

biology09

12-13th February 2009

zoology

University of Bern and Natural History Museum Bern
Charles Darwin's 200th Birthday
150 years „Origin of species“

botany

Abstract book of posters (alphabetical 1st authors)

mycology

Uni S - room 303

Invited speakers...

Clive Brasier

Fredrik Ronquist

Nina Wedell

James Bullock

John Pannell

systematics



Institute of Ecology
and Evolution -
University of Bern



Natural History
Museum Bern

1 Macroinvertebrate oviposition and the success of river restoration efforts

Maria Alp, Christopher Robinson

Morphological heterogeneity of a river determines habitat diversity which is linked to the diversity of aquatic organisms. Morphology includes not only variability in depth and width, but also the presence/size range of substrates in the stream. Large stones in a river can provide different “services” to biotic communities by enhancing hydraulic heterogeneity, offering habitat/shelter as well as substrate for oviposition by aquatic organisms. The role of boulders for biotic communities is pronounced not only at the local, but also at the regional scale, as stone availability may be crucial for the reproduction of many aquatic insects by influencing dispersal during the adult phase. Dispersal/recruitment of aquatic organisms is getting more interest in the context of river restoration. The aim of most restoration efforts is to create a healthy and diverse biotic community by offering organisms a variety of habitats. However, results of many restoration projects have been disappointing, indicating that not only habitat availability but also dispersal barriers and the regional species pool are crucial limitations for successful colonization of restored sites. Field experiments in two Swiss lowland rivers investigated the importance of substrate availability for the oviposition and recruitment of aquatic invertebrates. We manipulated substrate availability in reaches with different morphology and recorded oviposition through the adult flight season on added and naturally present substrates. The results revealed that oviposition substrate availability can be an important constraint for the reproduction and dispersal of many aquatic macroinvertebrates and thus must be considered when planning restoration efforts.

2 Projection of the butterfly diversity in Switzerland considering climatic changes until 2050

Florian Altermatt, Michael Nobis, Matthias Plattner

Butterflies are very sensitive to climatic changes. Therefore, they are often studied in the context of the current global warming. Among others, changes in the phenology, range shifts to higher latitudes and altitudes have been reported. There exist, however, no large-scale projections on how these changes influence the composition and diversity of whole butterfly communities in the future. Within the context of the Swiss Biodiversity Monitoring (BMD), we made for the first time a projection of the butterfly diversity in Switzerland until 2050. In the BMD, butterfly species richness is measured in about 500 transects that are regularly distributed all over Switzerland. Based on these field-measured data, we modelled nationwide the actual distribution of the butterfly species richness using environmental variables such as altitude, mean annual temperature, or forest cover. We then used this model to predict future butterfly species richness. The predictions were calibrated with actual climate data and depended on possible future climate scenarios. We assumed an increase in annual mean temperature of 2 °C until 2050. We found that many butterfly species expand their range to higher altitudes. As a consequence, butterfly species richness increases above 1200 m. In the future, we expect that several butterfly species may occur in alpine areas, which are currently not present. At lower altitudes such as in the Plateau and in the Jura, however, we predicted a decrease in butterfly species richness. Changes in the microclimate or changes in the vegetation may be possible explanatory mechanisms. Because the species loss at lower altitudes affects a much larger area than the species increase at higher altitudes, the mean butterfly species richness in Switzerland decreases slightly. Our model does not predict which species will be affected most by the changes. Possibly, generalists expand their range to higher altitudes, and species richness increases. At the same time, they may become competitors of alpine specialists and displace the latter.

3 How urgency levels in alarm calls influence the forager's response in Meerkats.

Valérie Amsler, Marta Manser

Many social animals exchange information about threats in their surrounding environment through vocalization. Several studies have shown that alarm calling increases the probability of not being

predated, especially during foraging activities, when individuals focus on maximizing their food intake in a minimal amount of time. Many animals using such calls convey either information on the type of approaching predators, or on the speed needed to escape from a predation threat. Meerkats (*Suricata suricatta*) inform other group members about surrounding threats through several types of alarm calls, which encode the predator type and the level of urgency simultaneously. This field study focuses on evaluating how the information transmitted in alarm calls of different levels of urgency influence the foraging receiver. By performing playback experiments of alarm calls recorded at different levels of urgency, I investigate how they influence the meerkat's foraging behaviour. In particular I test how the meerkat deals with a certain level of predation pressure depending on the energy already invested in acquiring a specific food resource. Results show that using levels of urgency enables meerkats to adapt their response to a potential threat: they increase their foraging efficiency by making trade-offs when an alarm call is heard. The more time and energy they spend on chasing a certain prey, the more they tend to take risks.

4 Effect of genetic drift in Arbuscular Mycorrhizal Fungi (AMF) on their response to a change of environment

Caroline Angelard and Ian Sanders

Arbuscular mycorrhizal fungi (AMF) form symbioses with the majority of plants, improving plant nutrition and promoting plant diversity. They grow and reproduce clonally by producing hyphae and multinucleate spores. These eukaryotic fungi are known to harbour genetically different nuclei and we already know that genetically distinct isolates of *Glomus intraradices* have different phenotypes. We recently found that single spores of AMF do not necessarily inherit the same genetic material due to unequal segregation of nuclei during spores' formation. Moreover, this genetic drift results in genetic and phenotypic divergence between single spore lines. The aim of this study was to determine whether single spore lines respond differently to a change of environment. We initiated "drift lines" of AMF from single spores of "parental lines" and we cultivated these lines on different host species. After several generations, we compared the phenotypes and genotypes of drift and parental lines. Results indicate that genetic drift can lead to lines responding to a change of host with phenotypic and genetic changes. Interestingly, we observed strong interactions between the AMF lines and host species. The effects of this type of drift could have important consequences for the coevolution of the plants and AMF and should be considered in future research to understand these important soil organisms.

5 Effective habitat connectivity measures for European tree frogs in Switzerland

Angelone, Sonia^{1,2}; Holderegger, Rolf¹

Swiss authorities support habitat connectivity measures to enhance the exchange of individuals among fragmented populations. Following a genetic approach, the effectiveness of connectivity measures can be evaluated by choosing independent landscapes differing in population density and implemented measures. We retraced the population history of the European tree frog (*Hyla arborea*) in the Reuss and Thur river valleys, performed a comprehensive population sampling to infer the genetic structure at eleven microsatellite markers, and used assignment tests to evaluate recent exchange of individuals among populations. The Reuss valley lost more breeding sites (56 vs. 27) and exhibited double genetic grouping ($K = 6$ vs. 3) than the Thur valley. However, almost identical numbers of first generation migrants were detected in both valleys (26 and 24). In the Reuss valley, 21 of these events occurred within the clusters identified, whereas in the Thur valley the migration pattern was diffuse. The analyses show that the connectivity measures implemented for the tree frog in the Reuss valley warranted effective migration among breeding sites within distances of 4 km to 5 km. However, the gene pools in the Reuss valley showed strong differentiation, which still reflect the impact of present barriers to tree frog movement. In contrast, a large number of populations have been preserved in the Thur valley and high population admixture indicated regular gene exchange among populations at distances of up to 13 km. Responsible authorities should continue implementing

connectivity measures with the long-term prospect to establish connections among the identified genetic clusters.

6 I crossed the ocean! What now? – linking dispersal, diversification and changing climates.

Alexandre Antonelli, Rafael Wüest, Peter Linder

What is the link between long distance dispersal and diversification in plants? Understanding the ecological and evolutionary processes that take place following a dispersal event may help us predict how invasive species will behave in new environments. The current worldwide distribution of the grass subfamily Danthonioidae points to several long distance dispersal events in the past, especially frequent between Australia and New Zealand. This makes it a perfect study group to investigate the relationships of dispersal, diversification and changing climates. We use phylogenetic reconstructions, molecular dating and habitat optimization analyses to identify key shifts in niche preferences and diversification rates. Our main research questions are: How did climatic changes influence the geographic range of currently rare species and their dispersal rates? Following a dispersal event, do diversification rates flatten out as fewer niches become available? Can we detect the founder effect (narrower niche width of dispersed species compared to ancestral)? Are historical changes in niche availability correlated to diversification rates?

7 Hybridization in the Triticum-Aegilops complex

Arrigo Nils, Lappe Sylvain, Guadagnuolo Roberto, Felber François

The domestication of wheat (*Triticum* sp.), one of the major crop currently cultivated, results from allopolyploidization events that involved *Aegilops* species. The reproductive isolation of both genera is incomplete. *Aegilops* species are traditionally used by wheat breeders as sources of beneficial traits, and conversely, F1 hybrids between wheat cultivars and *Aegilops* species are regularly reported in agroecosystems. Despite these observations, long term consequences of a transfer of wheat genes in the *Aegilops* genetic pool are poorly documented. This topic is however especially of concern for risk assessment studies associated for instance to the potential release of transgenic wheat. My Ph.D thesis assessed the presence of wheat genetic markers within three European *Aegilops* species. In the following talk, I present the approaches and tools that were developed during this study: 1. The surveys of European populations of *Aegilops* species. We collected populations that grew along wheat field borders and compared them to individuals sampled in wheat isolated areas. This survey provided the basis of my investigation. 2. The use of AFLP markers to detect the potential wheat gene flows that occur in *Aegilops* populations. This analysis requested the development of analysis tools with R CRAN. A first outcome was the development and release of RawGeno, a new freeware scoring algorithm that allowed a quick and reliable analysis of our AFLP datasets. The second outcome was the confirmation that a long-term introgression of wheat markers occurred in *Aegilops* populations collected near to crop cultivations.

8 Food habits of long-eared bats: the Swiss menu and its conservation implications

Ashrafi, Sohrab; Bontadina, Fabio; Beck, Andres, Arlettaz, Raphaël

The discovery of new cryptic species demands a re-evaluation of the previous knowledge regarding the recognised species and clarifying the ecological traits of the new species. Recently, molecular evidence has proven the existence of a sympatric cryptic species, *Plecotus macrobullaris*, in the alpine region. In this study we aimed to study feeding habits, niche breadths and overlaps, seasonal and regional variations in diet compositions of three *Plecotus* bat species, including the newly found *P. macrobullaris* in Switzerland. We collected 899 faecal pellets of the three *Plecotus* bat species

(*Plecotus auritus*, *P. austriacus* and *P. macrobullaris*) from eight colonies where the species was determined by DNA. The faeces were collected from individuals returning to their roost after feeding, in monthly intervals from May to September in the cantons Valais and Argovia. We found fragments of 21 orders and families of arthropods in the food remains. These bats eat predominantly Lepidoptera (41%, 88% and 87% in *P. auritus*, *P. austriacus* and *P. macrobullaris*, respectively). The major food items in all three species were Lepidoptera, Coleoptera, Diptera, Dermaptera, Arachnida and Chilopoda. Finding fragments of diurnal and flightless insects revealed gleaning behaviour only in *P. auritus*. Results showed a much wider niche breadth in *P. auritus* than in the other two species. The species show different niche overlaps, possibly explaining their current pattern of distribution in Switzerland. Abundance and diversity of moths, the major food of *Plecotus* bats, should be considered in species conservation programs.

9 Identification of candidate genes and physiological pathways involved in unexplained gonad deformation in whitefish (*Coregonus lavaretus*, L.) from Lake Thun, Switzerland

D. Bittner, A.R. Cossins, L. Excoffier, C.R. Largiader

Recently, fishermen reported the sudden appearance of unusually deformed reproductive organs in whitefish (*Coregonus lavaretus* L.) from Lake Thun, Switzerland. Despite intensive investigations, the causes of these abnormalities have remained unknown. Using gene expression profiling, we aimed at identifying new candidate genes and physiological processes associated with observed gonad deformations, in order to gain new insights into their potential causes. Using in situ-synthesized oligonucleotide arrays, we compared the expression levels at 21'492 unique transcript probes in liver and kidney tissue of male whitefish with deformed and normally developed gonads, respectively. The fish had been collected on spawning sites of two genetically distinct whitefish populations of Lake Thun. Analyses included gene expression profiles of 56 individuals, i.e. 14 individuals of each phenotype and population respectively. Gene by gene analyses revealed weak expression differences between normal and deformed fish, while we found very strong differences between the two whitefish populations, i.e. ca. 50% of all genes showed significant expression differences in both tissues. At the level of physiological processes, we identified significant enrichment of co-regulated genes in particular gene ontology (GO) categories, when comparing deformed and normal fish in both populations. In particular, we found categories involved in the immune system in both tissues, with genes primarily concerned in complement activation (up-regulation in deformed fish of both populations). Further congruencies were found in genes related to extracellular region and proteolysis in the liver and GTPase activity and Ras protein signal transduction in the kidney. We discuss the potential involvement of xenobiotic substances with focus on immunotoxicology.

10 The effect of land use on lichen diversity in the Biodiversity Exploratories

Steffen Boch, Dominik Hessenmöller, Daniel Prati, Markus Fischer

In geographically different regions of Germany three research sites for large-scale and long-term functional biodiversity research were established. The aim of this study is to analyze (1) the impact of different land use types and intensities on the lichen diversity and the species composition and (2) how the diversities of different species groups (vascular plants, bryophytes and lichens) are related to each other. We sampled 635 forest relevés with a plot size of 400 m², and 379 grassland relevés with a plot size of 16 m². The plots were selected randomly stratified across land use gradients. We recorded all vascular plants, bryophytes, lichens and different structural parameters. In forests we found a total of 200 lichen taxa. Species densities per plot varied between one and 53. Highest mean lichen species densities were found in the forests of the Schwäbische Alb (18.8), intermediate densities in the Schorfheide-Chorin (6.0), and lowest densities in the Hainich area (5.0). The lichen species densities in comparable forest types within one Exploratory varied slightly under different forest management regimes. We found no relationships between lichen and vascular plant diversity, but we found a positive relationship between lichen and bryophyte diversity. In grasslands we

recorded a total of 111 lichen taxa. Species densities per plot varied between zero and 30. We found positive relationships between lichen vs. vascular plant and lichen vs. bryophyte diversity.

11 Detecting shifts in competitive interactions under climate change in a long term dataset

Odile T. Bruggisser; Gilles Blandenier; Louis-Félix Bersier

Climate change is expected to affect species interactions within natural communities. This question is of key importance for modelling; however, up to now only changes in phenology and distribution have been documented. Here, we present a method based on wavelet analyses of multiple time series (inspired by neurobiology) to detect pairs of potentially interacting species. Wavelet analysis allows the consideration of different time scales, with negative correlations assumed to represent competitive dynamics. Changes in the structure of interactions over time are identified with a sliding window approach. We present results of bench tests and apply the method to a weekly dataset spanning over 11 years of a ballooning spider community in Switzerland.

12 Identification of key volatile compounds used in host location by the parasitoid *Cotesia marginiventris*

Virginie Brunner

Maize seedlings (*Zea mays* var. Delprim) infested by the herbivore *Spodoptera littoralis* (Lepidoptera: Noctuidae) emit different volatile blends than uninfested plants. These herbivore-induced plant volatiles are used by the parasitoid *Cotesia marginiventris* Cresson (Hymenoptera: Braconidae) to locate its host. However, the key compounds responsible for the attraction are still unknown. To gain insight into the nature of possible attractants we used selective filters to trap specific parts of the total blend of herbivore-induced volatiles which was tested in a four-arm olfactometer. It was found that extracts of a silica containing filter, which retained 30% of all detected compounds, were highly attractive and more attractive than the total blend. The highly attractive silica extract was separated by preparative gas chromatography in several steps using different columns. Some fractions were significantly more attractive than others, but lost this property after sub-fractionation. These results imply that there is not just one compound involved in this attraction but several acting in synergy. We tested synthetic versions of some compounds found in the silica extract. (E)-nerolidol and (-)-linalool were attractive but (+/-)-linalool was repellent. These results support the notion that multiple compounds are involved and that the chirality of a molecule is important for attraction. The eventual identification of the most attractive compounds will help to select crop varieties that are more attractive to natural enemies of herbivores.

13 Effect of fruit size and fruit abortion in a plant/seed predator system

Anne Burkhardt and Giorgina Bernasconi

Plant-pollinator interactions are well-known examples of mutualism, but are not free of antagonism. Antagonistic interactions and defenses/counter-defenses are expected particularly in nursery pollination, where adult insects, while pollinating, lay eggs in flowers, and juveniles consume seeds from one or several fruits, thereby substantially reducing plant fitness. The outcome of such interactions will depend, for the plant, on the balance between pollination vs. seed predation and for the larvae on the balance between food and shelter provided vs. costs imposed by plant defenses, e.g., through abortion of infested fruits. Here, we examine costs and benefits to the larvae in the nursery-pollination system *Silene latifolia* / *Hadena bicruris*. Using selection lines that varied in flower size (large- vs. small-flowered plants), we investigated the effects of variation in flower/fruit size and of a fruit abortion, on larval performance. Larger flowers gave rise to larger fruits with more seeds, and

larvae that were heavier at emergence. Fruit abortion was frequently observed (ca. 40% of infested fruits). From aborted fruits, larvae emerged earlier and were substantially lighter than larvae emerging from non-aborted fruits. The lower mass at emergence of larvae from aborted fruits suggests that abortion benefits the plant by limiting both resources invested in attacked fruits, as well as the risk of secondary attack. Moreover, by reducing mass at emergence of seed predators, fruit abortion likely reduces survival prospects of larvae. This strongly suggests that selective fruit abortion is an effective defense that may contribute to the stability of mutualism in this non-obligate system.

14 Do habitat suitability models reliably predict the recovery areas of threatened species?

Carmen Cianfrani, Anna Loy, Alexandre H. Hirzel, Gwenaëlle Le Lay

Predicting the locations of the areas suitable for the spatial recolonization of threatened species is essential to support efficient conservation policies. Habitat suitability models (HSM) predict the species distribution. As they rely on the ecological niche concept, the consistency of their predictions depends on the validity of the species-environment equilibrium hypothesis. In the case of expanding species, the non-equilibrium situation addresses the reliability of the species absence data to feed the HSM. We considered a recovering threatened species, the Eurasian otter (*Lutra lutra*) in southern Italy. We used data before recolonization events to produce HSMs, one using presence-only data (Ecological Niche Factor Analyses, ENFA) and a second using presence-absence data (Generalized Linear Model, GLM). We used data from the recolonization event to validate these models. We also compared the spatial predictions of these models to a second set of models, using the recolonization data. Our results demonstrated that taking into account absence data can produce wrong predictions of the areas suitable for the recovery of the species. The presence-absence model built with data before recolonization disagrees with the other models about the environmental factors important for that species and the location of the suitable areas. As a conclusion, in non-equilibrium situations, such as in the case of threatened species naturally recovering or for invasive species, the prediction process could be fooled by misleading absence data. If the problem is ignored, it may misinform wildlife conservation efforts to the point that management actions are non- or counter-effective.

15 Stochastic modelling of prey depletion processes

Thomas Clerc; Anthony C. Davison; Louis-Félix Bersier

Classically, prey-predator interactions are modelled using ordinary differential equations, but this has the drawbacks of assuming continuous population variables and of being deterministic. We propose a very general approach to stochastic modelling based on the concept of functional response for a prey depletion process. Our model could involve any kind of functional response, and permits a likelihood-based approach to statistical modelling. To illustrate the method we use the Holling–Juliano functional response and compare the outcomes of our model with a deterministic counterpart considered by Schenk and Bacher (2002), who observed the depletion of *Cassida rubiginosa* due to its exclusive predator, *Polistes dominulus*. The predation was found to be Holling type III, reflecting the ability of the predator to regulate its prey. Our approach corroborates this result, but suggests that the prey depletion census should have been done more often, and that the predation features were significantly different between the two years for which data are available.

16 A hybrid zone of two deeply diverged green toad taxa in north-eastern Sicily

Colliard C., Sicilia A., Turrisi G. F., Arculeo M., Perrin N., Stoeck M.

One of the key questions in evolutionary biology is the amount and speed of reproductive isolation accumulating in allopatric speciation (Coyne and Orr 2004). Our knowledge is especially scarce in

Western Palearctic frog lineages. Endemic green toads from Sicily (*Bufo siculus*) are phylogenetically closer to North African *B. boulengeri* than to neighbouring Italian Peninsular-origin *B. balearicus*. Using new microsatellite and mtDNA (Colliard et al. *Mol. Ecol. Res.*, in press) in a phylogeographical and population genetic framework, we demonstrate that *B. siculus* and *B. balearicus* co-occur in north-eastern Sicily, reproduce and form a hybrid zone. Since originally allopatric *B. balearicus* has been separated about 2.75 (1.19–4.9) My from the *boulengeri-siculus* clade (Stöck et al., *BMC Evol. Biol.* 8: 56, 2008), this hybrid zone results from a secondary contact after *B. balearicus* reached Sicily. Laboratory F1-hybrids are viable, but none were found in the wild. However, apparent F3- or F4-hybrids imply that at least rare F1-hybrids occur and backcross. Different degrees of mtDNA-introgression were observed, creating strong cytonuclear disequilibria in many hybrid zone individuals. MtDNA introgression is bidirectional, with *B. balearicus* mtDNA introgressing into the *B. siculus* gene pool (from the *balearicus* geographic range into the *siculus* range) and vice versa. Reciprocal F1-hybridizations are possible since we found mtDNA introgression in both directions. The cline of the nuclear genome introgression is much steeper than that of the mtDNA. Merging of both nuclear gene pools was not observed suggesting selection against hybrids and that both species maintain their identity.

17 Food or nesting place? Identifying the factors limiting wryneck population

Valérie Coudrain

In the last few years, several studies on wryneck populations have contributed to a better ecological understanding of this endangered bird. However, the ongoing decrease of the population called for an assessment of the factors limiting its occurrence. Our study addressed this issue by comparing known breeding territories and random territories in function of two ecological particularities of the wryneck: its food specialisation and its need of existing cavities to breed. In three regions of Switzerland, we compared the offer at breeding cavities, food abundance and vegetation structure of known breeding territories and random territories. Additionally we tested if wrynecks showed preferences for certain habitat types. Since ants are the main prey of wrynecks, we investigated the environmental variables affecting ant nest distribution and size. Breeding territories were mainly characterized by the conjoint presence of breeding cavities and higher ant abundance. Additionally, wrynecks appeared to prefer heterogeneous habitats with an amount of bare ground around 45%. Semi-vegetated vineyards and orchards were positively selected by the wryneck, whereas fields and grasslands were avoided. Ant nest density and size were especially large in semi-vegetated vineyards and small in grasslands. Temperature and the amount of bare ground were important determinants of ant abundance. Our results suggest that Wrynecks can adapt their distribution in function of nesting possibilities and food availability. Installation of nest boxes in habitats managed in an ant-friendly way should promote wryneck expansion. Habitats that combine vegetation and bare ground surfaces, such as semi-vegetated vineyards and low-stem orchards, appear particularly favourable.

18 Evidence for purifying selection among genetically different nuclei within one individual of the symbiotic fungus *Glomus intraradices*

Daniel Croll, Ian R. Sanders

Arbuscular mycorrhizal fungi are important plant symbionts with a unique genetic organisation. Individuals harbour genetically different nuclei within hyphal filaments and spores. Genetic heterogeneity within an individual and its transmission over generations pose a challenge to the classical view of selection acting mostly between individuals of a population, as selection could also act among the genetically different nuclei within an individual. Large-scale sequencing data from expressed sequences of one *Glomus intraradices* individual was used to identify patterns of single nucleotide polymorphism. A substantial amount of polymorphism was found, confirming the genetic differences among nuclei within an individual. The identified polymorphism was classified depending on whether it affects the amino acid sequence of encoded proteins (non-synonymous vs. synonymous changes). A majority of the coding regions exhibited a bias towards synonymous changes and more

than two dozens of predicted genes showed significant evidence for purifying selection. This suggests that mechanisms of selection exist within the individual to eliminate mutations with an effect on the protein sequence. However, a substantial number of predicted genes showed non-synonymous polymorphism indicating potentially deleterious effects on the functioning of the mycelium. The relative importance of the within-individual selection is likely to shape the evolution of these fungi and provides a unique framework to study selection at multiple levels.

19 Regional differentiation in skin peptide composition among color morphs of *Agalychnis callidryas* from Panama & Costa Rica

L.A. Robertson, J.M. Zamudio, K.R. Rutschow, H.L. Van Wijk, K.J., Sun, Q.I., Haribal, M.M.

The red-eyed treefrog *Agalychnis callidryas* is a widely distributed Neotropical frog that ranges from southern Mexico to Colombia. Tremendous variation in color, pattern, and body size has been documented from populations of *A. callidryas* in Costa Rica and Panamá. Here, we examine geographic variation in peptide composition to investigate isolation among these differentiated regions. Over two dozen peptides have been isolated from the skin extracts of *A. callidryas*; however, we know very little about the geographic variation among populations across this range. We collected skin peptide samples from 200 individuals from 13 different populations representing each of five, phenotypically distinct regions throughout Costa Rica and Panamá. Skin peptides were collected using a Transcutaneous Amphibian Stimulator which uses a mild electrical stimulus for skin secretion. Frog skin exudates were swabbed with sterile Qtips and stored in methanol. Peptide samples were analyzed by HPLC on a Luna RP-300 with a 5m analytical column (Phenomenex) using a gradient system of 0.2% TFA in water and acetonitrile and molecular weights were determined using MALDI-TOF MS/MS. We compared the chromatogram patterns of individuals within and among locations to quantify divergence in peptide components. Our data suggest a pattern of non-clinal and strongly regionalized variation in peptides among sampled populations. We used matrix correspondence tests to assess the correlation of this phenotype with other differentiated phenotypes in this species. These data will contribute to our understanding of the population differentiation and biogeography in this region; our results highlight the use of skin secretion peptides as a character for studies of population differentiation and biogeography.

20 Parasitism and winter survival in the common vole

Godefroy Devevey, Alia Mafli, Natacha Luximon, Andreas Sanchez, Philippe Christe, Pierre Bize

Effects of parasites on host reproduction have been demonstrated many times, with parasitized hosts producing fewer offspring that are less likely to survive until adulthood. However, very little is known about the role played by parasites outside the reproductive period, especially in temperate areas where host populations experience strong energy bottleneck during winter. In an ongoing experiment ran on the green roofs of the Biology Building of Lausanne, we are investigating effects of macro-parasitism on body mass maintenance and survival of free-living common voles *Microtus arvalis*. Preliminary analyses after the first 3 months of study on body mass maintenance and survival rate of voles from parasitized versus control populations are presented.

21 Behavioural attainability of evolutionarily stable strategies in repeated interactions

Dobler Ralph, Mathias Kölliker

Theory for the evolution of social interactions based on continuous strategies often assumes for simplicity that expressed behaviours are independent from previous encounters. In reality, however, such dependencies are likely to be widespread and often strong, generating complex behavioural

dynamics. To model this process and illustrate potential consequences for the evolution of behavioural interactions, we consider the behavioural dynamics of the interaction between caring parents and their demanding offspring, a prime example for long series of interdependent and highly dynamic interactions. These dynamics can be modeled using functions describing mechanisms for how parents and their offspring respond to each other in the interaction. We establish the general conditions under which the behavioural dynamics converge towards a proximate equilibrium and refer to such converging interactions as behaviourally stable strategies (BSSs). We further demonstrate that there is scope for behavioural instability under realistic conditions; that is, whenever parents and/or offspring 'overreact' beyond some threshold. By applying the derived condition for behavioural stability to evolutionary models of parent-offspring conflict resolution, we show by numerical simulations that evolutionarily stable strategies (ESSs) of current models are not necessarily behaviourally stable. Because behavioural instability implies that expressed levels of behaviours deviate from the ESS, behavioural stability is required for strict evolutionary stability in repeated behavioural interactions.

22 Root herbivore-induced shoot resistance: A physiological explanation for a counterintuitive phenomenon

Matthias Erb and Ted Turlings

Root herbivory can change shoot physiology and increase resistance of plants against aboveground attackers. Little is known about the mechanisms that are involved and if such interactions have any adaptive value. We therefore investigated if, how and why maize seedlings infested with the root herbivore *Diabrotica virgifera* develop resistance in their aboveground parts. Leaves of *D. virgifera*-infested plants displayed increased resistance against both the pathogen *Setosphaeria turcica* and the herbivore *Spodoptera littoralis*. Root herbivory furthermore reduced leaf-water contents and triggered accumulation of abscisic acid (ABA), ABA-dependent defense gene expression and secondary metabolite synthesis. By chemically inhibiting ABA-biosynthesis, we show that the induction of ABA-dependent aboveground changes by itself is a tolerance response of the plant. Direct treatment with ABA also reduced growth of the pathogen, whereas the shoot herbivore was not affected by the hormone, but was sensitive to changes in the plant's water balance caused by root herbivory. These changes were most pronounced under water-limited conditions. We conclude that *D. virgifera* induces shoot resistance against *S. turcica* and *S. littoralis* by triggering ABA-mediated drought-tolerance and upsetting the plant's water balance, two phenomena that are most likely physiological constraints resulting from the interaction between the root herbivore and its host plant.

23 Species abundance patterns in food webs

Yvonne Fabian; Louis-Félix Bersier

The niche hierarchy model (Sugihara et al. 2003) hypothesises a link between the abundance distribution of a group of species and its functional organization. We use information from food-web data to build dendrograms of niche similarity, concentrating only on intermediate species (i.e. having prey and consumers). First, we find generally a negative relationship between the nestedness of species in a dendrogram and their abundance, as expected by the theory. We find that dendrograms built with prey information (dietary similarity) or with predator information provide equivalent results. Thus, when describing the niche of a species, resources and consumers are both important to understand community organization.

24 Microbial enzyme activities as indicators of metabolic hot spots

Frossard Aline¹, Gerull Linda², Mutz Michael² and Gessner Mark¹

Metabolic hot spots are patches in the environment showing disproportionately high metabolic reaction rates relative to the surrounding matrix. The patchiness of riverine landscapes provides scope for such metabolic hot spots, particularly in catchments during early stages of succession. Accordingly, we hypothesized that in an experimental catchment newly created in a post-mining area, metabolic reaction rates are highest in groundwater upwelling zones within stream channels and lowest in soils adjacent to channels, with other instream sites showing intermediate rates. Eight sites were selected in each of three streams and sampled at four occasions. To assess specific metabolic rates, potential activities of enzymes were measured with substrate analogues linked to fluorescent molecules, 4-methylumbelliferone (MUF) or 7-amino-4-methylcoumarin (AMC): 4-MUF-phosphate, 4-MUF- β -D-glucopyranosid, 4-MUF-N-acetyl- β -D-glucosaminid dihydrate, 4-MUF- β -cellobio side, 4-MUF- β -D-xylopyranoide, aspartic acid-AMC, L-glutamic acid β -AMC, L-leucine-AMC. Polyphenol oxidase (PPO) and peroxidase activities were also tested using L-3, 4-dihydroxyphenylalanine (L-DOPA) as substrate. Preliminary analyses suggest that enzyme activities differ greatly among sites and the spatial patterns broadly reflect water availability, although individual enzymes vary in their responses.

25 Molecular systematics of long-legged flies

Christoph Germann, Marc Pollet, Marco V. Bernasconi

Systematic and phylogenetic studies in biology are important in many ways and encompass a wide area from evolutionary biology, pharmacology to conservation biology and many others more. Our study group represents one of the most speciose families of Diptera with more than 7000 described species. Alone in Europe, more than 800 species are known. Dolichopodidae are mostly predaceous and feed on small soft-bodied arthropods, as larvae as well as adults. They have been considered beneficial for pest control; in particular, Medetera species are predators of economically important bark beetles (Curculionidae, Scolytinae). Moreover, Dolichopodidae are excellent bio-indicators for the evaluation of natural areas. Concerning studies on sexual selection, Dolichopodidae have a huge potential as suitable model organisms with outstanding male secondary sexual characters. Despite of their species richness and conspicuous morphological characters, few authors have considered Dolichopodidae phylogeny and hardly any with molecular methods. We present a preliminary overview of the systematics of Dolichopodidae based on mitochondrial (12S, 16S, COI, Cyt-b) and nuclear DNA (ITS-2, 18S) from more than 320 specimens in about 300 species.

26 How does eutrophication lead to plant diversity loss?

Yann Hautier, Pascal A. Niklaus & Andy Hector

Human activities have dramatically increased the availability of nutrients in terrestrial and aquatic ecosystems. In grasslands this eutrophication causes loss of plant species diversity. Surprisingly, we lack a mechanistic understanding of how eutrophication decreases plant diversity even though alternative hypotheses were suggested decades ago. Here, we present a novel manipulation of experimental grassland plant communities which prevented the loss of biodiversity caused by eutrophication through experimental addition of light to the grassland understory. This result supports competition for light as a major mechanism of plant diversity loss following eutrophication and explains the particular threat of eutrophication to plant diversity. Our conclusions have implications for grassland management and conservation policy and emphasize the need to control nutrient enrichment if plant diversity is to be preserved.

27 Valuation of non-native species invasions: a mental models approach

Franziska Humair, Christoph Kueffer, Peter Edwards, Michael Siegrist

Biotic invasions by non-native species are considered one of the main threats to native biodiversity and ecosystem services. However, invasive species often have both positive and negative values in the invaded areas. Accordingly the perception of impacts of non-native species may considerably differ among stakeholder groups. A better understanding of an adequate valuation of impacts of non-native plants has therefore to be based both on a biological understanding of the effects on societal values – such as ecosystem services, biodiversity or agricultural production, by non-native species and a clarification of the valuation of these effects by stakeholders. Consequently, interdisciplinary collaborations among natural and social scientists are needed to study impacts of invaders. We present the conceptual framework of a new interdisciplinary project at ETH Zürich, where a biologist, a psychologist and two invasion biologists collaboratively study the stakeholder perception and valuation of plant invasions in Switzerland. The project focuses on five model species (*Ambrosia artemisiifolia*, *Heracleum mantegazzianum*, *Fallopia* spp., *Solidago* spp., *Buddleja davidii*). The project builds on the psychological concept of mental models. Mental Models reflect the beliefs and concepts of experts and stakeholders and show the gaps between the model and the current knowledge. Data will be collected through indepth interviews and standardised surveys among different groups of experts and stakeholders.

28 The fate of the grasshoppers during meadow harvesting

Jean-Yves Humbert, Jaboury Ghazoul, Thomas Walter

Agricultural mowing techniques have evolved considerably through mechanization in recent decades, and yet scientific knowledge on their impacts on field fauna is limited. Few studies have investigated this topic, and there remain considerable uncertainties that need to be addressed to develop effective guidelines for the conservation of diversity rich meadows. In nine low input meadows, the density of the grasshoppers population was measured 2 hours before mowing and again at the end of the harvesting process (after baling). In average the grasshopper density decreased more than 80%. But what happened, did the grasshoppers die or leave the meadow? To investigate this question, we conducted capture-mark-resight experiments to measure the proportion of grasshoppers killed during the harvesting stages (mowing, processing and removing the grass). Mowing and processing the grass killed between 40% and 50% of the individuals, while removing the grass killed about 60% of those having survived the previous stages. The impact of the whole harvesting process reached 80% mortality. This show that the grasshoppers are highly exposed during the harvesting of the grass and only a few can survive. Because no practicable meadow harvesting processes are damage free, leaving uncut grass refuges is a simple and good practice that will benefit the grasshoppers as well as other field organisms. The project was initiated on a large interest from the stakeholders and is supported by local authorities (13 Swiss cantons).

29 Evolution MegaLab: a European snail hunt

Eva Inderwildi (Schweizer Vogelschutz SVS), Bruno Baur (Universität Basel)

Banded snails (*Cepaea nemoralis* and *C. hortensis*) can be found in several ground colours and different band patterns. The distribution of the different forms is influenced by their predators (song thrush) and the local climate. The results of the European snail hunt Evolution MegaLab 2009 will show if there is a visible influence of climate change and local diminution of the song thrush population on the geographical distribution of the colours and band patterns of *Cepaea*. Everybody is invited to participate in this snail hunt. An interesting way to contribute to research and learn more about evolution and biodiversity.

30 Sexual selection in the brown trout and the minnow: indirect genetic benefits from mating with dominant males?

Alain Jacob, Guillaume Evanno, Emanuela Renai, Beat von Siebenthal and Claus Wedekind

Male-male competition for access to females is common in many fish. It is, however, unclear whether females obtain indirect genetic benefits by mating with dominant males or with males whose characteristics indicate dominance. To test this question, we first determined dominance hierarchies under semi-natural conditions in wild-caught brown trout (*Salmo trutta*) and minnows (*Phoxinus phoxinus*). We found that dominance correlated with body size in both species. In the minnow, the number of breeding tubercles, a secondary sexual characteristic that is not necessarily correlated with body size, could also be used to predict dominance. It has been shown before that dominance correlates with reproductive success in the brown trout. We could verify this relationship in the minnow by determining the paternity of hundreds of embryos that were collected from a spawning place. To test for potential indirect benefits of mate preferences, we stripped male and female brown trout, used their gametes for full-factorial *in vitro* fertilisations, and recorded embryo and juvenile survival in different environments, including a natural streamlet. We found significant additive genetic variance in offspring survival, i.e. males differed in their genetic quality. However, neither dominance nor body size as an indicator of dominance could be used to predict offspring survival under these various conditions. Our findings suggest that females do not significantly benefit from indirect genetic effects when mating with dominant males.

31 Determinants of mating group size and sperm transfer success in a hermaphroditic flatworm

Tim Janicke, Lukas Schärer

A crucial question in sex allocation theory for simultaneous hermaphrodites is how social group size translates into mating group size. We studied how mating group size and sperm transfer success are affected by social group size, density and morphological traits such as body size, testes size and genital morphology in the outcrossing hermaphroditic flatworm *Macrostomum lignano*. Furthermore, we tested whether the mating role predicts sperm transfer success. To do this we used a recently established sperm-tracking method based on labelling of S-phase cells in the testes. We found that mating group size increases linearly with social group size. Moreover, we demonstrate that sperm transfer success depends on testes size and the shape of the male copulatory organ. Finally, in mating trials with two competitors, the individual that is in the second role on average managed to successfully transfer twice as many sperm to a mate than the individual that mated in first role. This suggests that second male sperm precedence operates in *M. lignano*.

32 Trans-sexual antennal transplants alter behaviour in a moth

Nicole M. Kalberer, Carolina Reisenmann, Heather Stein, Wendy Mechaber and John Hildebrand

Similar to other moths, the primary olfactory centers of *Manduca sexta*, the antennal lobes, contain a small number of sexually dimorphic glomeruli, the macroglomerular complex in males and the large female glomeruli in females. These glomeruli play important roles in sex specific behaviors, such as the localization of conspecific females in males and the selection of appropriate hostplants for oviposition in females. The development of sexually dimorphic glomeruli depends strictly on the ingrowth of sex-specific olfactory receptor cell afferents. Here we tested the role of female-specific olfactory receptor cells in mediating female-specific host-plant approach behavior and in determining the response of downstream antennal lobe neurons. For this, we generated male gynandromorphs by excising one imaginal disk from a male larva and replacing it by the corresponding antennal imaginal disk from a female donor. Most male gynandromorphs that emerged as adults had an apparently normal female antenna and a feminized antennal lobe with the female-characteristic large female glomeruli. These male gynandromorphs were tested for flight responses towards tomato plants, a preferred hostplant for oviposition in *M. sexta*. Male gynandromorphs landed on hostplants almost as often as normal females. Thus, the presence of the induced female-specific olfactory glomeruli was necessary and sufficient to produce a female-like, odor oriented behavior in male gynandromorphs.

33 Genetic divergence and variability within *Horismenus* parasitoids of bruchid beetles in Mexico

Sarah G. Kenyon & Betty Benrey

Determining levels of genetic variability and the population genetic structure of insects is fundamental for the understanding of dispersion patterns and for the phylogenetic resolution among species. In our tritrophic study system we are using nuclear and mitochondrial markers to determine the levels of genetic divergence and genetic variability of three species of *Horismenus* (Eulophidae) parasitoid wasps. These wasps attack bruchid beetle hosts developing in wild *Phaseolus* bean seeds. The three parasitoid species, *H. depressus*, *H. missouriensis* and the recently described, *H. butcheri*, were collected from infested beans in 10 populations in Central Mexico over a period of two years. These wasps have established ranges that vary in either the bean species on which they specialize or the altitude at which hosts are attacked. While each wasp has its specific range they coexist in the common bean, *P. vulgaris*. Sequence analysis of 28SD2 and ITS2 nuclear regions shows *H. butcheri* to be more polymorphic than either *H. depressus* or *H. missouriensis*, splitting into four separate genotypes, while each of the other species possesses only one genotype. This greater genetic diversity argues for increased genetic drift, either due to decreased dispersal ability between populations (perhaps due to a more limited altitudinal range), and/or an earlier establishment. Additionally, two individuals *H. butcheri* appear to harbor sufficient variation at both the ITS2 and 28SD2 region to indicate the possibility of a new taxon. Investigations into the extent and underlying causes for this diversity are ongoing.

34 The Evolution of Antennal Courtship in Parasitoid Wasps of the Subfamily Diplazontinae (Hymenoptera, Ichneumonidae)

Seraina Klopstein, Salome Steiner, Donald Quicke, Christian Kropf

Because of their potential to cause reproductive isolation, characters associated with courtship behaviour are believed to play an important role in the diversification of life. In the species-rich insect order Hymenoptera, the use of the antennae during courtship is very widespread, but the reconstruction of its evolutionary history is obstructed by the lack of courtship data for most species. Recently, we reported a new mode of antennal courtship in the parasitoid wasp *Syrphoctonus tarsatorius* where the male curls its antennae in double-coils around the antennae of the female. We developed a method to reproduce this movement in amputated antennae which allows retrieving information about antennal courtship from museum specimens. Applying this method to the parasitoid subfamily Diplazontinae, we obtain courtship data for 40 species. To reconstruct the evolution of antennal courtship in diplazontines, we compiled a molecular phylogeny based on two mitochondrial and two nuclear genes. With one exception, the resulting phylogeny confirms the current genus-level classification. Mapping the mode of antennal courtship on the phylogeny, we found that the mode of antennal coiling is tightly linked to the position of antennal structures connected to internal glands. Moreover, a single origin is most probable for both single- and double-coiling, and coiling has been lost on three separate occasions. These results suggest a low speed of evolution of this character and contradict the hypothesis that antennal coiling had a major impact on the diversification of this subfamily.

36 Understanding and valuing the impacts of invasive plant species

Christoph Küffer

Invasions are considered one of the main threats to biodiversity. However, often impacts of invasive plants are poorly documented and their valuation is contested – as documented through expert workshops in Switzerland, Hawaii and the Western Indian Ocean. I discuss two reasons why research on impacts of invaders is underperforming. First, impacts are modulated by the local habitat context

including contingent factors such as anthropogenic disturbances. Therefore multifactorial analyses of concrete invasion scenarios are needed. Oceanic islands are ideal to compare impacts of invaders among replicated invasions. I present a comparison of invasive floras on 30 island archipelagos worldwide. While the number of problematic invasive plants per island group is well predicted by just two factors (habitat diversity, human population density), less than 20% of the species are problematic on more than two islands. I illustrate the relevance of the local context in plant invasions with two examples: Impacts on soil nitrogen availability by one of the fastest growing nitrogen-fixing invasive trees (*Falcataria moluccana*) was 100-times higher on young volcanic soils in Hawaii than on highly weathered soils in Seychelles. The invasion success of *Cinnamomum verum*, which makes up c. 80% of trees in Seychelles, is explained by a number of interacting factors. Second, the adequate assessment of impacts involves an understanding of both biological processes and stakeholder valuation (cf. <http://www.livingreviews.org/lrr-2008-2>). Collaborations between natural and social scientists are therefore needed – as illustrated by a new project at ETH Zurich involving a journalist/biologist, a psychologist and two invasion biologists.

37 Is genetically modified Bt maize combined with biological control a solution for sustainable pest management?

Géraldine Lécho, Claudia Zwahlen, Bruce Hibbard & Ted Turlings

Plants have sophisticated defence strategies to combat herbivores attacking them. A well known indirect defence strategy is to recruit natural enemies of herbivores by emitting volatiles, such as the (E)-B-caryophyllene emitted when maize roots are attacked by the corn rootworm *Diabrotica virgifera virgifera*, which attracts certain entomopathogenic nematode (EPN) species. Various transgenic *Bacillus thuringiensis* (Bt) maize varieties are also able to directly defend themselves against the same pest by expressing a toxic Cry3 transgene. The aim of our work was to investigate whether biological control using EPN and Bt maize can be combined to reduce the damage by corn rootworms, one of the major pests of maize. In the laboratory, we studied the attraction of EPNs to Bt maize varieties and their near isogenic control maize in belowground 6-arm olfactometers and measured the root volatile emission using GC-MS. Our results show that neither Bt maize nor the near isogenic control attracted EPNs, which is likely due to the low volatile emission in all varieties. Similar results were found in the field, where root damage caused by corn rootworm larvae was lower in Cry3-expressing Bt maize than any other varieties tested when corn rootworms only were present, but when EPN were applied to corn rootworm-infested field plots, root damage was not further reduced. This first evaluation of the compatibility of Bt maize and biological control implies that corn rootworm control could be improved with Bt maize lines producing more (E)-B-caryophyllene and other root signals attractive to EPN. Enhancing the plants' attractiveness to EPN should also help to slow down the development of resistance of corn rootworm to Cry3 toxins.

38 Ecological differentiation between coexisting sexual and asexual strains of *Daphnia pulex*

Mikko Lehto, Christoph Haag

In many closely related taxa there are both sexual and asexual strains or species. Closely related sexual and asexual strains often inhabit slightly different habitats. In Southern Finland asexual (obligate parthenogenesis) and sexual (cyclical parthenogenesis) *Daphnia pulex* populations often inhabit different rock pools, but the reason for the distribution has been unclear. We found differences in many ecological factors between ponds inhabited by sexual and asexual populations. A competition experiment in the natural environment showed that these differences are, at least partly, explained by adaptation to different environments indicating ecological differentiation between reproduction types. We suggest that geographical parthenogenesis in *Daphnia pulex* could be explained by environmental gradients. The distribution of reproduction types in South-Finland is showing small-scale geographical parthenogenesis. However, more studies are needed to explain the mechanism behind the differentiation and to generalize this explanation.

39 Queen or worker? (We will) Ask the hormones

Libbrecht R. and Keller L.

One of the great features of eusocial Hymenoptera is the existence of polymorphic castes. While reproduction is restricted to one or several individuals, usually the queens, individuals from the worker caste forgo reproduction to specialize on tasks such as nest building, foraging and brood care. A comprehension of the mechanisms underlying the determination of the caste is crucial to understand the ecological success of social insect species. Until a few years ago, the common dogma for female caste determination was that the differences between queen and worker were determined by nutritional, environmental and/or social factors affecting the larval stages. But recently, several examples of genetic caste determination and evidence for maternal effects on the determination of the caste have been documented. These findings jeopardize the idea that caste determination is only based on extrinsic environmental factors and call for studies on the proximate mechanisms of caste determination, in particular the roles and modes of action of hormones. Juvenile hormones and ecdysteroids are the most important groups of hormones in insects but their action on reproduction and caste determination differ greatly among social insect species. It would be worthy to investigate whether queens use these hormones (directly or as a signal) to determine the developmental fate of their offspring. Our idea is to experimentally manipulate the hormonal content of *Pogonomyrmex rugosus* queens to study the potential effect on the production of new queens.

40 PGDSpider: A program to exchange Population Genetics Data (PGD) between commonly used population genetics programs

Heidi Lischer, Laurent Excoffier

More and more population genetics data are produced as new sequencing technologies evolve. Proper analysis of this data requires the use of several analysis programs, which often need different data input formats. However data format conversion is an exhaustive, time consuming and error-prone work. I developed a new conversion program (PGDSpider) and a new general data format (PGD) to facilitate the data format conversion process. PGDSpider is able to deal with different data types and it can read the following 19 different input files: PGD, ARLEQUIN, BAPS, BATWING, CONVERT, FASTA, FSTAT, GDA, GENEPOP, GENETIX, HGDP-CEPH, Immanc (BayesAss), IM (IMa), MEGA, MIGRATE, MSA, NEXUS, PHYLIP or STRUCTURE. Furthermore, it is able to write 19 different file formats: PGD, ARLEQUIN, BAPS, BATWING, FASTA, FDist2 (datacal), FSTAT, GDA, GENEPOP, GENETIX, IM (IMa), Immanc (BayesAss), MEGA, MIGRATE, MSA, MSVar, NEXUS, PHYLIP or STRUCTURE. PGDSpider is user friendly in the sense that it provides a graphical user interface (in English, French, German and Italian) which is mostly self explaining. PGDSpider uses the newly developed PGD (Population Genetics Data) format as an intermediate step in the conversion process. PGD is a file format designed to store various kinds of population genetics data and to act as a general data format in the future. It is written in XML and is therefore independent of any particular computer system and extensible for future needs. The PGDSpider program as well as the new data format PGD will help to facilitate the analysis of population genetics data in future works.

41 Assessing differentiation of Whitefish species along an environmental gradient

Lundsgaard-Hansen B, Vonlanthen P, Seehausen O

A big amount of world's biodiversity is the result of the interaction between gene flow and selection leading to divergent adaptations to heterogeneous environments and to ecological speciation. Such species are reproductively isolated from each other by ecological mechanisms, i.e. extrinsic selection (post zygotic isolation) having the potential to induce mate choice (prezygotic isolation). When they

are of recent evolutionary origin, they have not yet evolved intrinsic reproductive incompatibilities. Therefore changing environments can induce interspecific hybridization. It has been shown multiple times that a loss of environmental heterogeneity can lead to fusion of species, but, especially in animals, there is far less evidence for interspecific hybridization having the potential to increase biodiversity. To measure the degree of reproductive isolation between two sympatric whitefish species of Lake Lucerne, we performed a quantitative sampling along an ecological gradient. We find indication that the recent environmental changes may have initialized secondary contact between those species and might have led to hybrid speciation; the formation of a hybrid species without disappearance of the parental species. The sampled whitefish species are divergent in neutral genetic differentiation, in spawning habitat as well as in morphological and life-history traits. The effect of changing environmental conditions on the interaction between gene flow and selection offers a great possibility to answer evolutionary biological questions. As environmental change affects most biomes, often due to human-induced habitat alterations, and is happening very fast, a proper understanding of the effects of environmental change on biodiversity is essential to conserve world's biodiversity.

42 The effects of environmental structure on eco-morphological and genetic differentiation of Lake Victorian cichlid fish populations

Isabel S. Magalhaes, Banz Lundsgaard-Hansen, Salome Mwaiko, Ole Seehausen

Theoretical models of ecological speciation in clines suggest environmental structure plays a major role in determining the extent of population divergence. Using this framework we investigated polymorphic populations of Lake Victoria cichlids living along environmental gradients that varied in slope and linearity. We sampled populations from three islands with replicate pairs of putative trophic morphs in the genus *Neochromis*, quantified morphology and dentition and typed population samples at 9 different microsatellite loci. Replicate pairs varied in extent of eco-morphological differentiation between one trait and more than 10 different traits. This variation was well predicted by variation in steepness and linearity of the resource gradient: the less steep and the more linear the gradient, the stronger the differentiation. However, neutral genetic differentiation is less well predicted by the environment, and does not correlate well with morphological differentiation. We find evidence for deviations from random mating between sympatric morphs, but significant differentiation only at the island with intermediate resource gradient and intermediate eco-morphological differentiation. The eco-morphologically most strongly and the least strongly differentiated morph pairs are both undifferentiated at neutral loci. Divergent and disruptive selection seems sufficient to maintain eco-morph differentiation in the face of nearly unrestricted gene flow.

43 Genetic diversity of *Chyphonectria parasitica* in Bosnia and Herzegovina assessed by microsatellite markers and vc types

J. Markovic, S. Prospero & D. Rigling

Chestnut blight, the most important disease of European chestnut (*Castanea sativa*) in Europe, is caused by the introduced fungus *Cryphonectria parasitica*. In Bosnia and Herzegovina, *C. parasitica* was first observed in the north-west in 1961, close to the border with Croatia. Afterwards, infested chestnut stands have been found in eastern and southern part of the country. Previous studies conducted in the Balkan Peninsula showed a variable diversity of vegetative compatibility (vc) types in *C. parasitica* populations. Vc-type diversity is relevant for the biological control of chestnut blight with hypovirulence, since the hypovirus is transmitted only between fungal strains with the same or closely related vc-types. In this study we investigated the diversity of six *C. parasitica* populations in Bosnia. Five populations were located in north-western Bosnia and Herzegovina and one in the south-eastern region. Approximately 50 cankers were sampled in each population. After isolation of *C. parasitica*, for all isolates vc-type and microsatellite genotype were determined. First results show that EU-1, EU-2, EU-12, and EU-13 are the most widespread vc types. In respect to frequency of vc types, the south-eastern population differ significantly from all the other populations. Although microsatellite

analyses have not been terminated yet, preliminary results indicate the occurrence of the same alleles as already identified in Switzerland and France.

44 Access to genetic resources from abroad and benefit sharing – Good practice

Susette Biber-Klemm, Sylvia Martinez

Whenever scientists intend to use organisms or parts thereof from abroad for research purposes, they need to adhere to a specific code of conduct as stipulated by the Convention on Biological Diversity CBD. The Swiss Academy of Sciences has elaborated a publication on Good Practice for non-commercial research. It offers easy to understand information about the international Access and Benefit Sharing system regarding basic research. It explains the necessary steps to take when requesting access to genetic resources for research purposes. It also sets out possibilities for benefit sharing within the academic context. <http://abs.scnat.ch>

45 Nectary and spur structure and evolution in rewarding and deceit-pollinated Orchidinae (Orchidaceae)

Merran L. Matthews, Salvatore Cozzolino and Florian Schiestl

Orchid flowers may be rewarding or rewardless, whereby non-rewarding flowers ensure pollination by deceit. In the sub-tribe Orchidinae, both flower types are present, sometimes within the same genus and often associated with a spur. Thus this group offers an excellent opportunity to compare rewarding and non-rewarding taxa and to gain a better understanding of their pollination biology. Due to poor molecular resolution however, existing phylogenetic trees are inconclusive regarding nectary evolution within the subtribe. As an alternative approach, comparative floral structural studies focussing on nectary (and spur) structure of both rewarding and non-rewarding taxa may provide additional insights into this problem. Using serial microtome sections of whole flowers, SEM studies and nectar measurements in the field we have sampled taxa from each genus within the sub tribe (plus outgroups), and have focussed on genera (or clades) with different character states. Our questions include: Is nectary structure the same within Orchidinae (indicating a possible common origin) or is it different (multiple origins)? Are vestigial nectaries present in non-rewarding taxa? And what is the relationship between the nectary, spur and pollination type? Preliminary results suggest that nectary structure is simple and mainly comprises unicellular papillae/hairs or a secretory epidermis. One clade has multicellular papillae lining the spur. These results provoke the question, 'does the structural simplicity of the nectary allow for the easy switching on or off of nectar production within the subtribe?' An additional spin-off will be that previously little known genera will also be described.

46 Fishery-induced rapid evolution and fishing-gear adjustment in population management

Sébastien Nusslé, Claus Wedekind

Size-selective fishing, i.e. the systematical removal of larger individuals, may affect life-history traits such as individual growth rate. We used long-term monitoring data to test for such effects in a well-defined population of Alpine whitefish in Lake Joux (Vaud, Switzerland) and found evidence for fishery-induced rapid evolution within only 20 years of intense gill-net fishing. We then used individual-based modeling and quantitative genetics to study the possible short-term and long-term effects of various mesh-size regulations and hence of catch size and age distribution. We found that certain kinds of mesh-size regulations that allow large fish to escape fishery could help populations to recover from the unwanted effects of fishery-induced rapid evolution. Our quantitative analyses may help to

reconcile short-term and long-term fishery interests with demographic and genetic aspects of fish population.

47 Interspecific hybridization amongst asexual *Epichloë* endophytes of *Hordelymus europaeus*

Martina Oberhofer and Adrian Leuchtman

Endophytic *Epichloë*/*Neotyphodium* species have been object of scientific research for the last 100 years due to their broad range of ecological impact on their host grasses, but also on the associated plant, animal and fungal community. Previous studies revealed an unusual high abundance of hybrid species among asexual *Neotyphodium* suggesting a selective advantage of hybridization for the mutualistic endophytes. This study is carried out on a woodland grass species, *Hordelymus europaeus* L., and tries to highlight the genetic diversity and associated host benefits of different genotypes of *Neotyphodium* endophytes found in this host grass along a South to North pan European transect. According to observations in Switzerland *H. europaeus* bears a hybrid and a non-hybrid strain. Reproductive tillers and corresponding spikes with seeds were collected in twenty populations along a transect covering about 3000 km. Here I will present the first data on infection frequencies of populations, genetic diversity of encountered endophytes and the distribution pattern of hybrid and non-hybrid strains. An ongoing glasshouse experiment using plants from selected populations that have been experimentally inoculated with hybrid and non-hybrid endophyte strains (both native and non-native) will assess mutualistic properties of different endophytes with regard to water stress and nutrient availability. Furthermore, a reinoculation experiment using two presumed parental strains simultaneously will be carried out to investigate and hopefully observe the process of endophyte hybridization in vivo. Sequencing of selected heteroploid genes followed by coalescence analysis should allow to assess the age and origin of the hybrid endophyte strains.

48 Assessing present and future species richness and evolutionary diversity hotspots for the Cape Proteaceae

Pio D. V., Guisan, A. & Salamin N.

Recent studies argue for the integration of evolutionary information in conservation prioritisation efforts, as some species are more distinctive than others and thus arguably deserve more attention. This paper examines for the first time the spatial relationship between predicted species richness (SR) (the main biodiversity measure currently used) and phylogenetic diversity (PD) in 149 Cape Proteaceae species. Distributions are based on climatic-matching modelling and used to reconstruct spatial patterns of SR and PD. Biodiversity hotspots are identified and the effect of future climatic changes investigated. Moreover, the coverage of protected areas and the PD contribution of uncommon species are quantified. A significant, non-linear relationship was found for PD and SR, at times resulting in contrasting spatial patterns for these two measures. Currently, 81% of SR and 90% of PD are well protected, but with climate change suitable habitat will diminish. Randomization procedures suggest that uncommon species do not contribute to a disproportionate amount of PD.

49 Mating order, reproductive success and mating strategies in Columbian ground squirrels (*Spermophilus columbianus*)

Raveh S., Dobson F. S., Coltman D.W. & Neuhaus P.

A major question in behavioural ecology is how competition within the sexes and conflicts of interest between the sexes shape the evolution of mating strategies. In many mammal species individuals engage in multiple mating, which may result in mixed paternity litters. Mating order can be crucial in

determining a males' reproductive success. We studied 4 populations of Columbian ground squirrels (*Spermophilus columbianus*) in Alberta, Canada to evaluate whether mating position affects male reproductive success. We observed the mating activity of oestrous females and used molecular analysis to determine paternity. Our results show a clear first male advantage in this species. Even though the majority of litters were multiple sired, single fathered litters occurred and were mainly produced by the first mating partner. Furthermore, we investigated whether males siring complete litters performed different mating behaviours than males siring offspring in mixed litters. Mate guarding and prolonged copulations increased chances of males to sire a litter alone while age and body condition did not have a significant effect. Our results suggest that male-male competition for early access to females and the coexistence of different male strategies may crucially shape the mating system.

50 Statistical modelling of food webs: exploring unexplained structure with latent traits

Rudolf P. Rohr; Heike Scherer; Christian Mazza; Louis-Félix Bersier

Food webs are complex objects that depict who eats whom in a natural system. Several models have tried to capture their architecture, often implicitly implying latent traits, i.e., non-measured characteristics. Here we adopt a statistical approach where we use log body-size ratio of prey on predator as explanatory variable, using a dataset of 12 highly resolved food webs. Body size typically predicts 20% of trophic links. We introduce a method to explore the unexplained part of the structure, which is based on the estimation of latent traits. For each species, one generality and one vulnerability trait are computed from the data, which dramatically improves the percentage of correctly predicted links (now 73% on average). These traits are useful to interpret the hidden structure of the food webs and can be related to external information (e.g. phylogeny, micro-habitat structure, or camouflage). We use taxonomic information on the species to show that phylogeny is in general closely linked to the latent traits.

51 Evolutionary Path to Terminal Differentiation and Division of Labor in Cyanobacteria

Valentina Rossetti, Zurich University

The transition from unicellular to multicellular organisms is not a well understood process in evolution. A common trait often associated with multicellularity is a division of labor achieved through cellular differentiation. However, the division of labor does not necessarily have to be constrained to a multicellular setting. In this study, we focus on the possible evolutionary paths leading to terminal differentiation in cyanobacteria. We develop mathematical models for two developmental strategies. One, of populations of terminally differentiated single cells surviving by the exchange of common goods. Second, of populations exhibiting terminal differentiation in a multicellular setting. We test the evolutionary stability of the two strategies with respect to resistance against disruptive mutations (i.e. "cheater" mutants). We also assess the ability to optimize the ratio of vegetative (carbon fixing) to heterocystous (nitrogen fixing) cells, which in turn leads to the maximization of the carrying capacity for the population density. We subsequently compare the predictions of the model with phylogenetic relationships derived from analyzing 16S rDNA sequences of different cyanobacterial strains. We find that the vegetative/heterocyst division cannot be maintained in homogeneously mixed single-celled populations, and requires the compartmentalization afforded by multicellularity to resist against invasion by cheater mutants. Additionally, we find that in the multicellular setting, the vegetative/heterocyst ratio, and as a result, the carrying capacity, can be optimized. Hence, for the class of interaction found in Cyanobacteria, multicellularity is a necessary condition for both the evolutionary stability of terminal differentiation and for the optimization of the division of labor.

52 Plant-phytophagous insect interactions : Reproductive succes of *Exapion ulicis* in relation with the phenology of his host plant, *Ulex europaeus*.

Romain Rouchet (realized at UMR Ecobio, University of Rennes 1)

Optimal oviposition behaviour and optimal synchrony with their hosts enable fitness optimization of phytophagous insects. The link between the fitness of *Exapion ulicis*, the gorse *Ulex europeaus* weevil, and both phenology and oviposition behaviour has been considered. Apion females are able to discriminate the pods containing most seeds to optimize a long and costly oviposition behaviour. Observations suggest that females mark the pod after oviposition and avoid superparasitism when parasitism rate is low and new pods are still produced by gorses. Pods are produced by the host plant from autumn to spring's end, but only pods produced in spring are parasited. Eggs deposited in spring have not enough time to complete their development and die because pods and larvaes have different growing speed. The reason is a gap between both growing speeds due to a different response to climatic conditions. Eggs deposited at the end of the spring are subject to a parasitism pressure by their parasitoid *Pteromalus sequester* and a interspecific competition pressure by *Cydia succedana*. Thus, there are strong constraints on apion phenology which cause a partial asynchrony with the host plant, preventing apion to benefit from the entire pod production. It is the first time that the interaction between *E. ulicis* and *U. europaeus* phenologies has been described on the insect side.

53 Pleiotropy in the melanocortin system, coloration and behavioural syndromes

Anne-Lyse Ducrest, Laurent Keller and Alexandre Roulin

In vertebrates, melanin-based coloration is often associated with variation in physiological and behavioural traits. We propose that this association stems from pleiotropic effects of the genes regulating the synthesis of brown to black eumelanin. The most important regulators are the melanocortin-1-receptor and its ligands, the melanocortin agonists and the agouti-signalling protein antagonist. On the basis of the physiological and behavioural functions of the melanocortins, we predict five categories of traits correlated with melanin-based coloration. A review of the literature indeed reveals that, as predicted, darker wild vertebrates are more aggressive, sexually active and resistant to stress than lighter individuals. Pleiotropic effects of the melanocortins might thus account for the widespread covariance between melaninbased coloration and other phenotypic traits in vertebrates.

54 Evidence of senescence in the Blue Tit (*Cyanistes caeruleus*)

Charlène-Aurore Ruppli, Olivier Gimenez, Philippe Perret, Jacques Blondel and Anne Charmantier

Aging, or senescence, yields to a decline in fitness with old age. Most of the studies designed to understand the mechanisms underlying its evolution have been performed under controlled conditions in laboratories. During the past two decades, the study of senescence in natural populations has provided evidence of a general decline in survival probability, or "actuarial senescence", over a large range of taxa. However, such evidence of a decline in reproduction still remains scarce, partly because of the difficult sampling of old individuals in the wild especially in short-lived species. Works focusing on reproductive senescence then usually do not take the variability in individual quality into account de-spite its strong potential effects on age-specific reproductive patterns observed at the population level. Using longitudinal data collected over 32 years, we analysed the age-specific individual trajectories of laying date, clutch size, the numbers of fledglings and of recruits per brood in Blue Tit females of three Mediterranean populations. We show that in spite of their short life-span, these birds undergo a significant specific decline mainly in the performance of their laying date and of their number of fledglings. Our findings also suggest that the senescent patterns observed can vary according to individual quality, i.e. the age of onset of reproduction and lifespan. This supports the existence of a reproductive senescence in a short-lived bird species, and highlights the importance of

accounting for interactions between various individual life-history traits to understand the real factors affecting the evolution of senescence in natural populations.

55 Predicted distribution of long-eared bats in Switzerland

Rutishauser Marianne, Bontadina Fabio, Kiefer Andreas, Braunisch Veronika, Ashrafi Sohrab, Arlettaz Raphaël

The discovery of a cryptic species causes knowledge gaps, not only in the new species but in all species involved. In 2002 a cryptic bat species, *Plecotus macrobullaris*, was newly-discovered in Switzerland. This requires a re-evaluation of the distribution of all three *Plecotus* species (*P. macrobullaris*, *auritus*, *austriacus*) in order to implement conservation action or to newly determine their red list status. This study aimed to assess the potential distribution and to determine the important ecogeographical predictors for the three *Plecotus* species at a large spatial scale. We collected samples of *Plecotus* specimen all over Switzerland from museums, bat researchers and conservationists. Fresh faeces and tissue samples were genetically identified. An Ecological Niche Factor Analysis (ENFA), was applied to explore the environmental niche and to localise suitable habitats for each species in Switzerland. First results show clear differences in the predicted distributions. *P. auritus* covers the largest area, has the broadest niche and prefers arboreal habitats. *P. macrobullaris* covers smaller areas and concentrates in alpine valleys together with lower zones in northwestern Switzerland. Semiopen sylvan structures and deciduous forest were preferred by this species. Some areas with highest suitability overlap with the best suitable habitats of *P. austriacus*, which shows a high specialisation in agreement with its rareness. The habitat suitability maps may help to identify priority areas for a re-evaluation of species occurrence and for local-scale habitat analyses.

56 Species abundance patterns in successive trophic levels

Nadine Sandau; Louis-Félix Bersier

Using food-web data sets where species abundance is documented, we explore abundance distributions in successive trophic levels. Our prediction is that the number of species and the complexity of the community will influence the shape of the distribution at the next trophic level. First, we find a positive relationship between species diversity in successive trophic levels. Second, there is a marginally significant relationship between diversity at one trophic level and evenness of abundance distribution at the next level. We interpret these results in the light of the niche hierarchy model.

57 Sperm precedence in *Macrostomum lignano*

Peter Sandner and Lukas Schärer

Sperm competition is a major force of sexual selection since it has implications for mating system and life-history evolution. Mechanistically, it can operate as a fair raffle or as a loaded raffle process, whereby one donor's sperm has a fertilization advantage. We here provide data on relative offspring (paternity) numbers of competing donors in the repeatedly mating turbellarian flatworm *Macrostomum lignano* by the use of microsatellite markers and propose a mechanism to explain the pattern of sperm utilization.

58 The influence of temperature and nutrients on the outcome of host-parasite interactions in hybridizing *Daphnia*

Corine Schoebel, Justyna Wolinska & Piet Spaak

Parasites as well as environmental factors are known to have important impacts on population dynamics. In *Daphnia* (waterflea) it was found that specific host genotypes are only susceptible at certain temperatures, and that infectability in general strongly depends on temperature and nutrient status. Previous work on a *Daphnia* hybrid system showed that the most susceptible taxon is not always the same; but the pattern differs between seasons and lakes. Therefore, the interactions between hybridizing taxa and their parasites are not a static, but a dynamic feature, and the environment plays an important role. In my PhD I focus on how hosts and their parasites co-evolve under a variety of different environments, and how this shapes genetic variation in both host and parasite. As a model system I study the *Daphnia galeata* x *hyalina* species complex and its naturally occurring protozoan parasite *Caullerya mesnili*. I will present the results of two independent cross-infection experiments. In the first one, I analyzed how two parasite isolates interact with six host clones (genotypes) at two temperatures (GHxGPxE). I found significant interactions between clones and temperature. In the second experiment, I tested the interaction between clones from 10 Swiss and North Italian lakes - with different nutrient status - and freshly isolated parasites under two nutrient conditions. Both lakes known for their parasite epidemics and lakes without parasites were analyzed. Preliminary results suggest that the nutrient status of a lake may affect the susceptibility of *Daphnia galeata*.

59 Effects of human disturbance on flight response of a key indicator species of alpine ecosystems

Rebekka Schranz, Patrick Patthey, Raphaël Arlettaz

Interactions between man and wildlife due to the rapid spreading of tourist activities are of growing conservation concern because they potentially induce costly behavioural responses and adaptations to disturbance. We tested if the level of winter disturbance influences flight initiation distances (FID) in the Black grouse (*Tetrao Tetrix*), a vulnerable species of alpine ecosystems where outdoor winter sports concentrate. Black grouse seemed to modify their behaviour through a lower flushing susceptibility, i.e. smaller FID in highly disturbed sites. This pattern which resembles a kind of habituation to human presence may be a way to compensate for the energetically costly and risky escape flights following disturbance. It remains, open, however whether this reaction is sufficient to keep a balanced physiology in winter. Based on our flushing distance data, we recommend implementing wildlife refuges surrounded by a buffer of 120 m (upper 95% CI of FID) in order to reduce interaction between birds and snow-sport people and limit population threats to this key indicator species.

60 Effects of human disturbance on activity budget of a key indicator species of alpine ecosystems

Rebekka Schranz, Patrick Patthey, Raphaël Arlettaz

Interactions between man and wildlife due to the rapid spreading of tourist activities are of growing conservation concern because they potentially induce additional energetic costs. If these extra physiological costs cannot be compensated for, they may lead to decreased survival and population declines. We tested if winter recreation influence activity patterns of the Black grouse (*Tetrao Tetrix*), a vulnerable species of alpine ecosystems where outdoor winter sports concentrate. Daily foraging duration increased with the intensity of winter recreation: radio-tagged birds started feeding earlier in the evening than control, undisturbed birds, while snow-sport people were sometimes still present on ski-slopes. This shows, firstly, that winter recreation induces behavioural adjustments, namely extra foraging activity, which are probably intended to compensate for the extra energetic costs caused by disturbance; secondly, that any additional feeding time is likely to increase the risks of conflict between

human and birds. Therefore we recommend to implement wildlife refuges in ski re-sorts for diminishing bird-human interactions, by providing undisturbed evening feeding sites to this declining indicator species.

61 Experimental tests of sex allocation theory using the RNAi-knockdown approach

Kiyono Sekii, Peter Ladurner and Lukas Schärer

How individuals invest their energy to male and female reproduction is an important aspect of an organism's life history. Sex allocation theory can provide successful predictions about this intriguing question, such as the sex ratio of sons versus daughters in gonochorists, the timing of sex change in sequential hermaphrodites and the resource allocation to male and female function in simultaneous hermaphrodites. However, the experimental examination of sex allocation theory is still limited, especially in simultaneously hermaphroditic animals, in part because it is difficult to manipulate their male and female allocation experimentally. We approach this question in an emerging model organism, the free-living flatworm *Macrostomum lignano*, by manipulating animals at molecular biological level. Firstly, we scanned available EST databases for genes that may be involved in male or female organogenesis. Next, we confirmed that the expression of these candidate genes is specific to male or female organs by in situ hybridization. Then we knocked down the function of these male- or female- specific genes by RNA interference (RNAi). We successfully isolated two genes, which are expressed exclusively in testis and play a role in spermatogenesis in *M. lignano*. The RNAi phenotype of these two genes show aberrant sperm in testis and no sperm in seminal vesicle, suggesting that these RNAi treated worms are male-sterile. Using these phenotypes, we plan to investigate the trade-off between allocation to male and female function, a fundamental assumption of sex allocation theory, and how male sterility affects the mating behavior.

62 Do tufa formation processes affect seasonal patterns of seston and drift in karst lotic habitats of the barrage system of Plitvice Lakes, Croatia ?

Sertic Peric M., Habdija I., Milisa M., Matonickin Kepcija R., Primc-Habdija B.

Karst streams represent special lotic habitats. An important characteristic of karst streams in this study is the formation of tufa from calcium carbonate precipitation and the development of various tufa habitats (underwater barriers, waterfalls, cascades, channels, fast flowing streams). Some authors suggest that aquatic biota of tufa habitats (cyanobacteria, bacteria, diatoms, algae, aquatic insects, mosses) affect tufa formation by their physical ability of accumulation, retention and encrustation of particulate organic and inorganic matter, and alternately by the chemical effects of photosynthesis. Through CO₂ uptake and out-gassing, photosynthesis as well as waterfall effects (accelerated flow velocity, enhanced air-water interface) cause supersaturation of water with respect to carbonate minerals followed by precipitation of calcite, following the reaction: $\text{Ca}^{2+} + 2\text{HCO}_3^- \rightarrow \text{CaCO}_3 (\text{solid}) + \text{H}_2\text{O} + \text{CO}_2 (\text{gas})$. The aim of this study was to evaluate seasonal patterns of macroinvertebrate drift and transport of particulate organic and inorganic matter in the karstic Plitvice Lakes hydrosystem in relation to hydrochemical characteristics associated with tufa formation. Results show that lower temperatures and flow velocities, accompanied by lower water turbulence and decreased CO₂ efflux, seasonally change carbonate hydrochemistry that favours calcite (tufa) dissolution. Higher decomposition of tufa deposits has an equivalent effect on the removal and downstream transport of mosses and particulate organic and inorganic matter within the barrage system, while drifting macroinvertebrates only partially follow this pattern.

63 Plant species diversity on 1500 grasslands plots of different land use types

Stephanie Socher, Steffen Boch, Jörg Müller, Henryk Baumbach, Dani Prati, Markus Fischer

Land-use and changes in land-use intensity are one of the most important drivers of plant diversity, particularly in the cultural landscape of Central Europe. This relationship is investigated as part of the Biodiversity Exploratories which were recently established in Germany (North, Central and South) as a platform for biodiversity research. The focus of the program is on land-use mediated changes in biodiversity and the evaluation of land-use effects on ecosystem processes. We focus on plant diversity and aim to understand how the type and intensity of land use affect species richness and functional diversity, how regional species pool and how disturbance affect the diversity and productivity of plant taxa. We recorded vegetation in 500 grassland plots of 16m² in each of these regions on different land use regimes (low intensity use to highly intensive land-use). In each Exploratory 50 out of 500 plots were chosen as representatives for the land use type. Criteria for plot selection were the soil types and the current land use. Vegetation relevés will be taken in 2008 and 2009 to be able to analyze temporal changes in species composition and diversity. Our poster presents results from the first season on how species diversity and composition differ according to type and intensity of land use and site conditions. We assessed the relative importance of land use, land site- and region-specific characteristics on the number, composition, and abundance of plant species and plant functional groups. In conclusion, our data will highlight the importance of large-scale, multi-site analyses of vegetation data to identify important drivers of biodiversity.

64 Bryophyte communities in alpine and subalpine calcareous alluvial zones of Switzerland

Julie Steffen, René Amstutz, Jean-Michel Gobat

Bryophytes are not well studied in the alpine and subalpine alluvial zones of Switzerland, despite their high diversity in these zones. Phytosociological studies are particularly lacking.

The aims of this study are: (1) performing a typology of bryophyte communities in alluvial calcareous alpine and subalpine zones, and (2) identifying the main ecological factors that drive them. We assume that altitude, microclimate and substrate quality are the factors that characterize the ecology of different moss synusiae. In addition, that the synusiae are related to the degree of evolution of the herbaceous phytocoenoses.

The work was done in Gasternal (subalpine zone, Bern) and Gemmi (alpine zone, Valais). The four typical vascular plant phytocoenoses of active alluvial zones (pebble beds, marshes, alder and willow forests) were sampled using three random quadrats of 25 m² per phytocoenosis. Phytosociological relevés and typology were done according to the methodology of integrated synusial phytosociology, and the stratification of the synusiae was performed as a function of substrate type (terricolous, epiphytic, lignicolous and saxicolous). Emphasis was put especially on soil factors, like humidity, temperature, microtopography and humus forms.

Preliminary results indicate that herbaceous pioneer communities are characterized by terricolous moss synusiae, whereas the other herbaceous phytocoenoses have a larger diversity of microhabitats and therefore, of moss communities. Furthermore, these results confirm that the nature of substrate plays a primary role in bryophyte establishment. Species from the Campyliaceae that are typical of moist habitats will be presented.

65 Estimation of Demography and Settlement History of Orkney Voles from Genetic Data

Rahel Struchen

The common vole (*Microtus arvalis*), a rodent species widespread on the European continent, can be found nowhere in Great Britain except on Orkney, an archipelago north of Scotland. This puzzling geographic distribution has posed many questions such as how and from where the voles came to Orkney. Most likely, they have been introduced by Neolithic settlers from Western Europe. This study aimed to investigate the genetic relationships among *M. arvalis* populations from Orkney and continental Europe, and to estimate demographic parameters associated with the colonisation of

Orkney. We performed phylogenetic analyses and simulated the colonisation of Orkney from the continent under an Approximate Bayesian Computation framework using a dataset of 14 microsatellite loci. Phylogenetic trees revealed a clear separation of Orkney from the continent indicating a separate evolution of the Orkney voles for a large number of generations, probably thousands of years. Demographic parameters such as the time of the colonisation of Orkney were relatively well estimated. Estimates of the time of colonisation were more recent than suggested from 4,800 year-old fossils found on Orkney. This result and the difficulty to clearly locate the origin of the Orkney voles on the continent might be explained by the loss of signals of the colonisation due to strong genetic drift having occurred since the arrival of the voles on Orkney. The estimates might also indicate a second colonisation event suggesting that there have been several introductions of voles to Orkney. The common vole on Orkney thus seems to have a complex demographic history and further investigations will be necessary to refine it, which would be valuable since the colonisation history of the voles provides a proxy for the study of human migration.

66 PAC - Friend or foe?

C. Tellenbach, C. Grüenig, T. Sieber, O. Holdenrieder

Endophytic fungi are located somewhere between mycorrhizal fungi and pathogens on the interaction continuum, which ranges from mutualistic to parasitic. Endophytes differ from mycorrhizal fungi because they do not form any distinct mycorrhizal structures. On the other hand, they normally do not behave pathogenic. Many endophytes are thought to rest latently for prolonged time periods in the host tissue which they quickly attack when the host becomes weakened by senescence, environmental stress or when the infected tissue dies. Dark septate endophytic fungi (DSE), which mainly belong to the ascomycetes, are the dominant root colonizers of a broad range of plants in alpine and subalpine habitats. In coniferous trees the most abundant species of DSE are members of the *Phialocephala fortinii* s.l. – *Acephala applanata* species complex (PAC). Despite their high abundance, the impact of PAC species on host plants is largely unknown. Data from literature are in part contradictory and indicate that the PAC covers the entire interaction continuum. Sometimes, results were even contradictory for the same strain on the same host species. In all cases, however, only few strains were used, and the experimental setup varied among studies, which complicates the comparability of the experiments further. A recent inoculation experiment with 36 well-defined strains in our lab demonstrated a pronounced strain- and species-specific pathogenicity of PAC on Norway spruce (*Picea abies*). The ecological role of PAC in forest ecosystems is discussed.

67 Chytridiomycosis-induced mortality varies between populations of *Alytes obstetricans*

Ursina Tobler, Benedikt R. Schmidt

Infectious diseases can strongly alter community dynamics and population survival and thus pose an important risk for biodiversity. Chytridiomycosis is a fungal disease of amphibians that has been involved in frog mass mortalities and extinctions world-wide. In Europe, the fungus causing the disease is wide-spread and the disease caused extinctions of midwife toads (*Alytes obstetricans*) in a natural park in central Spain. The midwife toad has suffered a 50% decline in Switzerland since the mid 1980s. Because the fungus that causes the disease occurs in about almost half of the ponds in Switzerland, but no mass mortality of any amphibian has been observed so far, we measured the impact of chytridiomycosis on Swiss *Alytes obstetricans* populations in a laboratory experiment. Results show that there is high mortality due to chytridiomycosis after metamorphosis, suggesting that chytridiomycosis also threatens midwife toad populations in Switzerland. Further, mortality varies strongly between populations. This implies that there are either different pathogen strains or differences in environment, genetic variation, skin peptides or other characters between the populations that affect susceptibility to chytridiomycosis.

68 On-going natural selection on flower color polymorphism and its geographic variation in *Geranium thunbergii* (Geraniaceae)

Takashi Tsuchimatsu, Hiraku Yoshitake, and Motomi Ito

Pattern of interactions between plant and its herbivore varies among local populations and it would result in a geographic variation of strength of selection on natural variations (e.g. Benkman et al., 2003; Amer. Nat. 162:182). In a system involving *Geranium thunbergii* (Geraniaceae) and a weevil (*Zaclarus transversicollis*) as a seed predator of *Geranium* species, we investigated the geographic variation of the oviposition behavior and the herbivore pressure by weevils. First, we found a flower color dimorphism of *G. thunbergii* and its clear geographic cline: white morph tend to be found in west Japan and red morph in east Japan although there are many populations where both red and white exist in the middle part of Japan. Two-year field survey showed that weevil significantly prefer white flower to red flower in Meiho population, where two color morph coexist, while there was no significant preference on flower color in another coexisting population, Ibuki. In Ibuki population, we found that a relative species of *G. thunbergii*, *G. yezoense*, was also flowering in the same season and that weevils significantly preferred *G. yezoense* to *G. thunbergii*. Variation of community assembly among local populations, especially the coexistence of sympatric relative species may affect the strength of selection on natural variations.

69 *Armillaria* spp. in virgin beech forests in the Ukraine

Tsykun T., Prospero S., Rigling D.

Species of the basidiomycete genus *Armillaria* are important components of the mycoflora in most forest ecosystems worldwide. They can behave as saprotrophs, contributing to wood decomposition and mineral cycling or as pathogens, causing root and butt rots on woody plants. We investigated the *Armillaria* diversity in an area of 14 600 ha of unmanaged virgin beech forests of the Carpathian Biosphere Reserve.

Armillaria rhizomorphs were collected on a regular grid in 43 plots both from the soil and from the root surface. DNA was extracted from 270 rhizomorphs and *Armillaria* species was identified by PCR-RFLP analysis of the intergenic spacer region (IGS) of the ribosomal DNA.

First results show that the saprotrophic *A. cepistipes* is the dominant species in the study area (69% of the samples), followed by *A. gallica* (29% of the samples), which is another saprotrophic species. *Armillaria ostoyae*, a more pathogenic species, is rare in the investigated forests (2 %). The three *Armillaria* species most likely contribute to decomposition of dead trees and sustainable functioning of virgin forest ecosystem without causing significant tree mortality. The distribution of *Armillaria* rhizomorphs was significantly affected by soil acidity. The optimum soil pH for the occurrence of *A. cepistipes* and *A. gallica* rhizomorphs was between 4.1-5.0. Below pH 3.5 rhizomorphs were rarely found.

Although RFLP patterns were consistent with previous reports for European *Armillaria* species, in some samples a combination of a *A. cepistipes* and *A. gallica* pattern was observed. This finding may be explained by the presence of populations of *A. gallica* and *A. cepistipes* which still may form interspecific hybrids. Further analysis will be conducted to test this hypothesis.

70 Colour polymorphism in *Oreina* beetles

Tom H. van Noort, Martine Rahier and Russell E. Naisbit

Oreina is a genus of leaf beetles that can be found throughout the mountains of Europe. It consists of a dozen closely related species that are morphologically difficult to identify in the field. In Switzerland you are very likely to encounter these splendidly coloured beetles on the broad-leaved understory in damp, shaded areas along mountain streams. Their gem-like colours vary from green to black, from blue to bronze, with or without blue or red stripes. All beetles have glands that can produce toxic fluids

in defence against predators. Their colours are thought to advertise this defence potential. If a predator experiences negative effects after feeding on a beetle it will associate the effects with the colour and ignore it on the next encounter. Brighter coloured animals are perhaps more easily recognised and remembered, and thus have a higher chance to survive and produce offspring. Through this mechanism, the so-called warning colours can evolve and spread through populations of defended prey animals. So far so good you would think. However, as described before, our protagonists occur in many forms and after several years of research it does not appear that one particular colour is becoming more abundant than others. Given the theory above, that is something unexpected and thus worth investigating. We are now doing that through a combination of field and lab experiments on selection and the role of colour in predation.

71 Tolerance of whitefish embryos to an opportunistic bacterium is linked to genetic and maternal effects, and reduced by previous exposure

Beat von Siebenthal, Alain Jacob, Claus Wedekind

Juvenile or adult fish can alter their behaviour and rely on an innate and adaptive immune system to avoid/counteract pathogens, while fish embryos have to depend on egg characteristics and may be partly protected by their developing immune system that is building up from a certain age on. We developed an infection protocol that allows testing the reaction of individual whitefish embryos to repeated exposures to *Pseudomonas fluorescens*, an opportunistic bacterial fish pathogen. We used a full-factorial in vitro breeding design to separately test the effects of paternal and maternal contributions to the embryos' susceptibility to different kinds of pathogen exposure. We found that a first non-lethal exposure had immunosuppressive effects: pre-exposed embryos were more susceptible to future challenges with the same pathogen. At intermediate and high levels of pathogen intensity, maternal effects turned out to be crucial for the embryos' tolerance to infection. Paternal (i.e. genetic) effects played a significant role at the strongest level of infection, i.e. the embryos' own genetics already explained some of the variation in embryo susceptibility. Our findings suggest that whitefish embryos are largely protected by maternally transmitted substances, but build up some own innate immunocompetence several days before hatching.

72 A strain of the bacterial endosymbiont *Regiella insecticola* protecting aphids against parasitoids

Christoph Vorburger, Lukas Gehrler, Paula Rodriguez

Bacterial endosymbionts play an important role in the ecology of aphids. Apart from the obligate endosymbiont *Buchnera aphidicola*, which serves a nutritional function, aphids may harbour several facultative endosymbionts. Two of these, *Hamiltonella defensa* and *Serratia symbiotica*, have been shown to increase resistance to hymenopteran parasitoids. A third bacterium, *Regiella insecticola*, affects susceptibility to fungal pathogens as well as host utilization of aphids, but has never been associated with resistance to parasitoids. However, in Australia we detected an entirely resistant clone of the peach-potato aphid, *Myzus persicae*, which harboured *R. insecticola*. To test if resistance was conferred by the endosymbiont, we cured this clone with antibiotics and experimentally transferred the symbiont to two uninfected clones of *M. persicae* and one clone of another species, *Aphis fabae*. Exposure to the parasitoid *Aphidius colemani* showed that the previously resistant clone became susceptible after elimination of *R. insecticola*, and the previously susceptible clones became resistant after acquiring *R. insecticola*. The endosymbiont also had a positive effect on aphid body size, but did not significantly affect fecundity. This supports that this Australian strain of *R. insecticola* protects its host against parasitoids, an ability that is predicted to evolve readily when symbionts are faithfully transmitted across generations. Harboring this strain was not associated with any obvious costs, raising the question why it is not more common in natural aphid populations.

73 Gammarus fossarum in Switzerland - unexpected diversity due to the presence of cryptic species

Anja Westram, Irene Keller, Jukka Jokela

Cryptic species make up an often underestimated part of the world's biodiversity. Even though these species are morphologically indistinguishable, they can be highly diverged genetically and can differ significantly in their ecological role and in their interactions with other taxa. Recognizing cryptic species and the differences between them therefore is important for understanding species ecology and may also be highly relevant in a conservation context. For our model organism, the ecologically important amphipod *Gammarus fossarum*, previous analyses suggest that it actually represents a complex of three different cryptic species. Using molecular markers, we are analysing their distribution across Switzerland. Our first results suggest that the species are geographically sorted, but co-occur in a large contact area. These results underline the importance of molecular genetic analyses in addition to classical morphological taxonomy.

74 Identification of putative isolation genes in *Ophrys* by using cDNA representational difference analysis (RDA)

Shuqing XU, Philipp Schlüter, Ueli Grossniklaus, Florian Schiestl

Species of the Mediterranean orchid genus *Ophrys* mimic mating signals of their pollinators and are pollinated by sexual deception. In previous studies, it was shown that the specificity of pollinator attraction is determined by the ratio of different compounds (alkenes) in floral odors. The genes that are responsible for the production of these compounds may thus be "isolation genes", since they are directly linked to the reproductive isolation among plant individuals. However, the large genome and limited available sequence data makes the identification of these genes in *Ophrys* difficult. In this study, representational difference analysis (RDA) was used on flower tissue of two closely related *Ophrys* species, *O. sphegodes* and *O. exaltata*. The analysis showed that most differentially expressed (or divergent) genes were involved in terpenoid and steroid biosynthesis and pathways, which play roles in floral odor production. The expression level and sequence divergence of selected genes were confirmed by further RT-PCR and RACE experiments. Our results indicate that RDA is a useful method to identify putative isolation genes among closely related species, which have large genomes.

75 Genetic analysis of migration in two avian influenza vectors: Tufted duck (*Aythya fuligula*) and Common pochard (*Aythya ferina*)

Yang Liu, Irene Keller, Gerald Heckel

The highly pathogenic avian influenza virus (HPAI) H5N1 poses a serious risk to human and animal health, and caused the deaths of tens of millions of domestic birds and more than 200 humans since its first emergence in 1997. Wild waterbirds have been identified as HPAI virus carriers in several instances, although their actual role in maintaining and spreading the virus is far from being clear, and much debated. Common pochard (*Aythya ferina*) and Tufted duck (*Aythya fuligula*) are particularly likely vectors as they cover long distances during east-west migration, and the virus has in fact been detected in European populations. This project uses a population genetic approach based on nuclear and mitochondrial DNA to infer the migration patterns of these two species throughout Eurasia. The analysis provides the first quantitative assessment of gene flow, genetic differentiation and the extent of mixing within the species' Palearctic ranges. Together with ring-recovery and bird census information, our data will allow a comprehensive investigation of the likelihood of virus spreading and transmission by these species. Preliminary results from mtDNA sequences show moderate levels of genetic variability in both *Aythya* species. East Asian birds display relatively low levels of genetic differentiation from European birds. Some frequent haplotypes are shared by ducks from European and Asian origins. Further analyses will resolve whether these genetic patterns are indeed due to the

capacity for long-distance movements and extensive mixture between European and Asian populations.

76 Suitable nest boxes influence settlement decisions of a secondary cavity breeding bird in intensive agricultural landscape

Silvia Zingg, Raphaël Arlettaz, Michael Schaub

1. Provisioning of nest boxes is a popular conservation action to enhance populations of endangered cavity breeding birds. However studies on the consequences of provisioning nest boxes in intensive agricultural environment are rare, particularly the effects of different nest box types are little known. 2. This study presents the results of a nest box addition experiment on a wryneck *Jynx torquilla* population. The study was conducted in Valais, where we surveyed a nest box population since 2002. These nest boxes were designed for the larger hoopoe *Upupa epops*, but were frequently also used by wrynecks. In 2008, we installed additional nest boxes which we supposed to be particular suitable for the wryneck (smaller entrance hole and brood chamber). We studied the effects of the two different nest box types on territory choice and reproductive success of this endangered bird species. 3. The additional wryneck nest boxes had a positive influence on territory choice and were preferably occupied. 4. The number of breeding pairs increased after the installation of the new nest boxes, but reproductive success was the same in both nest box types. 5. Our study shows that the attractiveness of a territory is enhanced when additional cavities are available, leading to a positive population response. Further specially designed nest boxes are preferred over larger nest boxes. Provisioning of nest boxes can thus be an efficient conservation action, but should be tailored to the specific needs of the focus species.

77 Foraging distances and their impact on reproduction in native bees

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Native bees have suffered a considerable decline in local species diversity and population size during the last few decades due to a decrease of resources needed for successful reproduction, such as suitable nesting sites and flowers. The knowledge about how bees spatially use plant resources is crucial to understand population dynamics of endangered species. In the present study, spatial aspects of resource use by bees were investigated with the solitary and pollen-specialist species *Hylaeus punctulatus*, *Chelostoma rapunculi* and *Hoplitis adunca*. Experiments were conducted in a landscape lacking the species-specific host plants. Maximum foraging distances were determined by subsequently moving patches of potted host plants away from the nesting site. The impact of foraging distance on reproduction was estimated by comparing the number of brood cells provisioned per unit time for different distances between nest and host plant patch. For all three bee species, unexpectedly long maximum foraging distances of 1000m and more were found. However, increasing foraging distances resulted in a considerable reduction in the number of brood cells provisioned per unit time. In *H. adunca*, 23% less brood cells are provisioned when foraging at a distance of 375m compared to 225m, and 26% less cells when foraging at 450m compared to 150m. Similarly, *Ch. rapunculi* provisions 40% less brood cells when foraging at a distance of 1000m compared to 500m. In conclusion, although bees can use resources on an unexpectedly large spatial range, already minor changes in the spatial arrangement of bee resources considerably affects bee population dynamics.