SNPs in the genes hppy, Doa, Eip75B and sickie. This approach demonstrates that individual SNPs have significant effects, and can both extend or shorten lifespan. We discuss these results in the context of life history evolution.

Early farmers from across Europe directly descended from Neolithic Aegeans

Oral presentation

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The introduction of farming and sedentism was one of humanity"s major evolutionary steps. Farming first appeared in southwestern Asia during the early Holocene and later spread to neighboring regions, including Europe, along multiple dispersal routes. One of the most enduring and widely debated questions in prehistoric archaeology concerns the origins of the European earliest farmers: Were they the descendants of local hunter-gatherers, or did they migrate from southwestern Asia, where farming began? Palaeogenomic data from five Neolithic individuals from northern Greece and northwestern Turkey spanning the time and region of the earliest spread of farming into Europe demonstrate a direct genetic link between Mediterranean and Central European early farmers and those of Greece and Anatolia. The European Neolithic migratory chain unbroken back to the Aegean precludes the notion that farming spread into and across Europe via the dissemination of ideas but without, or with only a limited, migration of people.

The extent, direction and temporal dynamics of gene flow in an introgession zone in the genus *Arabidopsis*

Poster

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In the genus *Arabidopsis*, gene flow between species, major evolutionary lineages, and even across ploidal levels is common. However, apart from two allotetraploid species that have been investigated in detail, the extent and temporal dynamics of gene flow and hybridization are not well understood. An introgression zone, with tetraploid *A. arenosa* introgressing into *A. lyrata* subsp. *petraea* in the Eastern Austrian Forealps and subsequently expanding northwards, was described previously and provides an outstanding study system, as adaptive introgression might be responsible for their colonization of northern habitats dominated by siliceous bedrock. We investigate this complex system in unprecedented detail using whole-genome data. With a combination of nuclear and chloroplast data, the extent, direction and temporal dynamics of gene flow are further elucidated. Genetic clustering of nuclear data confirms the introgression zone, but also reveals that hybridization is more common than previously thought. Using chloroplast phylogenomics based on complete chloroplast genome sequences and secondary calibration, we date the first establishment of hybrids is dated to the Pleistocene, likely during one of the last interglacial periods and with secondary contact at the northern and possibly southern border of the introgression zone occurring in the Holocene.

Local adaptation remains local: environmental associations of climate-related candidate SNPs in *Arabidopsis halleri* using an independent population set

Poster

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Numerous landscape genomic studies using next-generation sequencing and environmental association analyses have published lists of genes or genomic regions that are potentially involved in adaptation to the environment. However, most of these studies did not explicitly validate the generality of their findings, i.e. tested if the patterns and associations found also hold true in independent datasets such as in different areas of the natural range of a species. In this study, we aimed at testing whether 74 putatively adaptive and climate-related SNPs of the Brassicaceae *Arabidopsis halleri* show the same association to topo-climatic factors in an independent set of 18 populations. The candidate SNPs were previously identified in five populations using whole-genome next-generation pooled sequencing and a combined outlier/environmental association analysis. For the independent dataset, we used the same environmental association approach and individual SNP genotyping. Although 40% of the SNPs showed an association to at least one environmental factor in the independent dataset, only 5% of the SNPs were associated with the same factor as in the original dataset. Our results suggest that the loci and patterns identified are truly local and that their generality is not given. Our findings imply that the generality of a locus being under selection has to be explicitly tested.

Sub-lethal effect of a neonicotinoid insecticide in the house sparrow

Poster

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Neonicotinoids pesticides are commonly used in agriculture and can be ingested by non-target species via coated seed and arthropods. Both sources of food constitute an important part of the diet of many passerine birds especially while raising offspring. We experimentally tested the effects of a non-lethal dose of acetamiprid on house sparrow *Passer domesticus*, a species that feeds both on seeds and arthropods during the breeding season and is strongly linked to human activities. A total of 112 birds were dispatched in 14 aviaries and divided in two groups receiving an oral dose of acetamiprid or a placebo. We collected feathers and blood samples before and after the experiment to investigate markers of physiological and oxidative stress. The ingestion of acetamiprid had no effect on the oxidative status of birds. However, although all individuals seemed to reduce the amount of the stress hormone corticosterone deposited into their feathers during the experiment, males dosed with acetamiprid maintained higher levels of corticosterone. Our results show that very small doses of acetamiprid may disturb the hypothalamus-pituitary-adrenal axis and impair the regulation of stress in males. This finding is to be seriously considered because such sub-lethal effects add up to the many perturbations that modern agricultural practices cause to bird populations.

Are polyploids ecologically and genetically different from their diploid progenitors: The case of *Aegilops* spp.

Poster / FlashTalk

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Polyploid organisms result from the merging of genomes from the same or different species. To what extent the addition of two genomes affect ecological requirements is largely unknown. Here, we investigated the ecological niches of eight mostly Mediterranean *Aegilops* species: four diploids that differentially combined in four derivative tetraploids. A common background study for all eight species was designed based on biomes distribution and precise georeferenced occurrence data. It was used to define species niches based on 20 environmental factors. The additivity of diploid parental niches compared to that of the derived polyploid was tested using “ecospat” Rpackage. For three polyploid species, the analyses demonstrated strong niche stability with an expansion towards more temperate ecological requirements. In contrast, one polyploid species showed an important niche retraction compared to those of its diploid progenitors. Consequently, the results support an evolution of the polyploid niche in relation to the genetic origin of polyploids, which may be a key factor in the success of polyploidy.

An identification key for habitats in the agricultural landscape

Poster

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ALL-EMA is a long-term biodiversity monitoring program of the agricultural landscapes in Switzerland. For a reproducible habitat type identification a classification key was developed. In the key 86 habitat types of the agricultural landscape are distinguished, following the habitat typology of Delarze et al. (2008) on habitat type level. The identification of the habitat types with the key only takes an average of 3.5 min. Controls showed that over 90% of the habitats had been allocated correctly. The key yields fast and reliable results, given that the user has profound botanical knowledge.

Evolution of pheromone mimics in sexually deceptive orchids *Ophrys*

Poster

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Pollination by deception is very common amongst orchid species, with nearly one third being food deceptive and another 400 species being sexually deceptive. Sexually deceptive orchids attract male pollinators by mimicking the pheromones of female virgin bees. In many species of the sexually deceptive orchid *Ophrys*, plant pheromone mimics are comprised of alkanes and alkenes, with each species having a unique blend of hydrocarbons, varying in chain length and double bond position. Pollination is highly specific as each orchid species usually attracts one species of pollinator, and the pheromone mimics mediate reproductive isolation in the genus *Ophrys*. The genes underlying biosynthesis of these hydrocarbons may potentially be speciation genes. Hydrocarbon synthesis involves fatty acid elongation by β-keto-acyl-CoA synthase (KCS), putatively responsible for chain length differences. Since different species of *Ophrys* produce varying chain lengths, they might either have different KCS variants or differential expression of KCS. In this project, phylogenetic analysis was carried out to investigate the evolutionary history of the orchid KCS gene family. This allowed us to test for lineage-specific genes, and to hypothesize when functional change (or gene expression change) arose, if changes occurred in parallel, and if any of these genes were likely under selection.

Strategic adjustment of helping behaviour in the cooperatively breeding cichlid *Neolamprologus savoryi*

Poster

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Helping behaviour in cooperative breeding systems has been intensively studied in many species of birds and mammals, and in a few species of fish. Here, helpers engage in brood care, territory defence and shelter maintenance. These tasks can be unequally shared among group members, depending on their body size, sex, and status. Shelter maintenance involves digging out sand, which is costly in terms of energy expenditure, but essential for protection from predators. The highly social cichlid *Neolamprologus savoryi* is a hitherto little studied model system for the adaptive value of seemingly altruistic helping behaviour. We asked how breeders and helpers in this species share the costly effort of shelter maintenance, and how their investment is influenced by the presence of dependent young. Therefore, we conducted a field experiment aiming to increase the workload of group members by adding sand to the breeding shelter. Groups were selected according to the presence or absence of helpers and dependent young. We find clear evidence that the presence of dependent young increases the workload of digging, which is highly skewed toward breeding females and large helpers. The latter's effort reduces the workload of females, and is strategically adjusted to need. Our results highlight the specialisation of brood care helpers in a costly cooperative task in a highly social cichlid fish.

Phylogeography of the middle spotted woodpecker *Leiopicus medius*

Poster

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The climate of the last 2.5 million years was dominated by alternating glacials and interglacials. Expansion of glaciers and tundra in the Holarctic region led to shrinking of suitable habitats for many species and to population isolation in southern refugia. During interglacials dispersal into formerly unsuitable regions was possible again. These processes shaped the current genetic structure of many species and left signatures that are often still detectable in today's populations. The middle spotted woodpecker is widely distributed in the southern West Palearctic and specialized to old deciduous forests. We used environmental niche modelling to infer the location of glacial refugia for this species based on past climate models. Multigene phylogeographic analyses were applied to reconstruct its population history. We found strong genetic divergence between populations to the west and east of the Bosporus, implying a split at 1.5 million years ago. Both clades showed signs of population expansion after the last glacial maximum. The data suggests glacial refugia in southeast Europe for the western populations and in the Caucasus or Iran for the eastern populations. Interestingly however, the middle spotted woodpecker is morphologically a rather homogeneous species. Moreover, such a phylogeographic pattern was not described in birds before.

Preweaning mortality in wild brown hare leverets (*Lepus europaeus*)

Poster

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Increased postnatal leveret mortality – i.e. low recruitment – was identified as an important factor explaining the decline of brown hare (*Lepus europaeus*) populations in Switzerland. However, direct measurements of factors affecting leveret mortality are sparse. This might be because brown hare leverets behave very cryptically, which makes them difficult to study. We used thermal imaging (hand-held and airborne) and a specially trained detection dog to locate brown hare leverets. We radio-tagged 65 leverets in two different study sites in the Swiss lowlands, in order to monitor their individual fate. As agriculturally managed landscape is the main habitat for the hare, we were interested to see which agricultural land-use types are positively related to leveret survival. More specific we wanted to know whether survival in fallow land particularly designed for the needs of leverets ('hare fallows') are indeed positively related to leveret survival. We were further interested in the effect of precipitation, minimum temperature, field size and distance to the edge on leveret survival. Results show that survival varied according to different agricultural land-use types while sugar beet was positively related to leveret survival. Precipitation had a negative effect on leveret survival yet all other factors did not influence leveret survival. We found a large positive effect of 'hare fallows', indicating that its design does not miss the intended effect.

Patterns of neural activation during helping in a cooperative breeder

Poster

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To understand the evolution of proximate mechanisms underlying cooperation it is essential to integrate questions about the adaptive value with molecular genetics and neurophysiological approaches. Due to the diverse and complex nature of the information that needs to be integrated during decision-making processes in a cooperation context, patterns of brain activation might differ from those in other types of social interactions. We quantified the expression of egr-1, a marker for neural plasticity, in four major brain regions following a helping stimulus in a cooperatively breeding cichlid fish. First, we searched the genome for potential targets of the transcription factor coded by egr-1. Second, we investigated whether the exposure to a helping stimulus influenced egr-1 gene expression. We found that egr-1 is likely to regulate the expression of genes implicated in neural development and steroid hormone signaling pathways. Fish exposed to the helping stimulus expressed less egr-1 in the telencephalon and the cerebellum than control individuals. This was contrary to our expectation of enhanced neuroplasticity in the novel test situation. However, as potential targets of egr-1 included developmental genes that often act as repressors, a reduction of egr-1 expression might ultimately result in increased neuroplasticity.

Reproductive barriers and hybridization between co-flowering heterostylous primroses: integrating experimental and genomic approaches

Oral presentation

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Flowers enable the evolution of complex relationships with pollinators, promoting reproductive isolation (RI) and diversification. Features of corollas and reproductive organs can facilitate RI by attracting different pollinators or restricting interspecific pollen transfer. Floral RI is thought to play a major role in restricting interspecific gene flow, a notion largely relying on studies of specialized plant-pollinator systems. Knowledge about floral RI in plants with generalized pollination systems remains insufficient. We compared floral and postmating RI between distylous primroses (species with two floral morphs per population) pollinated by the same insect species with chemical, morphological, experimental, and genetic data. Floral scent and color differed significantly between species. Floral RI was absent in *Primula veris* and weak in *P. vulgaris*. Floral RI and early-acting, postmating barriers were weak and asymmetric between species and morphs. Natural hybridization rate was modest, suggesting that early-acting barriers prevent hybridization. Intermixed individuals were F1 hybrids, implying that strong, late-acting barriers prevent introgression. To conclude, floral isolation was negligible between *P. veris* and *P. vulgaris*, corroborating the theoretical expectation that it is less likely to evolve in plants with generalized than specialized plant-pollinator systems.

Weeds, their seed bank and seed predation in Swiss vineyards

Poster

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In order to create productive and sustainable agricultural systems requiring a minimum of external inputs, the interactions between the biological components of these systems and the influence of management on them have to be studied in further detail. Therefore, this thesis, which is embedded in the PromESSinG project, aims to investigate the interactions between the weed community, the soil seed bank and seed predation by ground beetles in Swiss vineyards and how these three parameters are influenced by weed management. Data on abundance and diversity of the biological components were collected in summer and autumn of 2016. The study sites were located in the canton of Valais and varied in their weed management in terms of no, complete or alternating (in every second row between the wine plants) removal as well as in removal technique (mechanical or chemical). Preliminary results show, that row treatment clearly influences weed abundance and might also have an effect on seed bank abundance and diversity. By disentangling the different aspects of weed management and interactions determining abundance and diversity of important biological parameters, the ultimate goal of this study is to contribute to the knowledge how weed management in vineyards can be at the same time economically profitable and supporting biodiversity in the production system itself.

Dynamics of global warming effects on the phenology of a widespread ectotherm

Poster

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In many organisms, the timing of life cycle events – known as phenology – has become substantially earlier in recent decades as a result of climate warming. These changes can have important ecological, economic and health consequences. Here we compile long term observations of 54 species of adult Odonata in Europe to show that sensitivity of apparent phenology to temperature changed from 1980 to 2013 along latitude and elevation. Our results suggest that sensitivity to temperature of ectotherms may either increase or decrease in the future depending mostly on the warming of winter and the current timing of the life history trait, that is whether the phenological event is before or after the peak photoperiod of the year.

Small Scale Spatial Patterns in Experimental Grasslands

Poster

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Recent ecosystem function and biodiversity research focuses on community or larger scale effects, and how these might change with biodiversity decline. Unfortunately, these studies provide only little insight to very small scale dynamics, which are the basis for the community wide observations. Specifically in grasslands, studies should consider the small plant individual size and their resulting small horizon for experiencing environment. In this study we exploit a gradient of functional diversity and species richness established in experimental grasslands of the Jena Biodiversity Experiment in 2010. We mapped the spatial grid patterns of plant species in 80x80 cm areas with a resolution of 1x4 cm. 138 communities differing in species number and composition have been sampled both in fall of 2014 and 2015. First explorative results indicate an increased stability of species specific spatial patterns with increasing species richness, whereas monocultures exhibit a higher non-directional fluctuation in area. By analyzing these patterns and their shift between years we expect to gain more insights into the association of plant species, their spatial organization, the stability of resulting patterns, and whether these are affected by diversity.

Functional diversity of peatland testate amoebae: finding relevant traits to assess the response of communities to ecological stress

Poster

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Human impact is increasingly threatening ecosystems. This affects living organisms and their functions and understanding these impacts and the ability of ecosystems to recover is essential. Most studies on ecosystem patterns focus either on taxonomic or on ecosystem processes, but typically ignoring the link between the two: the functional characteristics of species. Indices providing quantitative measures of key "ecosystem service providers" are required to estimate the ability of ecosystems to perform their functions effectively. One way to achieve this is to estimate services through the functional diversity of organisms in the ecosystem and focusing on key groups of organisms related to a given service. High functional diversity and redundancy and connections should allow ecosystems to be resilient towards stresses and disturbances. The diversity of functional traits of species involved in the response to environmental filters can be used to estimate ecosystem functioning. We address this question in a mesocosm experiment of Sphagnum peatlands with water table manipulation. We found that taxonomic and functional diversities of testate amoebae, a group of protists building a shell, were both strongly affected by the induced stress and indicate the evolution of the ecosystem by giving direct information on how changes in water table level impact ecosystem functioning.

Conservation biology of specific biotic interactions: the case of the lycaenid butterfly *Maculinea alcon*

Poster / FlashTalk

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Biotic interactions broadly influent organismal evolution and diversity. For instance, the strong association with a specific plant in a large number of herbivorous insects and consequent host plant-driven evolution have been acknowledged to explain the high species richness of insects. Here, we ask, whether host-based specialization is always supported by lineage sorting, by focusing on three morphologically similar ecotypic forms of the lycaenid butterfly *Maculinea alcon*. These ecotypes use each not only a specific host plant, but they socially parasitize distinct ants and occur in different type of habitats: hygric low-elevation, xeric low-elevation, and xeric high-elevation. Whereas such a multiple ecological constraint might be theoretially supported by a genetic differentiation of each forms, no significant distinctive molecular traits were revealed so far using classical Sanger sequencing, microsatellite or allozyme markers. In this study, we use a dataset of 1,393 Single Nucleotide Polymorphisms (SNPs) loci obtained by whole-genome RAD-sequencing of 26 specimens originating from an area ranging from Western to Eastern Europe. We discuss the results in light of how conservation strategies should apply to population-level genetic polymorphisms, when resulting phenotypes develop in contrasting ecological habitats.

The influence of Nardion grassland degradation on orthopterans in the Bernese Pre-Alps

Poster

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The Cantonal Office for Agriculture and Nature of Berne noticed a decrease in the rare species-rich *Nardion* grasslands within the last 30 years although these grasslands were extensively managed. To find key factors for the degradation of these grasslands we surveyed the vegetation in 52 grasslands of the Bernese Pre-Alps. The grasslands were either intact or degraded because of a cover increase of *N. stricta* or eutrophic plant species. In addition, we recorded orthopterans since they are good bioindicators for ecosystem degradation and include the degradation impact on higher trophic levels. We assessed their density and species richness with a biocenometer combined with additional visual and auditory survey. To investigate the management of the grasslands we interviewed farmers and analysed soil samples. The data shows that orthopteran richness and abundance is lower in meadows than pastures due to lower differences in vegetation height and direct mortality by mowing machines. Further on, an increasing cover of *N. stricta* reduces the species richness. Differently, species richness is positively influenced by the cover increase of eutrophic plant species. Both can be explained by the orthopteran preferences for diverse diet and plants with fine leaves. Conclusively, plant species-poor and *N. stricta* dominated *Nardion* grassland should be reduced with appropriate management practices.

Into the genomic wild: exploring real-time selective allele frequency shifts, in Stickleback, through a release experiment

Poster

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The fundamental question of how, and to what pace, genomic selection enables species to adapt to divergent environments remains open, and experiments addressing the molecular consequences of divergent selection, in real time, are scarce. The Stickleback (*Gasterosteus aculeatus*) from Konstanz Lake region, Central Europe, show divergence in phenotype and genotype associated with ecological differences, between lake and stream habitats. Using these populations, we established an experiment to investigate rapid evolution in allele frequencies driven by natural selection. We generated thousands of F2 hybrids, by crossing lake and stream individuals, then releasing the juvenile hybrids into the wild, on previously inhabited and controlled streams. One year after the release, we sampled the individuals that survived environmental selection and are establishing. We are now able to follow natural selection, in real time, based on whole-genome sequencing data, through the comparison of the genetic makeup of the survivor cohort with that of the initially released population. We will explore whether selective allele frequency shifts are strong enough to be detected, based on genome-wide markers, within a generation, thus contributing to shed light into the tempo and mode of selection in the wild, giving further understanding on the link between molecular evolution and ecology.

Long-term effects of wetland mowing on breeding birds: evidence from a 30-year experiment

Poster / FlashTalk

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Habitat destruction is the first cause of biodiversity loss worldwide. Wetlands are amongst the richest, yet most threatened types of habitats on earth. One major threat is the modification of water regime for human activities, which disrupts normal ecosystem equilibrium. In lacustrine wetlands, reduced flooding causes shrubs to take over, ultimately leading to a shift towards woody communities. To counter this, wetland managers have set up a variety of measures, including mowing, burning, and pasturing. Because of the short time frames of the previous studies on the subject, little is known on their potential negative side effects on the ecosystems. Here, we evaluate the long-term effect of mowing on breeding populations of the five most abundant bird species in our central European study area. This study of an unprecedented timescale (30 years) shows that rotational mowing as in our setup has no long-term detrimental effects on birds. However, optimal mowing regime for the birds might often be less frequent than what is usually applied. To overcome that, we discuss additional measures that could be implemented in complement to mowing. Because of the widespread distribution of the target habitat and species, our study provides readily applicable information for wetland managers worldwide.

A balance between biodiversity and hay production in mountain semi-natural grasslands

Oral presentation

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A long history of traditional management has resulted in a rich assemblage of species in Alpine semi-natural grasslands. However, in recent decades, pressure to increase agricultural productivity has led to management intensification, a practice that is known to have negative impacts on grassland biodiversity. To address this problem, we initiated an experiment in meadows across the Swiss Alps in 2010. The aim of this research project was to find a balance between hay production and biodiversity conservation. Field surveys demonstrated that plant species richness and phylogenetic diversity decreased under high intensification, but were maintained at low and medium intensification levels, compared to control plots. The abundance of ground beetles was positively correlated with intensification, while that of spiders was highest at low and medium intensification levels. As expected, hay production increased with management intensification and so did nitrogen yields, a measure of the hay quality. The study's results indicate that a tradeoff between biodiversity and yield could be possible at low to medium management intensity level, where an acceptable yield can be obtained while retaining considerable grassland. The study outcomes will contribute to the development of new guidelines for the future development of montane and subalpine agricultural systems.

Sexual reproduction as bet-hedging

Oral presentation

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In evolutionary biology, bet-hedging refers to a strategy that reduces the variance of reproductive success at the cost of reduced mean reproductive success. In unpredictably fluctuating environments, bet-hedgers benefit from higher geometric mean fitness despite having lower arithmetic mean fitness than their specialist competitors. We examine the extent to which sexual reproduction can be considered a type of bet-hedging, by clarifying past arguments, examining parallels and differences to evolutionary games, and by presenting a simple model examining geometric and arithmetic mean payoffs of sexual and asexual reproduction. Sex typically has lower arithmetic mean fitness than asex, while the geometric mean fitness can be higher if sexually produced offspring are not identical. However, asexual individuals that are heterozygotes can gain conservative bet-hedging benefits of similar magnitude while avoiding the costs of sex. This highlights that bet-hedging always has to be specified relative to the payoff structure of relevant competitors. It also makes it unlikely that sex, at least when associated with significant male production, evolves solely based on bet-hedging in the context of frequently and repeatedly occupied environmental states. Future work could usefully consider bet-hedging in open-ended evolutionary scenarios with de novo mutations.

Occurrence and evolution of six sexual development genes in Lake Tanganyika cichlid species

Poster

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Within the animal kingdom, sex determination mechanisms are particularly diverse in fishes including different genetic systems and environmental factors. In addition, the genetics of sexual development show some variations depending on the species studied. The three East African Great Lakes Victoria, Malawi and Tanganyika (LT) are home to the most diverse extant vertebrate adaptive radiations comprising ~2000 different cichlid fish species. The cichlid assemblage of LT is genetically and morphologically the most diverse one and benefits from a well-established phylogeny. With this, it is an ideal model system to investigate how is sex determined, how different sex chromosomes evolve and how this contributes to speciation eventually. This is so far unknown for all but a handful of cichlid species. As a first step, in this study, we analyzed the genomic region of six prime candidate genes implicated in sexual development (cyp19a1 (A-, and B-copies), amh, dmrt1, gsdf, wnt4 (A-, and B-copies), SOX3) in males and females of 250 Lake Tanganyika cichlid species. We investigate those genes for presence/absence in the cichlid genomes and their sequence evolution to determine how those sexual development genes contribute to the variability of sexual development, and to determine which genes are more conserved or derived between taxa.

Understanding the newcomers: ecological and socio-economic impacts of woody invasive alien species in East Africa

Poster

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During the last century, exotic woody species have been introduced in East Africa to provide goods and services to rural livelihoods. However, some of these species escaped from the original plantations and now invade agricultural land and natural ecosystems, having both positive and negative impacts at the same time. To be able to develop woody invasive alien species (IAS) management strategies and prioritize management efforts, it is important to better understand how positive and negative impacts of woody IAS relate to the cover of these species and what their net socio-ecological impact is. We hypothesised that the net impact is positive at low cover of woody IAS and becomes negative at higher cover levels. In each of four areas in Ethiopia, Kenya & Tanzania, ten communities were selected along a cover gradient; in each community, socio-economic impacts were assessed through household interviews and ecological parameters were measured in replicated field plots with different IAS cover levels. For a comparison of the environmental and socio-economic impacts, the results were integrated at the community level, using remote sensing for IAS cover data at the community level. Here we present combined ecological and socio-economic data collected along a *Prosopis* cover gradient in Kenya and discuss the possibilities such a direct socio-ecological integration and comparison offers.

Effects of an early-life stress exposure on adult resistance to oxidative stress, plumage color and sperm performance

Poster

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Early-life stressful conditions can shape individual phenotypes and ultimately influence fitness. Oxidative stress is a pervasive threat that affects many fitness-related traits and can modulate life-history trade-offs. Yet, the extent to which exposure to oxidative stress during early life can have long-lasting effects on key fitness-related traits remains to be elucidated. Using a wild-population of great tits, we experimentally mimicked an acute exposure to oxidative stress in 11 days-old birds by dosing them with paraquat, the active component of a widespread herbicide. One year later, we recaptured 39 of them as adult breeders and quantified effects of the paraquat exposure on their resistance to oxidative stress, plumage reflectance and male sperm performance. The pre-fledging exposure to paraquat had surprisingly positive effects on resistance to oxidative stress measured at adulthood. Further, paraquat-dosed females had a brighter plumage, an effect that was not observed on male plumage or sperm performance. For the first time in a natural population of vertebrates, we experimentally show that an early-life acute exposure to oxidative stress has long-term positive effects on individual ability to resist oxidative stress, and hence potentially on their fitness.

The genomic landscape of incipient speciation in the presence and absence of intrinsic barriers

Poster

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Incipient speciation is a key process that underlies the rapid emergence of biodiversity. Species from temperate environments in particular frequently evolved distinct adapted ecotypes during post-glacial range expansion, where gene flow between ecotypes is often still possible due to the lack of intrinsic postzygotic barriers. Alternatively, speciation can occur rapidly if such postzygotic barriers emerge, often resulting in ecologically similar yet geographically isolated species. While theoretical and empirical developments have advanced our knowledge on how patterns of genomic divergence evolve during ecology driven speciation, we lack direct comparisons to speciation events with intrinsic postzygotic barriers. Here we aim to fill this gap using population genomic data from across the post-glacial species range of North American *Arabidopsis lyrata*. Comparing the genomic architecture of substrate associated ecotypes with the architecture underlying the repeated shift from outcrossing to self-fertilization, we predict intrinsic postzygotic barriers such as self-fertilization to be associated with fewer yet broader peaks of divergence due to increased linkage disequilibrium. We find empirical evidence for our hypothesis and subsequently test how the shift towards self-fertilization may potentially also affect substrate associated ecotype formation.

Adaptive population divergence in *Asellus aquaticus*?

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Adaptive population divergence is often driven by divergent natural selection, but the agents of selection are rarely identified. Phenotypic differentiation during ecotype formation can arise because habitats vary in the number, identity, and interactivity of selective agents. However, experimental manipulations of selective agents are rare, and so we have poor mechanistic explanations for most instances of adaptive population divergence.

The freshwater isopod *Asellus aquaticus* occurs in both vegetated and non-vegetated habitats, and exhibits habitat specific variation in its level of pigmentation. Fish predation likely mediates the evolution of pigmentation, but this has not been tested experimentally. To test this, we performed an outdoor mesocosm experiment (40 x 1000L mesocosms) to test for the interactive effects of fish (stickleback: *Gasterosteus aculeatus*) and macrophytes (*Myriophyllum* sp. and *Chara* sp.) on the abundance, body size, and pigmentation of *A. aquaticus*.

We found that stickleback strongly reduced the abundance of *A. aquaticus*, but reductions were stronger in the absence of macrophytes. Furthermore, we found a strong positive relationship between pigmentation and body size, which however was modified towards stronger than expected pigmentation in vegetated mesocosms. Our results provide experimental evidence that fish and macrophytes can interactively affect adaptive population divergence of freshwater isopods.

Don’t overlook temperature fluctuations: Importance of Jensen’s inequality in predicting thermal physiology of ectotherms

Poster

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Climate change is a major threat to biodiversity, particularly to ectotherms. Constant temperature has generally been applied to investigate the ecological responses of organisms to climate warming. However, natural populations experience daily and seasonal variation of temperature, which may alter the physiological responses of organisms. Here, we (1) investigate the effect of temperature fluctuation on development rate of sepsid flies (Diptera: Sepsidae) and (2) predict physiological responses to temperature fluctuation using the thermal performance curve (TPC). We conducted a common garden experiment including three temperature treatments (18°C, 15-21°C and 11-25°C), two photoperiods (16L/8D, 12L/12D), and two populations for each of the four study species. We found that flies raised under high temperature variation and longer photoperiod had faster development rate, which reveals that fluctuating temperature induces faster development than occurs under constant temperature. We then used the TPC to theoretically predict the development rate under constant vs. fluctuating temperature, and correlated these predicted estimates with those observed in our laboratory experiment. We found a high correlation between the predicted and observed development rate, which highlights that TPC yields reliable estimates of the effects of both constant (average) and fluctuating temperatures.

Females of the cooperatively breeding cichlid fish *Neolamprologus pulcher* show size dependent mating preferences

Poster

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Mate choice is a central behavioural mechanism of sexual selection. Still, it is thought to play a minor role in cooperative breeders, where individuals may not have the opportunity to choose the optimal mate due to limited mating opportunities. Evidence of mating preferences in such complex social systems hitherto comes mainly from correlational studies on extra pair reproduction. There is currently a lack of experimental studies of mate choice in cooperative breeders. Here we investigated the role of mate choice in the cooperatively breeding cichlid fish *Neolamprologus pulcher* that shows a size dependent hierarchy, with larger fish having a higher probability to reproduce successfully. We investigated female mating preferences for large body size in a standardized choice experiment. When given the opportunity to simultaneously choose between two males of different size, females showed a high preference to spawn with the bigger males. This preference was absent when females were tested in a no-choice paradigm, where either one small or large fish was presented to the female. This is the first manipulative study demonstrating mate choice in a cooperative breeder. More generally, it increases our understanding of hitherto neglected mating preferences in systems where mate choice opportunities are limited.

Extreme sink and source manipulation experiment carried out in the large scale aeroponic system on the tropical tree *Ceiba pentandra*

Poster

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Carbon allocation within trees depends on the coupling of source organs (canopy) and sink organs (root system), but the extent and regulation by either environment and/or physiology are still largely unknown. This knowledge gap is mainly a result of the inaccessibility of the root systems. One of the approaches to address canopy-root system coupling and its regulation is sink and source manipulation. Often this is performed by affecting the source organs, e.g., leaf shading, stem girdling, branch removal. During this study we performed extreme manipulation on root system by reducing its mass by 0% (control), 33% and 66%. With the help of stable isotopes (13C) we were able to test whether and to what extent changing sink strength affects source activity and carbon allocation. For this project trees were grown in a unique large scale aeroponic system called Sarah Racine Root Research Laboratory at Tel Aviv University, Tel Aviv, Israel. To the best of our knowledge, the Root Laboratory is the only of its kind worldwide. Study results indicate fast response to the root manipulation suggesting that carbon allocation is strongly driven by sink strength.

Extrafloral nectary-mediated ant-plant interactions in temperate zones: Insights from the Swiss Southern Alps

Oral presentation

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Extrafloral nectaries (EFNs) mediate one of the most common facultative and often mutualistic ant-plant interactions: The EFNs secrete a sugary reward to attract the ants that, in return for this valuable food source, defend the plant from herbivores. These interactions are well documented in the Tropics and Subtropics, whereas they are poorly studied in the Temperate Zone. In this study, we focus on the diversity of EFN-bearing plants in the flora of the Swiss Southern Alps, where we explored their systematic diversity, functionality, and seasonal patterns in nectar secretion and interaction with ants. We confirmed EFNs presence in at least 25 species from 13 plant families, 1 fern genus and 16 angiosperm genera, half of which are exotics (incl. invasives). EFNs were functional and attracting ants in almost all species. The species surveyed in 2016 for seasonal patterns differed in their nectar secretion period due to different EFN phenologies. EFNs were active and ants present as early as late Winter (early March), though most activity in native species was observed in Spring, while that of non-natives extended into Summer. Therefore, EFN-bearing exotics likely represent an additional food source for local ant communities, raising new questions about their ecological role in the ecosystems where they occur.

Tiny but powerful – testate amoebae as indicators of past environmental changes

Oral presentation

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Testate amoebae (TA) are microorganisms abundant in wetlands all over the world. They play an important role in peatlands where they are top predators in the microbial food web. TA are used in palaeoecology to quantitatively reconstruct changes in water table depth over time. In the presented study we explored the use of functional traits of TA as an “early warning” indicators of disturbances affecting peatlands. Disturbances such as fire and peat extraction often cause water table lowering, with long lasting effects on local microbial communities. Under ongoing climate and land use changes disturbed peatlands may become carbon sources instead of sinks, and we need a tool to anticipate such risks. For this reason we analysed functional traits of TA from two Sphagnum peatlands which had experienced fire and peat extraction in the last 2000 years. We used structural equation modelling to test the effect of disturbances on the linkages between TA community structure, functional trait composition and functional diversity. Our results show that two traits: ‘mixotrophy’ and ‘plagiostomic apertures’ are related to disturbances over the long time-scales (decades to century). We observed a loss of mixotrophic TA and an increase of TA possessing plagiostomic apertures during and post-disturbance and we suggest that those two traits can be used as proxies for peatland disturbance.

Fungal and algal diversity within lichens

Poster

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As composite organisms, lichens (systematically lichenized fungi) consist of a fungal partner (mycobiont) and one or more photosynthetic partners (photobiont). Lichens act also as unique microhabitats for diverse fungal, algal and bacterial communities – microorganismal diversity that is still poorly known. We metabarcoded the fungal and algal diversity in 100 epiphytic lichen species from Switzerland using fungal- and algal-specific molecular markers in high-throughput 454 sequencing in a GS FLX System. Besides the expected mycobiont, many other fungi were identified within our samples – on average 10 fungal lineages per a lichen sample. Several of these were identified as highly specific lichen-associated or plant-associated fungi, while others seemed to be substrate generalists. The algal diversity comprised terrestrial green algal lineages specialized on lichen symbiosis (e.g. genera *Asterochloris*, *Symbiochloris*, *Trebouxia*) as well as free-living taxa (e.g. *Apatococcus*, *Chloroidium*, *Coccomyxa*). Only about ten percent of the sequenced taxa were identified to the species level using the NCBI nucleotide database as reference, indicating the lack of knowledge in lichen microorganismal diversity.

Maternal allocation of carotenoids increases tolerance to bacterial infection in brown trout

Oral presentation

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Life-history predicts that iteroparous females decide each breeding season how much of their resources they invest into somatic maintenance or reproduction. In salmonid fish, females often vary the size and number of their eggs and the compounds they allocate to their clutch, including various carotenoids whose functions are not sufficiently understood yet. We sampled 35 female brown trout from a natural population, experimentally fertilized their eggs, raised the developing embryos singly (n = 2,960), and either sham-treated or infected them with Pseudomonas fluorescens. We used female redness and their allocation of carotenoids to clutches to infer maternal strategies. Astaxanthin was the most prevalent carotenoid in eggs and largely determined their colour. Neither egg weight nor female size was correlated to this carotenoid. Astaxanthin content was positively linked to larval growth and to tolerance against P. fluorescens. Although higher astaxanthin contents in the eggs were associated with an improvement of early fitness-related traits, some females appeared not to maximally support their current offspring as revealed by a negative correlation between female red skin colouration and egg carotenoid content. This correlation was not explained by female size and supports the prediction of a maternal trade-off between current and future reproduction.

Comparative ecology of sexual and asexual parasitoid wasps

Oral presentation

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Different hypotheses predict that species characterized by sexual and asexual reproduction differ in certain ecological attributes, such as ecological generalism and the size of distribution ranges, with opposite predictions depending on the hypothesis. However, there are no studies that compare ecological attributes of sexuals and asexuals on a large scale, prohibiting inference of general patterns. Some insect groups present high proportions of asexual species and are thus good systems to test for ecological differences between species with different reproductive modes. In this large-scale comparative analysis, we investigated the ecology and distribution of sexual and asexual parasitoid and phytophagous wasps. Data on distribution and host species for more than 200 asexuals and 10’000 sexuals was retrieved from an exhaustive online database. We found that asexuals have more host species and wider distribution ranges than their sexual relatives. These generalist ecologies did not solely evolve after the transition to asexuality. We found that extant asexual lineages often derived from sexuals with relatively many host species and wide distribution ranges, indicating that these ecological attributes favour the transition to and/or success of asexuality. We discuss how ecological pre-adaptations in sexuals determine the evolutionary success of their derived asexuals.

The language of cooperation: Shared intentionality drives variation in helping as a function of group membership

Poster

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Language sets humans apart from all other animals, yet experimental game-theoretical studies aimed at explaining exactly how it affects our unique cooperation abilities are still scarce. With a novel paradigm presented as an optimal foraging problem, the ‘egg hunt’ game, we studied players’ natural language use and how it affected repeated decisions to help a partner at a cost. Unisex pairs composed of either ingroup or outgroup members could either talk freely or not at all. Both shared group membership and the possibility to talk led to increased cooperation and overall success in the hunt in an additive way. Importantly, in conversation in-group members displayed more shared intentionality, the unique human ability to share intentions and goals. In contrast, out-group members discussed more separate, individual goals. Females also helped more and displayed more shared intentionality in discussions than males. Crucially, using a mediation analysis we identify the psychological process driving an increase in spontaneous costly helping, specifically shared intentionality. In conclusion, by studying human specific cognitive tools like language and shared intentionality, we further our understanding of the conditions that both promote and hinder human cooperation in real life.

What makes Alpine swift ascend at twilight? Novel geolocators reveal year-round flight behaviour

Oral presentation

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Tracking to track the flight behaviour of an individual bird throughout its annual cycle is notoriously challenging. Therefore, we know very little about the relevance and year-round occurrence of twilight ascents. These ascents are suspected to play an important role in the orientation and navigation of birds, in particular during migration. Here, we present first results achieved with a light-weight multi-sensor tag about this behaviour from 34 alpine swifts (*Apus melba*) of four different populations. We tested if ascents occur mainly when birds are navigating through unfamiliar landscape or when the atmospheric conditions were changing at the current location of the birds. In contrast to our expectation, birds preformed most of ascents during the non-breeding residence period in Africa. Dawn ascents were twice as common as dusk ascents and occurred mainly when atmospheric conditions remained stable over a 24 hours period. We found no conclusive support that twilight ascents are essential for orientation. Supplementary data on the wing beat intensity rather suggests that alpine swift generally increase flight activity - also horizontal flight - during the twilight period and that ascents might be only a by-product of social interactions between birds during this period.

A new approach for measuring α- and β-diversity of plants in agricultural landscapes by an indicator species–based index

Poster

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To measure the effects of agri-environmental schemes on biodiversity, spatially explicit data on biodiversity play an important role. However, mapping and interpreting numerous biodiversity indices from full species records is costly. Thus, a new index was developed for rapidly measuring α- and β-diversity of vascular plant species in agricultural landscapes. The indicator species–based index for species diversity (iSpecDiv) is based on indicator species and habitat type data, and was developed by selecting the smallest number of indicator species per habitat type, where iSpecDiv still correlates with α- and β-diversity indices of vascular plants in the Swiss agricultural landscape. Results showed that iSpecDiv was a suitable index for α- and β-diversity across the agricultural landscape. The final iSpecDiv is based on expert ratings of 25 indicator species per habitat type that have to be sampled in the field. Thereby, iSpecDiv is saving approximately 85% of time compared to a full species survey. Due to the straightforward parameterization of iSpecDiv, this index can easily be extended to the habitat types of other ecosystems and possibly to other organism groups.

Oxidative costs of compensatory growth in Seba”s short-tailed bats

Poster

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Facing adverse conditions during early life might affect the growth of the individual, leading to many short and long term detrimental effects, for example on its reproductive success. To avoid a sub-optimal adult size, organisms may adjust their phenotypic development in response to adverse conditions. To reach the predicted adult size, two major mechanisms can interplay : compensatory growth, with an acceleration of the growth rate, and catch-up growth, implying to grow for longer. A major drawback of growing at the maximal growth rate is the generation of high levels of oxidative stress, leading to short and long term consequences for the individual. Indeed, oxidative stress can negatively impact a wide range of life history traits. Using dietary restriction, we experimentally impacted the early life of Seba’s short-tailed bats (*Carollia perspicillata*). We managed to impact the growth rate of the pup, leading to compensatory growth. We monitored the levels of antioxidant as well as the oxidative damages in the blood throughout growth, in the mothers and in the pups. I will present the short-term effects of the compensatory growth on the morphology and on the redox balance of the pups. Our results provide evidence for the existence of compensatory growth in Seba’s short-tailed bats, and will reveal the subsequent physiological effects on the redox status

Plant-galling arthropods in urban forests

Poster

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The impact of urbanisation on the environment can be diverse and manifold. In many cases urbanisation results in a fragmentation of habitats that have a longer warm growing season, but the forest edges are exposed to more variable temperatures and humidity. These types of environments can be exploited or benefit certain herbivorous organisms. Galling arthropods create an enlargement and/or proliferation of host plant cells or vascular tissue that protects them from the environment and provides them a continual source of nourishment. We tested if forest size, forest edges, and different gradients of urbanisation have an effect on the abundance of plant galls and their parasitism rates. We selected 20 urban to sub-urban forest sites in Basel and established in each forest site six 2 m2 quadrats (three at the forest edge and three at the forest interior) that had the presence of at least one of three common focal tree species: ash, beech, and sycamore. Saplings/branches within the quadrat between the heights of 30-250 cm were surveyed for presence of plant galls and assigned to morpho-species. In addition, 6 leaves with galls of each focal tree species was randomly selected and later opened up to identify the inhabitants and possible cause of mortality by predation or parasitoids.

Effect of adverse conditions in early life on exploratory behaviour of Seba’s short tailed bat

Poster

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Adverse conditions in early life can have long standing impacts on both the physiology and behaviour of an organism. Indeed it is well documented that early life malnutrition in rats alters behavioural responses. One such behaviour is exploration. Exploration allows organisms to become familiar with their environment and has important consequences for the life of an individual. Using dietary restriction, we experimentally created adverse early life conditions in captive mother-pup Seba’s short-tailed bats (*Carollia perspicillata*). The behavioural response to a novel environment was then assessed after a period of expected compensatory growth using the novel environment of a plastic maze. Both mother and pup were separately placed in the maze for 15 minutes, the number of novel areas visited and activity of the bat was recorded. We hypothesised that the pups exposed to dietary restriction would be less exploratory than control individuals, under the assumption that individuals that have experienced a ‘poor start’ take longer to habituate to novel situations. Our results will show the effect of dietary restriction on exploratory behaviour and highlight the impact of early life experience on an organism’s behavioural responses.

Extending trait-based approaches to multi-trophic levels to assess ecosystem processes

Oral presentation

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Many ecosystem functions rely on interactions among primary producers and other trophic levels. However, the mechanisms through which these interactions influence the functioning of ecosystems are poorly understood. How functional composition (community weighted mean trait values, CWM and community traits' variation, FD) mediate impacts of environmental change on ecosystem processes delivered by multiple trophic levels remains little understood. We present two examples illustrating a) a novel experimental framework to disentangle the relative effects of CWM and FD in leaf litter macrodetritivore model system, and b) a qualitative application of the response-effect traits framework on a plant–grasshopper trait linkage explaining variations in fodder production under different management regimes. We discuss about some possible drawbacks when replacing measured physiological and biomechanical traits underlying ecosystem processes and trophic interactions by trait database and literature values or by trait proxies that are either not directly related to the process under study or were not validated beforehand.

Tracing coco de mer's reproductive history: pollen and nutrient limitation reduce fecundity

Oral presentation

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The extraordinary Coco de Mer (*Lodoicea maldivica*) is an endangered, dioecious palm found on the islands of Praslin and Curieuse in the Seychelles. This giant island endemic produces the largest seeds in the plant kingdom (average 8.5 kg), and the nutrient costs of reproduction are high. However, much about the reproductive ecology of this important keystone species is unknown. A detailed study of persistent female inflorescences enabled us to track the reproductive history of individuals over seven years, and to investigate the factors determining reproductive success. We recorded large variation in reproductive output among individuals, and assessed how soil nutrient and pollen availability affected inflorescence and flower production. Habitat degradation resulted in reduced fruit set, and a higher fruit abortion rate, which substantially reduced overall fruit set. We also documented the largest variation in seed size in any species (16.3-fold range in fresh weight, N = 2415). We discuss the implications of our results for the sustainable management of this iconic palm species and more broadly, the factors that shape reproductive output in threatened plants.

Genomic divergence as a result of ecological disruptive selection: Evidence from haplochromine cichlids

Oral presentation

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Cichlid fishes are famed examples of rapid sympatric speciation and adaptive radiation, comprising about 5% of all vertebrate species on earth. However, among cichlids, species richness is unevenly distributed, with few lineages accounting for the majority of species. Although comparative studies revealed lake depth, solar energy and sexual dichromatism of the fish as the most important predictors of within-lake cichlid diversification, the underlying processes which promote or constrain speciation in cichlids remain obscure. To investigate these, we quantified phenotypic and genotypic diversity and divergence in three species-rich and three species-poor East-African cichlid lineages and inferred selection patterns to test whether the prevalence of disruptive selection predicts genomic divergence and whether this differs between species-rich and species-poor lineages. Our first results suggest that the level of genomic divergence between closely related taxa is highly correlated i) with the number of traits under disruptive ecological selection and ii) with the genomic variance within a lineage. Taken together, our results seem to suggest that both disruptive ecological selection and genomic variance, e.g. due to ancient hybridization, are needed for rapid speciation with gene flow in cichlids.

Using ADME genes to explore modern human evolution between Africa and Eurasia.

Poster

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ADME genes, a group of genes involved in drug metabolism, mainly interest physicians who seek to adapt drug therapeutic dosage to patients" profiles. However, because of their role in interactions between the organism and its environment, ADME genes are also potential targets for natural selection, thus allowing to study old and recent adaptations of human populations to different chemical environments, diets or lifestyles. From this assumption, the goal of our project is to describe genetic diversity of ADME genes from East Africa to Eurasia and, if differentiated patterns of diversity are found, determine whether they result from adaptive or demographic processes. To this aim, we will obtain genome-wide genotypes from 100 individuals in 4 different countries: Czech Republic, Greece, Oman and Ethiopia. Moreover, enzymatic activities of 7 ADME genes will be investigated in the same persons. Because these countries are distributed along a latitudinal transect, we assume the existence of different environmental conditions which could promote population-specific selective regimes or intensities in ADME genes. Furthermore, our sampling transect extends over the areas where supposed early migrations of modern humans took place. With these data, we will describe associations between genotypes and phenotypes and search for potential signals of selection.

Speciation or not: Two ecologically divergent populations of *Astatoreochromis alluaudi*

Poster

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Cichlids are well known for their large diversity and high rate of speciation, with several hundred species in the East African great lakes. However, not all lineages diversify equally rapid. While some lineages have evolved a great number of species, others remain species-poor. One of the latter lineages is the genus *Astatoreochromis*, which only contains two species. *Astatoreochromis alluaudi*, the species of this genus dwelling in Lake Victoria, can be found in many different habitats. In our project we compare two populations of two ecologically very different habitats. One population comes from Makobe island, a rocky off-shore island with only little vegetation and clear water, the other population is from Sweya, a vegetation-rich, swampy stream. We will investigate into the phenotypic, ecological and genomic divergence between these two populations, using linear morphometrics, stomach content and stable isotope analyses, and RAD sequencing. We found significant differences between the two populations in traits relevant for swimming performance and nutrition. We also found significant differences in stable isotope ratios, indicating ecological divergence between the two populations. By comparing these results with the speciating lineages of Lake Victoria, this study will help us to better understand factors contributing to or constraining speciation in East African cichlids.

Fossils and ancient DNA shed light on the evolution of East African cichlids

Oral presentation

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Speciation and adaptive radiation are processes that take place over long time periods, and are commonly studied by investigating extant populations and species. While many aspects of these processes are being successfully revealed that way, others are difficult to elucidate using extant data alone. The colonisation history of habitats, the presence of competitors, extinctions, and the trajectory of within-lineage evolution can much better be inferred from long-term records. Time-series data on an evolutionary time scale would therefore be highly desirable to tackle outstanding questions in diversification research. However, such data is difficult to obtain, as the duration of speciation and adaptive radiation typically exceed the professional career of researchers, or even that of historical records. Natural archives, such as lake sediments, can yield highly resolved records of the paleohistory of biota and can also be used to glean ancient genetic information. To improve our understanding of these aspects of diversification, I am using cichlid fish fossils from East African lake sediments to reveal changes in abundance, morphology, ecology, and genetic evolution through time. Here I present results from this approach that shed light on the beginning of Lake Victoria's spectacular cichlid radiation and showcase the promises - but also the limitations - of this approach more generally.

How do ambrosia beetles decide when to leave home?

Poster

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Field and laboratory studies on fungus farming ambrosia beetles showed that delayed dispersal of sexually mature females is a fundamental precondition of cooperative breeding in this taxon. While staying in their natal gallery, females groom other colony members, remove waste and tend the mutualistic fungus garden serving as food. However, at some point females decide to leave their natal gallery to start breeding independently elsewhere. Theory predicts that dispersal decisions should be based on information about the relative fitness effects expected when dispersing or staying at home. Our data show that in native ambrosia beetles, the state of the fungus garden, the number of dependent offspring, and environmental parameters such as humidity, the degree of wood decay and barometric pressure critically influence dispersal decisions. We shall outline how the use of internal and external information helps optimizing life history trajectories in cooperatively breeding ambrosia beetles.

Integration of feedbacks among global change drivers, biodiversity and ecosystem variables through meta-analysis.

Poster

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Global change drivers are phenomena such as climate change, habitat change, pollution and over-exploitation, that affect the Earth system and its capacity to sustain life. Biodiversity plays an important role in the maintenance and resilience of ecosystems to global change. While there are numerous studies reporting the effects of these drivers in changes in biodiversity levels and disruption of ecosystem functions, data is reported in heterogeneous ways and remains largely scattered. Moreover, there are synergistic effects of global change drivers for which is necessary to also look at feedbacks and interactions at different scales, as opposed to studying them in isolation. In this meta-analysis, I show the results of a preliminary study of the feedbacks within 3 variables: land use/land cover change, species richness and net primary productivity. I integrate data on the effects among these variables between the years 2000-2016 in order to report a net effect of one variable in the other, conjointly. Furthermore, I quantify the proportion of the heterogeneity of data available that can be explain with different moderators, most importantly type of ecosystem where the effect was reported and intensity of the effect variables. In all, I highlight global patterns that may be hard to appreciate with non-quantitative, non-integrative reviews.

Morphological divergence among populations of the livebearing fish *Jenynsia multidentata* (Anablepidae, Cyprinodontiformes) along a salinity degree

Poster

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Species living in heterogeneous environments provide interesting model systems to investigate local adaptions. This work aimed to analyze shape and size variation in the livebearing fish *Jenynsia multidentata* from habitats with different salinity degrees along the Atlantic Coast of Brazil. Geometric morphometric analyses (13 landmarks) were performed in 155 specimens (97 females and 58 males) from freshwater, brackish water, and coastal stream habitats. Both sexes showed similar results. The centroid size of the coastal stream populations was bigger than of brackish or freshwater ones. Mean body shape was also different among these habitats. PCA results indicate that about 70% of the variation in males and females is explained by the first five and four PCs, respectively. The morphospace analyses show that coastal stream specimens showed a mean body shape represented by a larger head, a more dorsal positioning of the pectoral fin and shorter caudal peduncles compared to brackish water fish; freshwater populations showed an intermediate pattern. The CVA results confirm the differences between the three habitats, suggesting local adaptation in this species. As a next step, we will investigate the genetics of local adaptation in *J. multidentata*.

Fitness consequences of variation in exaggerated foreleg size of male *Drosophila prolongata*

Oral presentation

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Sexual selection can result in the evolution of condition-dependent variation in expression of sexually selected traits among males that reflects the individuals' condition. Since sexual traits are a critical component of fitness gains, it is expected that males will benefit by maximizing their resource allocation to such traits. However, with the amount of energy available to any individual being finite, an individual's investment in a sexual trait may be determined by the viability cost of trait expression. Males of the fruit fly *Drosophila prolongata* have prominently exaggerated forelegs that they use in fights against other males and during courtship of females. By rearing males under different dietary conditions we were able to assess how condition-dependent expression of forelegs can affect the outcome of male-male competition and the reproductive success of males. We observed the behavior of each male when competing with another male in the presence or absence of a female. We assessed the reproductive potential of males (given unlimited access to females) as well as the realized reproductive success under a competitive setting. Finally, we measured each male's foreleg and evaluated how the size of such trait affected the performance of males on each experiment.

What determines range limits in North American *A. lyrata* subsp. *lyrata* ?

Poster

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A major question in ecology is: Why do species have their actual distribution? An alternative hypothesis to drastic changes in the ecological factors defining the ecological niche of the species is, that population at edges of distribution are small due to bottlenecks and isolation, have low genetic variation and accumulate deleterious mutation, resulting in a fitness decrease called drift load, constraining further adaptation and colonization of new environments. This hypothesis will be tested in the next three years on the North American species *A. lyrata* subsp. *lyrata*, by assessing the heterosis effect of crosses between population of different sizes and genetic diversity. This effect will be analyzed in a common garden experiment, and in laboratory with a focus on heat, drought and pathogen stresses, with a following RNA-Seq study to assess the effect of drift load on previously identified genes related to environmental adaptation, and discover new potentially related genes.

Biased gene conversion drives codon usage in human and precludes selection on translation efficiency

Oral presentation

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In humans as in all other mammals, synonymous codon usage (SCU) varies widely among genes. In particular, genes involved in cell differentiation or in proliferation display a distinct codon usage, suggesting that SCU is adaptively constrained to optimize translation efficiency in distinct cellular states. However in mammals SCU is known to correlate with large-scale fluctuations of GC-content along chromosomes, caused by meiotic recombination via the non-adaptive process of GC-biased gene conversion (gBGC). Here, we disentangle and quantify these different factors driving SCU by analyzing the relationships between functional categories, base composition, recombination and gene expression. We show that the gBGC model explains 70% of the variance in SCU between functional categories and translational efficiency less than 1%. We argue that the strong heterogeneity of SCU induced by gBGC precludes any optimisation of the translation efficiency.

Does the presence of an odd individual affect group choice by coral reef fishes?

Poster / FlashTalk

Quattrini Fausto, Redouan Bshary & Dominique G. Roche. Éco-Éthologie, Institut de Biologie, Université de Neuchâtel

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Group formation (shoaling) in fishes is common and provides several antipredator benefits. However, coral reef fishes often form mixed-species shoals, which can generate costs for some group members. The oddity effect posits that individuals that stand out from a group are more likely to be targeted by predators. Thus, the presence of an odd fish might reduce the risk of predation to other group members; alternatively, it might attract predators and increase predation risk for the group as a whole. In collaboration with Lizard Island Research Station (14°40’S; 145°28’E), we investigated whether three species of coral reef fishes chose to associate with conspecifics over heterospecifics and whether they associate or avoid shoals containing an odd individual. One species actively avoided associating with shoals of heterospecifics. However, no species showed either active avoidance or preference for shoals containing an odd individual. Lower predation risk to individuals associating with an odd fish might be negated by greater predation pressure on the group as a whole.

Is schooling behaviour affected by lateralization; a study with three coral reef species

Poster

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Brain lateralization (i.e. asymmetrical organisation of brain hemispheres) usually results in directional biases in behaviour (e.g. handedness). Lateralized individuals can benefit from several advantages such as an increased ability to multitask. Conversely, population-level lateralization (i.e. when the majority of individuals present the same directional bias) might present costs, notably by making behaviour predictable to predators. Yet, population-level lateralization is common in nature. One explanation might be that uniformity of lateralization helps coordinating movements by members of a group. To test this hypothesis, we studied three species of coral reef fishes that live in groups (shoals). We examined whether group cohesion and alignment increases when shoal are composed of highly lateralized individuals. All species contained lateralized individuals but only two were lateralized at the population level. Overall, we found no evidence that lateralization influenced shoal compactness or alignment. In one species, group compactness was influenced by size differences among shoal members: shoals exhibiting a greater size range were generally more compact. Our findings suggest that group cohesion is affected by factors other than lateralization in the species we examined.

The impact of interspecific hybridization in conservation and evolution: a general model

Oral presentation

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Human activities have impacted species distribution through the modification of natural habitats, translocation of invasive species and climate change. These disturbances have enhanced the likelihood of interbreeding between species or populations that have never been in contact before. Similarly, antibiotic resistant bacteria or genetically modified organisms can spread their genes into neighboring populations or species. To investigate how genes and phenotypes are transmitted when two populations hybridize, we developed a general model that integrates for the first time the main genetic, demographic and ecological processes. We first show that analyses based on a single gene can lead to biased conclusions about the threat to a species due to hybridization, while the use of two or more genes can correct this bias. We also find that demographic influences can amplify or balance the genetic effects, evidencing the need to integrate both processes in the analyses. We then illustrate the utility of our approach by investigating how introduced mallards (*Anas platyrhynchos*), the most widely translocated dabbling duck, can threaten local species through hybridization. We finally demonstrate how hybridization can facilitate biological invasions. This model can solve questions in a variety of fields, such as evolution, conservation, agriculture and epidemiology.

Selection for mitochondrial quality drives evolution of the immortal germline and the aging soma

Oral presentation

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The origin of the Weismannian germline-soma distinction is a fundamental unsolved question, with implications for understanding aging and mortality. Plants and basal metazoans such as corals and sponges do not sequester a specialized germline, but generate gametes from pluripotent stem cell lineages in adult tissues, and are capable of asexual reproduction and seemingly unlimited regeneration. In contrast, bilaterians set aside a specialized and protected germline early in development, but also have complex bodies with many terminally differentiated tissues that deteriorate with age. In this talk I will show that the strict germline-soma dichotomy could have evolved as a strategy to improve mitochondrial genome quality in metazoans with high mitochondrial mutation rates. The evolutionary transition likely coincided with the increase in atmospheric oxygen levels and the origin of predation in motile metazoans in Cambrian explosion. The evolution of the germline enabled unconstrained differentiation in somatic tissues, but also marked the origin of senescence and death.

Adaptive divergence in East African cichlid fish: testing for pre- and postzygotic reproductive barriers

Poster

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Divergent natural selection leading to phenotypic differentiation between populations exploiting different environments is thought to be a primary cause of adaptive radiation. The East African cichlid fish *Astatotilapia burtoni* is a habitat generalist and thus represents an ideal model to study adaptive divergence across an environmental gradient. Various lake-stream population pairs exist in Lake Tanganyika and affluent rivers that rest at different stages of the 'speciation continuum'. To evaluate the degree of reproductive isolation between genetically divergent *A. burtoni* lake and stream populations we performed a mate choice experiment in a semi natural setting in experimental ponds at our field site at lake Tanganyika. Reproductive isolation in the presence of male–male competition was assessed from genetic parentage. Moreover, to investigate the direct fitness consequences of morphological divergence, we tested the performance of stream fish, lake fish and lake-stream hybrids in lake habitat in a transplant experiment. Relative fitness of hybrid and parent genotypes was assessed based on survival and growth rate over several weeks. Together these experiments contribute to a better understanding of the evolution of reproductive barriers in *A. burtoni* lake-stream pairs.

The physiological and root microbial ecology of wild and cultivated rooibos (Aspalathus linearis) populations

Poster

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Rooibos, an endemic legume shrub of the South African Fynbos, is a jack of all trades in mineral nutrient acquisition for thriving in exceptionally infertile, acidic and water-deprived soil. As an emerging, locally adapted crop plant, it offers great opportunities for a minimally environmentally invasive and resource-efficient agricultural production. This project aims at identifying those groups of plant-beneficial root-symbiotic microbes which could confer nutritional advantages and environmental stress tolerance. By observation and manipulation, repeated patterns of microbial community composition and structure coinciding with better plant performance are sought. The poster presents total leaf nutrient concentration and ð15N, ð13C, and ð18O isotopic signature data of a field survey in adjacent cultivated and wild populations of the tea bush. Taking ð15N as a time-integrated indicator of symbiotic N2 fixation, plants from the wild seem to profit more from rhizobia, and taking ð13C and ð18O as long-term integrators of drought stress, plants from plantations seem to be better off than plants from the wild. Rhizobia, glomeromycetes and oomycetes are the functional and phylogenetic target groups whose selective association with roots of rooibos will be studied in a field survey, soil manipulation experiment and inoculation trials.

Natural forest regeneration at Mt. Kilimanjaro

Poster

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Mt. Kilimanjaro represents one of the few mountain ecosystems in East Africa. However, its forests and woodlands, which provide essential ecosystem services for the local population, are threatened by climate change and land use. Furthermore, the impact of former and ongoing disturbance on tree abundance and diversity is highly unknown. As adult trees show a delayed response due to longevity, it is crucial to assess the early stages of a tree`s life, which highly determine population dynamics. Therefore, we assessed the regeneration of all woody species in a 20 x 5 m area on 65 plots, covering all main habitat types along the whole elevational and land use gradient of the southern slopes of the mountain. We recorded species, height and diameter of all stems between 25 and 130 cm. Initial results show a hump shaped pattern along elevation with a peak of regeneration at 2000 m.a.s.l., which coincides with the maximum of precipitation. Still ongoing disturbance in form of land use at the lower zones reduced regeneration significantly. However, former disturbance in form of logging and fires at the higher zones did not show a significant effect. This indicates, that the habitat protection at the higher zones is working and facilitating natural regeneration.

Adaptive genetic changes in rapidly coevolving host and virus populations.

Poster

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Dramatic demographic fluctuations are often observed in coevolving systems, but it is to a large extent unknown how this affects genomic variation. Understanding how demography (via drift), selection and their interplay shape genomic variation is particularly interesting in a setting where adaptation of one species changes selection pressure for the other and vice versa (eco-evolutionary dynamics). We use an experimental setup where host (*Chlorella*) and virus (Chlorovirus) populations reciprocally evolve resistance and counter-resistance mechanisms over 90 days. Previous research has shown reproducible demographic and ecological dynamics occurring over multiple replications of coevolution. These initially reflect an "arms race" between virus and host strains, then change into a state where both species co-occur at stable densities, but fluctuating phenotypic distributions. My PhD work will track evolution at the genomic level. We established a sequencing approach to generate whole-genome population (Poolseq) data for both species simultaneously and have sequenced multiple time points during coevolution. This dataset now has allowed us to identify adaptive genetic changes by their change in frequency over time, which is the next step towards understanding what drives the observed eco-evolutionary dynamics.

Early programming of the stress axis affects social behaviour and stress responsiveness in a cooperatively breeding cichlid fish

Oral presentation

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In vertebrates, early social adversity can influence social behaviour, stress responsiveness and altered programming of the hormonal stress axis during later life, suggesting a link between early exposure to stress hormones and long-term effects of social experience. In the cooperatively breeding cichlid *Neolamprologus pulcher* we manipulated the early programming of the stress axis to evaluate its causal role for differences in later life performance. Twenty-six fish were assigned to either of three treatments applied by water baths repeatedly during the first 2 months of life: (i) the stress hormone “Cortisol”, (ii) the blocker of the glucocorticoid receptor GR1, ”Mifepristone” or (iii) control. At age 163 d, we measured their stress responsiveness as the difference between basal and stress levels of cortisol, using the fish holding water technique. At age 167 d, we tested their social behaviour and ability to defend a resource. Individuals treated with Mifepristone won more contests over the resource than controls, and fish treated with Cortisol and Mifepristone showed more threat behaviour than controls. Moreover, the social behaviour was interactively influenced by the rearing treatments and stress responsiveness of the fish. Concluding, our early manipulation of the stress axis had long-term effects on stress regulation and social behaviour of individuals.

Exploring the relationship between genetics, morphology and geography in human populations

Poster

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The demographic history of populations has been studied through several complementary fields. Among the first data gathered to infer relationships among human populations is the measurement of non-metric morphological trait frequencies. More recently, with the advent of high-throughput sequencing, genetic data has exponentially increased and has allowed to re-investigate in an integrative way some fundamental questions relative to human dispersals. In this work, we assemble large genomic datasets of worldwide human populations (including the 1000 genome and the human genome diversity projects) and compare these data with cranial metric traits of geographically matching populations. We study the relationship between those two types of datasets and the geographic distance that separates the sampled populations. We explore the results and highlight some factors that impact the degree of correlation among datasets.

Body covering of bone and teeth: What does it take for it to emerge?

Poster

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Dental structures are found in the head of extant vertebrate lineages and derive from cephalic neural crest cells. These structures are absent from the trunk presumably because the trunk subpopulation of neural crest cells cannot trigger odontogenesis. However, in several extinct lineages, extra-oral dental structures (odontodes) are found in the trunk in association with an underlying dermal bony plate. Today, the Loricarioidei catfish group is an exceptional living lineage bearing trunk dental structures which are also associated to an underlying bony plate. By investigating this lineage, we ask if the underlying bony plate is a prerequisite for unlocking the odontogenic potential in trunk neural crest cells. We first study the presence of dermal bony plates and of odontodes in all loricarioid families. Then, we do a thorough phylogenetic analysis with a new, 10-gene dataset, and determine the evolutionary relationships among these families. We time-calibrate this phylogeny with eight calibration points, and reconstruct the ancestral state of the ancestor to all Loricarioidei, finding that it had odontodes on the trunk, but not dermal bony plates. These results show that dermal bony plates are not necessary for unlocking the odontogenic potential of the trunk NC. We also show that in loricarioids, when trunk odontodes are not associated with dermal bony plates, they are associated to other underlying bones such as ossified fin rays or the exposed pectoral girdle. Finally, we suggest future avenues of genetic experimentation for studying how the odontogenic potential of the trunk NC can be unlocked.

Spatial relationship between recolonizing wolves and their ungulate prey

Poster / FlashTalk

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Wolves recolonizing the canton of Valais, Switzerland cause considerable conflicts with local communities, especially sheep breeders and hunters. However little is known about the habitat selection of the Valais wolves. We investigate if the prevailing prey densities (mainly red deer, but also roe deer and chamois) affect spatial recolonization patterns. Based on 4 years of snow-tracking along 218 1km transects we predicted relative ungulate densities across the study area. Prey densities, along with other environmental factors, were then used to analyse the habitat selection patterns of the spreading wolves, using data from the Swiss wolf monitoring and own camera traps. After accounting for detection probability, red deer densities at the transect sites were found to be more or less stable over time, with only minor spatial fluctuations. Similar results we found for roe deer and chamois. Robust density estimates along transects will now allow generating area-wide predictions of both prey and wolves. Understanding the habitat selection of recolonizing wolves and predicting spatial patterns of population re-establishment will help to better anticipate future conflict zones. In the long run, the ungulate-wolf monitoring will allow assessing (and objectifying the debate around) predator-prey-interactions, and provide the necessary objective basis for management decisions.

Environmental factors driving local adaptation in the Alpine Brassicaceae *Arabis alpina*

Poster

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Fitness differences among individuals are mostly genetically determined, and it is therefore important to study the genetic processes behind local adaptation in order to understand the responses of individuals to changing environments. Here we investigate the extent of adaptive genetic variation that can be found in genic and non-genic regions of the genome. Three hundred six individuals of the Alpine rock cress *Arabis alpina* were sampled in different environments in four regions of the western Swiss Alps. We preformed association analyses of 400,000 SNPs, identified through whole-genome re-sequencing, with various environmental factors derived from LIDAR data and evaluated in-situ. The results will help us assessing the predictive power of the environmental factors in driving local adaptation, and knowing which genes are involved in this important evolutionary process. Moreover, the spatially hierarchical sampling of individuals will allow us to assess the scale of local adaptation. On-going analyses will identify transposable elements in near genic regions, elucidating the role of the non-genic part of the genome in local adaptation.

Global macroecology of size, sexual size dimorphism, dispersal and range size in drosophilids

Oral presentation

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Macroecological rules describe conspicuous trends in potentially adaptive phenotypic variation across large spatial scales and environmental gradients. Although these “rules” are supported by empirical data and underlie theory, the predictive power of Allen’s, Bergmann’s, Rensch’s and Rapoport’s rule is strongly limited across taxa, and patterns in insects tend to be especially equivocal. We here investigate these patterns in common fruit flies (Drosophilidae). Previous research has focused on intraspecific variation while interspecific patterns have received little attention in this group. Also, potential interactive or confounding effects between macroecological patterns are only rarely addressed. We here reconstruct the evolutionary relationship between 191 species of drosophilids and use comparative analyses as well as faunistic data from across the globe to test Allen’s, Bergmann’s, Rensch’s and Rapoport’s rule and their interrelations. We find support for several macroecological patterns in thorax length, wing size, dispersal capacity, sexual size dimorphism as well as range extents, although their manifestation varies considerably across clades. Furthermore, we explore and discuss potential confounding effects between traits and their possible role in maintaining the idiosyncrasy of macroecological patterns generally observed in insects.

Using wild tomato endosperm transcriptomes to assess the involvement of genomic imprinting in seed failure and reproductive isolation

Oral presentation

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The endosperm is a triploid seed tissue controlling embryo development. Imprinting, or parent-specific gene expression, has been found to occur in the endosperm. Parental imprints may be necessary for embryo survival and seed viability. Accordingly, hybrid seed failure in crosses between closely related species may be a consequence of mismatches between diverging imprints in the endosperm. The aim of our study is to test these hypotheses using three wild tomato species: *S. peruvianum*, *S. chilense* and *S. arcanum* var. *marañón*. We identified imprinted genes in (i) three intraspecific crosses and (ii) three interspecific crosses with variable levels of seed abortion. Endosperm tissue was recovered at pre-globular stage and Illumina-sequenced. In both intra- and interspecific crosses, we found more maternally imprinted genes (MEGs) than paternally imprinted genes (PEGs). We identified 43 MEGs and 17 PEGs conserved in the three intraspecific crosses. We compared maternal expression proportions between intraspecific and hybrid crosses having the same mother. The hybrid endosperms of abortive crosses were characterized by an elevated maternal expression together with the gain and loss of imprinting. This reveals molecular perturbations of gene expression involving parental effects. Perturbed imprinting may contribute to reproductive isolation in wild tomatoes.

Free-living house mice carrying a selfish genetic element are more likely to emigrate

Oral presentation

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Selfish genetic elements (SGE) are genetic loci that increase how often they are copied ("drive") to the detriment of the rest of the genome and organism, resulting in conflict. This conflict creates selection on the rest of the genome to counteract the drive and counter-selection on the SGE. The t haplotype (t) is an SGE in house mice. It drives in its male carriers and is transmitted by them in high frequencies. It is less frequent in natural populations than predicted based on its drive because of homozygous lethality and low sperm competitiveness. Thus, it is prone to extinction in small (drift) and large (multiple mating) populations, yet it has survived for two million years and is found throughout the world. We hypothesized that increased emigration propensity could support the survival of the t. We tested this by analysing data on juveniles disappearing from and migrating within a long-term free-living house mouse population. We found that t-carriers were indeed more likely to emigrate from the population as juveniles, particularly during times when the juvenile population size was large. Thus, t likely evolved to increase emigration propensity in its carrier, probably because the fittest t haplotype variant is one that most consistently spreads to new populations and is hence the least harmed by local extinctions.

Provenance oblige - the consequence of adaptation on host range for an RNA virus

Oral presentation

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RNA viruses characteristically exhibit high flexibility in their host range, often infecting very distantly related species. Still, most infections deriving from a reservoir host (spillovers) cause only temporary epidemics in the recipient species, while the establishment of a persistent infection chain appears to be a major evolutionary challenge. We study the evolutionary constraints of host-range expansion in a natural system of Tula hantavirus (TULV) and its rodent reservoir host *Microtus arvalis* (common vole). While spillovers into other Arvicoline species are reported, in the reservoir host the infection range of different TULV strains appears to be highly constrained by parapatric evolutionary lineages. We found high consistency between the spatial distribution of TULV strains and host genotypes in a natural hybrid zone of two common vole lineages indicating within-species specialization. Despite high overall genetic divergence, only five percent of fixed genome-wide nucleotide differences between TULV strains are nonsynonymous, resulting in a small number of potentially adaptive substitutions. Our system provides a unique opportunity to explore RNA virus fitness landscapes in nature and shows strong trade-offs between adaptation and host-range expansion.

Wing shape clines of yellow dung flies originate from biogeographic history and local adaptation on different continents

Poster

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Geographic clines provide insights into putative targets and agents of natural selection, but biogeographic history can lead to identical patterns of trait divergence. Using a population genetic framework derived from microsatellite analysis we examine the evolutionary forces affecting geometric wing morphology in the yellow dung fly *Scathophaga stercoraria* worldwide (North America, Europe and Japan). Our results indicate that both adaptive and demographic processes contribute to geographic variation in wing morphology leading to inconsistent wing shape clines across North America and Europe. Furthermore, in agreement with theoretical considerations, we find a strong influence of biographic history in North America, which presumably has been colonized recently by flies of Eurasian ancestry as inferred from microsatellite variability patterns. By contrast in Europe where the species exists for much longer time and where no molecular pattern of isolation is evident, local adaptation appears to be the dominating process leading to geographic clines in certain dimensions of fly wing shape. Our findings illustrate the importance of detailed biogeographic information when interpreting clines of dispersal traits in an adaptive framework.

How does phenotypic plasticity affect population differentiation with gene flow?

Oral presentation

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Species are heterogeneous entities, and populations (although connected by gene flow) could differ from each other in their phenotypic and genotypic composition. The potential causes are diverse, including random genetic drift, divergent selection and phenotypic plasticity. Although verbal models exist, theoretical work is missing that describes explicitly the effect of phenotypic plasticity on population differentiation. To this end we extended a quantitative genetic model and describe the genetic and phenotypic differences between two populations in dependence of the strength of divergent selection, the migration rate and phenotypic plasticity. We complemented the approach with individual-based simulations to parameterize the model and investigate neutral genetic dynamics. We show that phenotypic plasticity decouples genetic from phenotypic differences between populations, and demonstrate under which conditions countergradient variation can be found and why PST can be a bad surrogate for QST. The simulations further show how phenotypic plasticity decouples the effective migration rate from census migration rate and thereby shapes genetic differentiation in allele frequencies FST and FSTQ. In line with verbal models, we show analytically under which conditions genetic or phenotypic differences observed in nature do not point in an adaptive direction.

Reciprocity and kin selection - two alternative mechanisms underlying cooperation in Norway rats

Oral presentation

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Social groups contain individuals with varying degrees of relatedness. Group members may help each other at some cost without receiving immediate benefits from their collaboration. Evolutionary mechanisms responsible for cooperation include kin selection and reciprocity. The interplay between these alternative mechanisms has been little studied. We tested to which extent cooperation among Norway rats (*Rattus norvegicus*) is affected either by relatedness or by previously experienced help. Under natural conditions, rats live in colonies of various sizes consisting of related and unrelated individuals. In our study, right after weaning brothers were separated for 15 months and then tested for sibling recognition, which they indeed accomplished. In the experiment, test rats experienced either unfamiliar kin or unfamiliar non-kin, which either provided food to them or not. Subsequently, test rats could provide food to the same social partners. Focal rats provided more food to previous food donors than to uncooperative partners, irrespective of relatedness. This shows that direct reciprocity apparently can explain cooperation both among related and unrelated individuals. Interestingly, test rats overall provided more food to non-kin than to related social partners, suggesting an increased investment into social relationships with unrelated conspecifics.

Holocene treeline changes in the Canadian Cordillera are controlled by climate and local topography

Poster

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Climate change is expected to lead to an upward shift of mountain forests, but secondary controls such as topography and geomorphology might be important as well. We aim to determine if vegetation change in response to past warm periods in the Canadian Cordillera was regionally synchronous or if local factors caused divergent responses. To address this question, we analyzed post-glacial sediments from three lakes at or just below the present treeline for pollen, macrofossils and charcoal. At two lakes, highest macrofossil concentrations occurred in the warmer-than-present Early Holocene, indicating highest treeline position and forest density in response to higher temperatures. At the third lake, a divergent vegetation history with highest macrofossil concentrations in the mid-Holocene suggests that local topography was an important control of mountain forest dynamics. We conclude that summer temperature is the primary driver of mountain forest dynamics, but the establishment of closed forest depends on adequate moisture availability, which is controlled by topography and geomorphology. We therefore expect a rapid upward shift of treelines during the 21st century in response to warmer temperatures, but only where deep soils or favorable aspects provide sufficient moisture for tree growth. Upward forest expansion will be patchy and occur first in favorable microsites.

The effect of food quality during growth on spatial memory consolidation in adult pigeons

Oral presentation

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Poor environmental conditions experienced during early development can have negative long-term consequences on fitness. Animals can compensate negative developmental effects through phenotypic plasticity by diverting resources from non-vital to vital traits such as spatial memory to enhance foraging efficiency. We tested in young feral pigeons (*Columba livia*) how diets of different nutritional value during development affect memory. Parents were fed either with high- or low-quality food from egg laying until young fledged, after which all young pigeons received the same high quality diet until the memory performance was tested at 6 months of age. The pigeons were trained to learn a food location out of 18 possible locations in one session, and then their memory of this location was tested 24 hours later. Birds reared with the low-quality diet made fewer errors in the memory test. These results demonstrate that food quality during development has long-lasting effects on memory, with moderate nutritional deficit improving spatial memory performance in a foraging context. It might be that under poor feeding conditions resources are redirected from non-vital to vital traits, or pigeons raised with low-quality food might be better in using environmental cues like the position of the sun to find back where food was hidden.

Social huddling and physiological thermoregulation are related to melanism in the nocturnal barn owl

Poster

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Endothermic animals vary in their physiological ability to maintain a constant body temperature. Since melanin-based coloration is related to thermoregulation and energy homeostasis, we predict that dark and pale melanic individuals adopt different behaviours to regulate their body temperature. Young animals are particularly sensitive to a decrease in ambient temperature because their physiological system is not yet mature and growth may be traded-off against thermoregulation. To reduce energy loss, offspring huddle during periods of cold weather. We investigated in nestling barn owls (*Tyto alba*) whether body temperature, oxygen consumption and huddling were associated with melanin-based coloration. Isolated owlets displaying more black feather spots had a lower body temperature and consumed more oxygen than those with fewer black spots. This suggests that highly melanic individuals display a different thermoregulation strategy. This interpretation is also supported by the finding that, at relatively low ambient temperature, owlets displaying more black spots huddled more rapidly and more often than those displaying fewer spots. Assuming that spot number is associated with the ability to thermoregulate not only in Swiss barn owls but also in other Tytonidae, our results could explain geographic variation in the degree of melanism.

The influence of predator- induced maternal effects on offspring growth and anti-predator behaviours

Poster

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Through non-genetic maternal effects, mothers pass essential information to their offspring, which may be beneficial to both mothers and offspring. Predation risk is an important ecological variable influencing life history evolution and can even promote sociality, such as in the cooperative cichlid *Neolamprologus pulcher*. Predation risk perceived by mothers is expected to enhance offspring growth and predator avoidance behaviour. In this study, predation risk was simulated by showing egg laying *N. pulcher* females repeatedly to either videos of natural predators or control. We present the results of the first part of this experiment, in which we compared clutch size, initial offspring size and growth. Subsequently, these offspring were tested for predator escape and anti-predator responses at 3 and 4 months respectively. We then discuss our plans for the following experiment, in which we will compare maternal effects at the level of egg composition. We will measure total fat and amino acid content along with maternally passed transcripts of the two main somatotrophic hormones namely, IGF-1 and GHR. Our study will promote general understanding of the phenotypic effects, and the respective costs and benefits of predator-induced maternal effects, and in particular bolster the importance of predation risk in the life histories of highly social cichlids.

Testing for reproductive isolation between two geographically and genetically distant populations in the haplochromine cichlid *Astatotilapia burtoni*

Poster

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The event of speciation and the understanding of how it is driven by selection is a ubiquitous topic in biology. Reproductive isolation may evolve as a by-product of the accumulation of differences between two geographically distant populations. The radiation of East African cichlids in Lake Tanganyika is an important model for studying patterns of speciation. Here, we focus on mating patterns in a haplochromine species, *Astatotilapia burtoni*, which occurs within Lake Tanganyika and surrounding rivers. We use two experimental setups involving two geographically and genetically distant lake populations to assess the level of reproductive isolation. In the first experiment, where only visual cues were considered, the number of eggs laid next to each male serves as a measure of female preference. The second experiment allows direct contact between males and females (i.e. all cues available), and mate choice is determined via genetic paternity testing. The results of these experiments allow us to infer at which stage of the speciation continuum the populations are resting.

Indicator ecosystem functions and the many dimensions of multifunctionality

Oral presentation

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Research on the factors determining the ability of ecosystems to provide multiple functions and services simultaneously (multifunctionality) has increased during the last decade. However, how we evaluate ecosystem multifunctionality is hindered by limited budgets or scientific expertise, reducing the number and variety of functions that can be measured in research projects. We therefore lack information on the reliability and comprehensiveness of the multifunctionality indicators used in different studies. Here, we used large forest and grassland datasets, each including multiple ecosystem functions, to i) search for “indicator functions” (those related to other functions and services), ii) quantify the dimensionality of multifunctionality, i.e. the minimum set of functions needed for its reliable measure (considering synergies and trade-offs between functions). Our results show that P retention and soil C are best correlated with multifunctionality and with most individual functions, suggesting them as “indicator functions”, similar to the indicator taxa used in biodiversity research. Ecosystem multifunctionality has 6 dimensions, which is the minimum number of ecosystem functions needed to obtain a reliable multifunctionality index. Lastly, we explore the role of land-use intensification and biodiversity in the trade-offs and synergies between ecosystem functions.

Methylome wide association study of two mating season phenotypes in a wild Round Goby population

Oral presentation

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Condition-dependent alternative reproductive behavior is one of the best studied examples of phenotypic plasticity in animals. However, it is unknown when and how an organism evaluates the environment. Epigenetic marks such as DNA methylation are known to change with different environments and have an effect on gene expression. Here we investigate the relationship between epigenetic marks and two mating season phenotypes in a population of *Neogobius melanostomus* in the Rhine River. We found an association between DNA methylation and the phenotype. Additionally, we also saw that premating season fish seem to be epigenetically more closely related to either one or the other phenotype. Overall, this indicates a certain epigenetic predisposition during development towards becoming a mating season phenotype.

Leave no stone unturned: challenges in Ichneumonidae palaeontology

Oral presentation

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The importance of an accurate placement of fossils becomes evident in the context of palaeo-ecological and molecular dating studies, where results heavily rely on the correct taxonomic position of the fossils. There are many factors that can bias the identification of fossil specimens. First of all, imperfect fossilisation hinders taxonomic placement in any group of organisms, as body parts that contain synapomorphies might not be preserved. In Ichneumonidae, another factor that impedes correct placement is widespread homoplasy: several groups have often independently acquired identical character states due to a similar life style, e.g., adaptation to the same host. We describe five new fossil species and two new genera of Ichneumonidae from the Green River Formation (~ 50 Ma) including *Mesoclistus*? *yamataroti* sp.nov, the first record of the subfamily Acaenitinae for the locality. Additionally, we revise the ten previously described ichneumonid fossils from Green River. Generic positions of most of the revised species proved to be unclear and four of the species have been moved from their subfamilies into Ichneumonidae *incertae subfamiliae*. In the light of these outcomes, we discuss the aforementioned challenges and give suggestions for future practise that can reduce mistakes related to erroneous fossil placement.

The importance of 3D flower shape and its modularity in complex plant-pollinator interactions

Oral presentation

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The 3D shape of flowers has, until the advent of modern 3D dataset acquisition techniques, remained as elusive as it was thought to be crucially important for pollination. We present here patterns of 3D flower shape variation gained in the study of two systems: the sexually deceptive orchid *Ophrys* and the heterostylous *Primula*. In *Ophrys*, we show that floral shape is more tightly correlated to the shape of the male bee (pollinator) than it is to the shape of the female bee (object of mimicry). We show that the parts involved in pollen transfer belong to well-supported shape modules, both in the bee and the flower. In Primula, we present a novel, multidimensional approach to quantify and analyse heterostyly. The best-supported shape module for flowers of both morphs together involves the apex of the stamens and the corolla mouth, both of which restrict the access of pollinators to the floral tube in one morph. Taken together, our analyses of the modularity of flower shape, in two unrelated systems, challenge the established paradigm of a division of flowers into modules of “attraction” vs. “reproduction”, and support a division into a module of parts that are directly in contact with pollinators vs. a module of parts that are not. Our results emphasise the relevance of modularity in flower shape and provide new perspectives into a rapidly expanding field.

Bayesian divergence time estimation and skull shape evolution in sea catfishes (Ariidae)

Oral presentation

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New geological evidence contests the commonly accepted age of the rise of the Isthmus of Panama, which constitutes an important calibration point for molecular clock based timing of phylogenetic trees. Here, we use Ariidae (sea catfishes) from the Northern Neotropics, a mainly marine lineage that diverged 65 Ma (Cretaceous-Paleogene boundary) and that has a growing Neogene fossil record, to identify and date patterns in lineage splitting events, using a new phylogenetic hypothesis based on RAD-seq data and fossil calibrations. Further, we investigate skull (neurocranial) shape evolution applying 3D geometric morphometrics in a phylogenetic context, and examine secondary freshwater adaptations, which have occurred repeatedly in ariid catfishes. Bayesian inference of phylogeny and lineage splitting events supports repeated closures and openings of the trans isthmian seaways and an earlier date for the initial rise of the Isthmus of Panama. The examination of skulls in twenty recognized ariid species suggests that skull shape changes are strongly associated with phylogeny rather than with habitat (fresh, brackish, salt water) transitions. We thus propose that adaptation to habitat in Ariidae might rather be located in the lower jaw and the soft tissues than in the neurocranium. However, morphospace analysis can therefore be used to identify specimens of unknown identity.

Effects of vegetation management on soil biodiversity, soil functions and grape quality in Swiss vineyards

Poster / FlashTalk

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The BiodivERsA/FACCE-JPI project PromESSinG (www.promessing.eu) investigates the links between ground management, soil biodiversity and ecosystem functions in vineyard ecosystems in five European countries (CH, F, D, A, ROM). The different ground management methods, which are characterized by different levels of spontaneous vegetation in Swiss vineyards, are evaluated with regards to their effects on soil biodiversity, ecosystem functions and services. Here, we present results from the first two study years (2015 & 2016) obtained in Switzerland. In particular, we study how soil management practices affect the diversity and community composition of different groups of organisms, such as plants, the microbial community, meso- and macrofauna. We also study the effects of management on soil functions like soil respiration and decomposition rates as well as nutrient regimes. Furthermore we evaluate the effects of soil management on different indicators of grape quality. Preliminary results show that biodiversity is generally negatively affected by vegetation removal whereas soil functions and grape quality seem to be selectively affected. These results suggest that reduced vegetation management in vineyards has an overall positive effect on soil health without compromising grape quality.

Microbial communities in *Maculinea alcon* caterpillars change following trophic shifts

Poster / FlashTalk

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Insects vary widely in their use of microorganisms for nutrition and physiology. In most cases, their microbiomes only change slightly with diet modifications. However, *Maculinea alcon* caterpillars undergo a dramatic change in diet, abruptly shifting from phytophagy to ant tending (feeding via trophallaxis) during their parasitic relationship with *Myrmica* ants. Is this shift in diet accompanied by a change in bacterial communities in caterpillars? To address this question, we used high-throughput 16s rRNA sequencing to track changes in bacterial community composition over the course of caterpillar development. To better understand the origins of bacteria present in *M. alcon*, we also sequenced the bacterial communities present in their surrounding environments (flower buds, and soil inside ant nest chambers), as well as in their ant hosts. Here, we present evidence of a major shift in microbiome composition during *M. alcon* development: to our knowledge, the first evidence of such a shift. We also draw parallels between caterpillar and ant bacterial communities, suggesting a transfer of bacteria from ant hosts.

Effect of the helpers on breeders" condition in the cooperatively breeding cichlid *Neolamprologus obscurus*

Poster

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Helpers in cooperative breeders are expected to reduce workload and increase condition of breeders. However, beneficial effects of helpers are often difficult to assess. We examined the effect of helpers in a cooperatively breeding cichlid *Neolamprologus obscurus*, which feeds on benthic invertebrates. Helpers increase the excavated stone area inside the breeder's territory by sand digging, which may be important to acquire food resources. However, helpers consume the same food as breeders, which make their effect unclear. Behavioural observation in a wild population revealed that the workload of breeders decreased and feeding behaviour of breeders increased according to the helper numbers. Using body mass data, breeder's condition increased according to the excavated stone area, but decreased with the helper number. Detailed analysis revealed that only larger helpers are most likely to improve the condition of breeders. This study shows novel aspect of helper's function in cooperatively breeding vertebrates.

Spatial predictions of essential biodiversity variables: A bird perspective

Poster

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The fact that the world is losing its biodiversity due to human activities causing habitat loss and fragmentation has been widely known and studied. Populations of sensitive species become more isolated and decrease in size as their suitable habitats become fragmented and degraded. Monitoring how landscape changes affect biodiversity should thus be a central component of landscape planning. For this reason, the concept of essential biodiversity variables (EBV) was defined, with the intent to identify key elements to monitor. One way to derive EBVs spatially may be through the use of niche-based species distribution models (SDM) based on quantification of species' habitat suitability. Environmental data to feed SDMs may come from existing mapped datasets but also from remote sensing technologies (mainly satellite imagery here). In this project, we aim to develop and test new approaches based on SDMs and remote sensing data to build spatial predictions of EBVs for birds. The developed tools should allow assisting bird monitoring in space and time, and ultimately help identifying priority bird conservation areas.

Asexuality takes over the front of invasion waves: a new explanation for geographic parthenogenesis

Poster / FlashTalk

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You are a Eukaryotic female, and say you have the choice between reproducing sexually or asexually. What should you do? It depends. What are the others doing in your population? Can you really reproduce on your own, or do you still depend on interactions with a male in order to complete parthenogenesis? Genetically, would your offspring be a perfect clone of yourself, or instead an extremely inbred version? And by the way, do you find yourself at the front of an invasion wave? This last question seems to be of special importance, and potentially even override the others. I propose a genetically- and spatially-explicit individual-based model, where asexuals mutants are able to take over the margins of an expanding sexual population. They do so thanks to various combinations of demographic and genetic features that are advantageous specifically on the margin, and those advantages depend on their way of achieving asexual reproduction, reflecting the variety of asexual forms in nature. Patterns produced by the model are also consistent with typical instances of geographic parthenogenesis proposed in the literature, such as an association of asexuality with higher altitudes, latitudes, on islands, in deserts, or disturbed areas, as the common denominator of those environments is a history of relatively recent colonization.

Climate change negatively affects the ontogeny of cognitive performance in cleaner fish

Poster

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Climate change is a major threat to coral reef ecosystems worldwide. Here, we present the immediate negative effects of extreme weather disturbances on the cognitive sophistication of cleaner wrasse *Labroides dimidiatus*. Cleaners are key organisms on coral reefs contributing to the maintenance of healthy fish communities through their removal of ectoparasites. We report a significant decline in the ability of cleaners to manage their own reputation and strategically prioritise clients, following recent perturbations. One location had been heavily impacted by cyclones in 2014/2015, while the other one had been exposed to coral bleaching during the 2016 El Niño event, i.e. just three months prior to our experiments. This implies that the reduced cognitive performance has ontogenetic causes. Lower cleaner densities emerged as key explanation for the observed loss in sophistication. In conclusion, contemporary climate change may cause diverse and unexpected effects on species interactions, including the loss of more complex cognition.

First complete species-level molecular phylogeny of Barn Owls and allies (Strigiformes: Tytonidae)

Poster

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Few examples of complete phylogenetic studies of cosmopolitan groups are found in the literature, and the avian family Tytonidae is a good model, majorly represented by the cosmopolitan Barn Owl, the "Tyto alba species complex", which contains more than 30 putative subspecies worldwide. Occurring in every continent across a wide range of habitats, including many islands, Tytonidae comprises 16 currently recognised species assigned to two genera: *Phodilus* and *Tyto*. To this date no densely sampled molecular phylogeny has been available for this group. Previous authors have made efforts to assess phylogenetic relationships, but while some have left out many taxa or key geographical regions, others have relied on small amounts of genetic data. It was clear that there was a need to increase inter- and intra-specific sampling, and to increase the range of geographical locations included, while using consistent taxonomic terminology. Taking advantage of field data and museum collections worldwide, we analyse, for the first time, all currently recognised species, and 50 out of 52 subspecies. Thus providing the most recent and densely sampled molecular phylogeny of the Tytonidae family to date.

Using life-history traits to predict arthropod responses to grasslands management amid species pool influences.

Oral presentation

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To maintain the characteristic biodiversity of semi-natural meadows, regular management by mowing is required to avoid vegetation succession. We use a trait-based approach to test the effects of three mowing regimes on several groups of grassland arthropods. We use literature data on phenology and larval substrate to identify which species are most likely to benefit from the changes in management. Mowing regime was manipulated by delaying mowing by one month or leaving an uncut grass refuge on 10-20% of the field in comparison to control meadows (first cut after June 15). Arthropod communities were assessed after 4-5 years of treatment. We only tested for legacy effects, i.e. before the first cut of the year. The various arthropod groups showed contrasting responses to the mowing regimes: we found positive effects of delayed mowing on parasitoid wasps and sawfly larvae, and of refuge apportioning on Lepidoptera larvae, whereas no effects were found on ground beetles, rove beetles, wild bees and hoverflies. Using the trait-based approach, we found that species with vegetation-dwelling species, and species with a later phenological peak can benefit from the alternative mowing regimes. We conclude that delayed mowing and refuge apportioning have lasting effects on biodiversity and can easily be implemented within the agri-environment scheme framework.

Community selection increases biodiversity effects in a grassland experiment

Oral presentation

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The ecological consequences of biodiversity loss are numerous and include the destabilization of ecosystem functions such as biomass production and nutrient cycling. Statistical and ecological mechanisms underlying these biodiversity effects have been studied at large, but this is not the case for evolutionary mechanisms. Nevertheless, it was previously found that short-term selection at the level of species increased biodiversity effects. Here we show that this also applies to short-term selection at the level of entire plant communities. We used a long-term field biodiversity experiment to select plant communities of different species richness levels over eight years and planted these selected communities next to unselected communities on co-selected or neutral soil. Over the subsequent four years of growth the selected plant communities produced more biomass and expressed stronger biodiversity effects than unselected communities. Soil co-selected with plant communities reduced biomass production but dampened variation between years. Our findings suggest that natural communities with a long history of community selection cannot simply be reconstructed by reassembling them with the same species but lacking the same community selection history; local extinctions may thus be less reversible than expected.

Offspring presence modulates predator defence in parents

Poster

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Ambient predation risk can influence animal life history strategies such as growth trajectories and the decision between natal philopatry and dispersal. Young animals may learn about predation risks from cues perceived by adult conspecifics. As exemplified by some birds and mammals, parents can deliberately modulate their behaviour to signal risk levels to the offspring (signalling hypothesis). On the other hand, parents may change defensive behaviours against offspring predators in response to perceived offspring vulnerability and risk. In either case, parental defence levels should differ depending on the presence of young offspring. Here we investigated aggression of parents towards a predator animation in the African cichlid *Neolamprologus pulcher*, when offspring were either present with the parents vs. when they were separated by an opaque divider. Males were generally more aggressive towards the predator stimulus than females. Surprisingly, both parents showed more aggression towards predator when the offspring were separated. This result objects the signalling hypothesis. Instead increased stress levels of offspring during the separation process or the absence of offspring may have been perceived by the parents as (risk of) offspring predation, which in turn may have invoked the stronger defence response in parents.

Discrete genetic elements drive diversity effects in conspecific plant communities.

Poster

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Ecological experiments have frequently found a positive relationship between the biological diversity and the productivity of communities. Such effects have, however, neither been fully explained at the functional level, nor have they received enough attention from a breeding perspective. I have examined positive genetic diversity effects in conspecific communities consisting of different Arabidopsis accessions, for which genetic mapping populations are available. Results from a quantitative genetic approach indicate that these effects can be driven by allelic variation at discrete loci. The mendelization and molecular cloning of such discrete genetic elements (at which allelic diversity between two accessions drives overyielding in genotype mixtures) is currently in progress. I have fine-mapped one locus with major effects to a two-centimorgan interval. This has led to the identification of a possible candidate DNA polymorphism in a gene known to mediate in a trade-off between growth and defense. The work provides proof-of-principle that a genetic approach can help identify genes, traits and mechanisms that underlie niche differentiation in conspecific plant communities, and (by the use of population genetics) allow for the study of evolutionary forces shaping biodiversity effects.

Ecological predictors of social organization in the Alpine silver ant

Poster

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Insect societies vary in their social organization, yet the influence of ecological factors on the maintenance of this variation remains poorly understood. In the Alpine silver ant *Formica selysi*, colonies headed by one queen (monogynous) or by several queens (polygynous) occur in the same populations. In the Alps, the proportion of monogynous colonies increases with elevation. Using a niche modeling approach, we aim to unravel the ecological factors shaping the species distribution and the distribution of each social form. We found that elevation, soil composition and Mean Diurnal Range are the main factors shaping the distribution of *Formica selysi* over its entire range. We will perform similar analyses to uncover the ecological factors favoring alternative forms of social organization. These results will provide insights into the impact of the environment on ant social organization at a continental scale.

Male × male × female interactions in *Drosophila melanogaster*

Poster / FlashTalk

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Unravelling variables explaining sperm competition success is crucial to resolve the processes of sexual selection and helps improve our understanding of sexual conflict and reproductive isolation. It seems likely that the outcome of fertilization is influenced by both male and female genotypes. However, the importance of physiological variables and how they interact remain a conundrum, partly due to the limitations in the study of post-copulatory selection in internally fertilizing species. Here, we used Drosophila melanogaster to competitively mate pairs of males with females in different combinations among given genotypes. The use of genetically modified male isolines producing sperm carrying non-identical fluorescent tags allowed us to resolve the effects of numerous variables on sperm competition success, including but not limited to in vivo sperm velocity, relative number of sperm stored and ejected by the female as well as relative numbers of offspring sired by each male. We examined the interactions between the different genotypes and traits, opening new insight into genetic compatibility.

Integrating biodiversity conservation in temperate agricultural landscapes

Oral presentation

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Biodiversity needs space and access to net primary production of ecosystems and therefore often competes with agricultural production. As land is limited and human population rising, this conflict is likely to increase further and calls for more researches on how to better integrate biodiversity conservation in agricultural landscapes. This study describes how the proportion of cropland, natural permanent grasslands and agri-environment schemes (AES) influence bird and butterfly diversity at landscape scale. The study was conducted in the Swiss lowland, where land use and biodiversity data from 90 different landscapes of 1 km2 were analyzed. We used three different indicators as proxy for land-use and management intensity. The results show that biodiversity of birds and butterflies can be maintained at intermediate land-use intensities. Particularly the proportion of AES (extensively managed areas) had a positive influence on species diversity and abundance. Nowadays there is an urgent need to define land-use strategies to integrate agricultural production and biodiversity conservation in landscapes. Our results show how biodiversity reacts to land-use intensity in temperate landscapes and that agri-environment schemes can effectively promote biodiversity.

Plant chemical defense indirectly mediates aphid performance via interactions with tending ants

Oral presentation

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The benefits of mutualistic interactions are often highly context-dependent. For example, the interaction between aphids and tending ants is generally considered beneficial, yet plant genetic variation may alter the effects of tending from mutualistic to antagonistic. In an attempt to identify the mechanisms underlying this effect, I could link the shift in strength and relative benefit of one ant-aphid interaction to plant genotypic variation in the production of a plant defensive compound. Using a field experiment with highly variable plant genotypes, I could show that plant defensive compounds are ingested by aphids, of which a subset is excreted in aphid honeydew without directly affecting aphid performance. Toxin content in plants directly determines contents in honeydew, and aphids excreting higher amounts of plant toxins received fewer ant visits, which reduced aphid survival. Plant defensive compounds without direct effects against herbivores may thus be revealed as important when multi-trophic interactions are considered.