

Biology05

24-25 February 2005, University of Basel

The Annual Conference of the Swiss Societies of Botany, Mycology and Zoology

A two-day scientific meeting of organismic and integrative biology. A forum for PhD students and PostDocs to present their research.

Abstracts

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Editor

Institute of Botany, University of Basel, Switzerland, 2005

Keynote lectures

Janne Bengtsson, Swedish U Agricultural Sciences, Uppsala, Sweden

Local and regional processes in human-dominated landscapes

I will talk about the importance of a landscape perspective on ecological processes, mainly in the context of landscapes influenced by agriculture and other human activities, but also in small aquatic ecosystems. Examples of effects of landscape structure and farm management on biodiversity, biological control and pollinators will be given from our research in mosaic agricultural and urban landscapes in Central Sweden. For example, we estimated that in 1999 natural enemies to aphid pests on spring cereals were worth about 40 euros per hectare to the farmer. Because natural as well as human-dominated ecosystems are dynamic and subject to disturbances (ecological, and socio-economic), I will suggest that the classical approach to biodiversity conservation in isolated static nature reserves may not be enough to preserve biodiversity and the ecosystems services humans depend on. The classic approach should be extended to landscape-wide management based on knowledge of natural and human disturbance regimes, involving conservation in both managed ecosystems and reserve networks. I will conclude with a reflection on the fact that agricultural sciences need a large dose of basic ecology to be of any use for sustainable management of agricultural landscapes. Ecologists, on the other hand, should realize that the basic ecological mechanisms are the same in most ecosystems. Thus ecology will profit from studying systems which are perceived by the public as both interesting and important for human welfare.

Meredith Blackwell, Louisiana State University, USA

Fungal associations with arthropods: an inordinate fondness for fungi

An inordinate fondness for fungi: Fungal associates of arthropods.

The discovery of novel arthropod-associated fungi, elucidation of their life histories and dispersal associations, and their phylogenetic relationships has been enhanced by the development of molecular and phylogenetics methods. Several different groups of fungi have been of special interest in these studies: Laboulbeniales and insect gut-inhabiting ascomycete yeasts (Saccharomycetes). Both groups are morphologically and genetically distinct and contain large numbers of species. Members of the Laboulbeniales are obligate ectoparasites of arthropods, especially insects, and are unusual among fungi because of their limited thallus with determinate growth. Development of the several hundred-celled thallus begins with division of the two-celled ascospore; mycelium does not develop. The unusual development and morphology caused taxonomic uncertainty for more than 100 years, and the Laboulbeniales have been classified as zygomycetes, ascomycetes, basidiomycetes, floridean red algae, and even parasitic worms. Phylogenetic analyses based on molecular characters strongly support placement of Laboulbeniales in a distinctive clade with certain mycelial ascomycetes that are insect dispersed. Members of the other group of interest, the distinctive well-supported ascomycete yeasts, have a broad variety of substrate associations. New taxa are being discovered at a rapid rate, and, especially importance in this context, several newly discovered clades are comprised entirely of insect-associated yeasts. The insect-associated yeasts occur in clusters scattered throughout the entire yeast phylogenetic tree. These analyses and other experimental data suggest speciation in certain insect-associated ascomycetes has occurred via their specialization on insects, isolation within insect populations, and subsequent rare horizontal transfers, resulting in large numbers of insect-associated fungi.

Peter Klinkhamer, Leiden University, The Netherlands

(Size dependent) sex allocation in plants

Sex allocation theory is well developed and leads to some clear cut predictions both on the level of comparisons of species with different reproductive strategies and on the level of individual species. Practical difficulties and some conceptual problems so far stood in the way of vigorous testing. Nevertheless, our increasing understanding of the processes shaping fitness gain curves has

allowed the formulation and testing a number of hypothesis. In particular the role of selfing, leading to a decreased investment in male function, and the effects of mode of pollination are well understood. More recently models have been developed to study the effects of selective embryo abortion on sex allocation. It was hypothesized that sex allocation in plants should be size dependent because many of the factors that determine the optimal sex allocation (the exponents of the gain curves, local resource competition, local mate competition, selfing rate) are different for small and large plants. Effects of individual size on the shape of the gain curves can be direct (e.g. taller plants disperse their pollen further) or indirect because bigger plants invest larger budgets in reproduction (e.g. leading to increased geitonogamy). Direct effects select for a complete gender change with increasing size, budget effects to a gradual change. Because budget effects will be present in most plant species a gradual sex change was expected to be most common in plants and this is indeed found. Evidence that sex change is adaptive comes, among other things, from a comparison of wind and animal pollinated plants.

Mark van Kleunen, University of Potsdam, Germany

Constraints on the evolution of adaptive phenotypic plasticity in plants

The high potential fitness benefit of phenotypic plasticity tempts us to expect phenotypic plasticity as a frequent adaptation to environmental heterogeneity. Examples of proven adaptive plasticity in plants, however, are scarce and most plastic responses actually may be 'passive' rather than adaptive. This suggests that frequently requirements for the evolution of adaptive plasticity are not met or that such evolution is impeded by constraints. In this talk, I outline requirements and potential constraints for the evolution of adaptive phenotypic plasticity, identify open questions, and propose new research approaches. Important open questions concern the genetic background of plasticity, genetic variation in plasticity, selection for plasticity in natural habitats, and the nature and occurrence of costs and limits of plasticity. Especially promising tools to address these questions are selection gradient analysis, meta-analysis of studies on genotype-by-environment interactions, QTL analysis, cDNA-microarray scanning and quantitative PCR to quantify gene expression, and two-dimensional gel electrophoresis to quantify protein expression. Studying plasticity along the pathway from gene expression to the phenotype and its relationship with fitness will help us to better understand why adaptive plasticity is not more universal, and to more realistically predict the evolution of plastic responses to environmental change.

Anders Pape Møller, Université Marie et Pierre Curie, Paris, France

Darwin Party talk

Oral presentations

Patrick Basset, Glenn Yannic, Harald Brünner & Jacques Hausser, U Lausanne

*Chromosomal rearrangements and gene flow in hybrid zones between shrews of the *Sorex araneus* group*

The species and races of the *Sorex araneus* group of shrews exhibit a huge range of chromosome polymorphism. European species and chromosome races of this group are parapatric and exhibit contact or hybrid zones showing an extraordinary variety of situations, from absolute genetic isolation to almost free gene flow. This variety seems to depend for a large part on the chromosome composition of populations, which are primary differentiated by various Robertsonian fusions of the same acrocentric chromosomes. Various data suggest that chromosomal rearrangements severely impede recombination in heterokaryotypes. In such circumstances, gene flow should be more restricted for markers housed on chromosomes involved in rearrangements than on chromosomes identical in both parent species.; In the present study we address the reality of such differentiated gene flow in the context of hybrid zones between species of the *Sorex araneus* group.

Laura Brändli, Lori Handley & Nicolas Perrin, U Lausanne

Phylogeography and demographic processes inferred from sex-specific markers; in the greater white-toothed shrew, Crocidura russula

Fifty-four males of *Crocidura russula* sampled throughout the species range were analysed using three regions of the mtDNA, four introns plus one coding region from the Y chromosome, and two X chromosome-linked introns, encompassing over 5kb of sequence data. Phylogenetic analyses of mtDNA, Y and X chromosomes are basically concordant, and indicate two highly divergent haplogroups, a western haplogroup (HW) comprised of individuals from Morocco and Europe, and an eastern haplogroup (HE) from Tunisia and Sardinia. Phylogeographic analyses indicate that European populations originate from Morocco, and mtDNA mismatch distributions suggest an expansion following colonisation, dated to approximately 70ky BP. Diversity was all but wiped out during colonisation, and equilibrium levels have not yet been restored on the European X and Y chromosomes (as opposed to mtDNA) owing to their low mutation rates. Accounting for time since expansion (as well as mutation rate and effective number of copies), the Y chromosome and mtDNA display a deficit in variance relative to the X chromosome in both ancestral and derived populations, which likely stems from selection on these non-recombining loci. However this deficit is less than published values for species with more typical mammalian breeding systems (polygyny and male-biased dispersal), highlighting the importance of male reproductive skews in reducing Y-linked polymorphism

Rolf Debrunner, Gwenaël Jacob, Kurt Bollmann & Felix Gugerli, Swiss Federal Research Institut WSL, Birmensdorf

Population size estimation of Capercaillies (Tetrao urogallus) in the canton of St. Gallen - Field estimates validated by genotyping faeces

The capercaillie is a grouse species inhabiting, in central Europe, coniferous forest in mountainous areas. The species has experienced a dramatic decline during the last century and is considered endangered in Switzerland. An action plan was initiated by St. Gallen cantonal authorities in collaboration with the Ornithological Station Sempach and the WSL, aiming at determining the causes of the decline and implementing management measures for the species. Direct capercaillie observations and the densities of tracks, faeces and feathers observed during field surveys are used to estimate the density of individuals. Additional information on the quality of the surrounding habitat is used to extrapolate the census sizes of the local populations. Molecular methods provide an alternative to estimate population census size, but also to determine the sex ratio and the relatedness among individuals within a patch. We extracted DNA from 147 faecal samples collected in 13 for; est patches in the canton St. Gallen. The samples were genotyped at 12 nuclear microsatellite loci and an additional sex-diagnostic locus. We identified 43 unique multilocus genotypes and extrapolated a population size of 60 to 100 individuals for the study area. Our result is 20 to 25 % higher than a previous estimate based on field surveys. The variance in census size estimates is low in patches with medium quality habitat and increases with patch quality and population density. The genetic-based methods of population size estimates are expensive and cannot be used routinely in conservation programs. Therefore, we recommend to validate field expertise by molecular methods when possible.

Thomas Fabbro & Thomas Steinger, U Fribourg

Evolution of herbivore-induced resistance in wild mustard (Sinapis arvensis)

Induced responses of plants to herbivore feeding are thought to play an important role in plant-herbivore interactions. Today, little is known about opportunities and constraints on the evolution of induced resistance. Several chemical, morphological, and life-history traits can be induced and their inducibility may be under selection by herbivores. However, an evolutionary response to selection may be constrained by a lack of genetic variation or by negative genetic correlations. We used a quantitative genetic approach with controlled crosses (paternal half-sib families), that allowed the estimation of additive genetic variances and correlations. In a greenhouse experiment we exposed *Sinapis arvensis* (Brassicaceae) to feeding by a specialist herbivore, *Pieris rapae*, and compared untreated control and herbivore damaged plants. Growth of *Mamestra brassicae* and

Spodoptera littoralis (two generalist herbivores) was reduced on herbivore damaged plants but growth of *Pieris rapae* was not affected. We found heritable variation for resistance against *Mamestra brassicae* on plants with herbivore damage and heritable variation for the inducibility of this resistance. In contrast, no heritable variation was found for resistance against *Spodoptera littoralis* and *Pieris rapae*. Glucosinolate concentration on herbivore damaged plants was almost doubled and exhibited heritable variation in control and herbivore damaged plants but no heritable variation for inducibility. We present patterns of phenotypic and genetic correlations among resistance traits and discuss factors that may influence the evolutionary dynamics of induced resistance.

B. Facon, P. Jarne, J.P. Pointier & P. David, U Lausanne

*Hybridization and invasiveness in the freshwater snail *Melanoides tuberculata*.*

Many invasive taxa are hybrids, but how hybridization boosts the invasive process remains poorly known. We address this question in the clonal freshwater snail *Melanoides tuberculata* from Martinique, using three parental and two hybrid lines. We combine an extensive field survey (1990-2003) and a quantitative genetic experiment to show that hybrid lines have outcompeted their parents in natural habitats, and that this increased invasiveness co-occurred with pronounced shifts in life-history traits, such as growth, fecundity and juvenile size. Given the little time between hybrid creation and sampling, and the moderate standing genetic variance for life-history traits in hybrids, we show that some of the observed trait changes between parents and hybrids were unlikely to arise only by continuous selection. We therefore suggest that a large part of hybrid advantage stems from immediate heterosis upon hybridization.

Anne-Marie Fiore-Donno, Cédric Berney, Jan Pawlowski & Sandra L. Baldauf, U Geneva

*Higher-order phylogeny of Myxogastrica (*Myxogastrina*)*

The Myxogastrica are common soil microorganisms with a life cycle comprised of a plasmodial trophic stage and large fruiting bodies generally visible with the unaided eye. Until now, their classification has been based exclusively on a combination of morphological, ultrastructural and developmental characters. Our study is the first attempt to examine phylogenetic relationships among these taxa using molecular data. Partial small-subunit ribosomal RNA and/or elongation factor 1- α gene sequences were obtained from eleven, mostly field-collected species representing the five orders of Myxogastrica. Nineteen sequences were obtained and subjected to phylogenetic analysis together with ten sequences available from GenBank. Separate and combined analyses of the two data sets support the division of Myxogastrica into three distinct groups. The most basal clade consists of the Echinosteliales, an order considered to have affinities with Protostelia. The three species examined possess unpigmented or slightly pigmented spores. The second group consists of Liceales and Trichiales, taxa characterized by the presence of clear, but pigmented, spores. The third group consists of the two remaining orders, Physarales and Stemonitales, both possessing dark spores. This suggests that spore pigmentation is an evolutionarily conservative character in myxogastrics, and that the simple morphology of echinostelids is not a derived feature.

Martin Grüebler, Zoological Institute, U Zürich & Swiss Ornithological Institute, Sempach

Breeding in a hurry: the timing of second broods in the Barn Swallow affects over-all reproductive success

A seasonal decline of reproductive performance is documented for many single-brooded bird species. In double-brooded species the trade-offs in optimizing the timing of breeding may be even more pronounced. Thus, time constraints due to the limited season may affect the performance of the second brood as well as the allocation of efforts among the two broods, and the timing of the first brood at the beginning of the season. A major problem in quantifying the fitness-relevance of the timing of breeding is that the seasonal trend may be caused or confounded by parental quality effects, namely if good quality parents breed earlier than low quality parents.; To disentangle the effects of timing and quality of parents on the condition and the post-fledging survival of juveniles,

we conducted a clutch exchange experiment with second broods of Barn Swallows. The results showed evidence for both the parental care and the date effect. Structural size of early second broods was affected by the treatment, while late broods showed no differences in size between groups supposing a declining effect of parental quality in the nestling period. However, experimental treatment did not reveal a parental quality effect in the declining post-fledging survival rates.; Thus, parent Barn Swallows face a trade-off between continuing the post-fledging care of first-brood chicks and an early start of their second clutch.

Felix Gugerli, Jean-Claude Walser, Katerina Dounavi, Rolf Holderegger & Reiner Finkeldey, WSL

*Fine-scale spatial congruence between taxon assignment based on leaf morphological characteristics and nuclear microsatellite variation in *Quercus petraea* and *Q. robur**

The genus *Quercus* has been extensively studied with regard to hybridization as a major mechanism in speciation processes. In central Europe, the species complex comprising *Q. petraea* and *Q. robur* shows distinct leaf morphologies and ecological preferences, but low differentiation in various types of molecular markers at a broad spatial range. Small-scale, spatially explicit genetic analyses of *Q. petraea* and *Q. robur* have not been performed. We studied a mixed stand located in the Swiss central plateau and used discrimination analysis of leaf morphological characters for grouping individuals and identifying putative hybrids. The two taxa were significantly differentiated at five nuclear microsatellite loci. Individual assignment based on maximum likelihood of multilocus genotypes grouped putative hybrid trees to the taxon that corresponded to the taxonomic status of the spatial neighborhood in which the respective trees were located in the stand. When building clusters of trees derived from their spatial positions, discontinuities in morphological and molecular distance matrices among these clusters showed high congruence. Based on our data and on the literature, we assume that reproductive incompatibilities, assortative mating, limited seed dispersal, and microsite-induced selection in favor of the locally adapted species at the juvenile stage may reinforce taxon-specific spatial aggregation that fosters species separation. Thus, we see *Q. petraea* and *Q. robur* as distinct species that share a relatively recent common ancestry and rarely hybridize.

Alessia Guggisberg, Sylvia Kelso & Elena Conti, U Zürich

*Testing the secondary contact model: the case of the *Primula egalikensis*-complex (sections *Aleuritia*/*Armerina*, *Primulaceae*)*

The sections *Aleuritia* and *Armerina* of *Primula* include diploid heterostyles and polyploid (4- to 14-ploid) homostyles, distributed all over the northern hemisphere, with a primarily high arctic range for the polyploids. A correlation between ploidy level, homostyly, and arctic distribution has been suggested, according to the secondary contact model that predicts geographic isolation of diploids during the Quaternary glacial peaks followed by connections and gene flow after glacial retreats. Isolated and partially differentiated diploid populations then come into contact and hybridise, giving rise to several polyploid systems. To investigate these hypotheses, we generated molecular phylogenies for the *P. egalikensis*-complex, using one nuclear (ITS) and five chloroplast genes (*rpl16* intron, *rps16* intron, *trnL* intron, *trnL-F* spacer, *trnT-L* spacer). This polyploid complex is of special interest, featuring a tetraploid homostyle, *P. egalikensis*, which is supposed to; be an intersectional hybrid between diploid heterostyles, *P. mistassinica* (sect. *Aleuritia*) and *P. nutans* (sect. *Armerina*). Preliminary results reveal high incongruence between the nuclear and chloroplast data sets, indicating conflicting position of polyploid taxa intermingled with the diploid ones. The topological discordance also highly supports an allopolyploid origin for *P. egalikensis* between *P. mistassinica* and *P. nutans*. Further, the high number of haplotypes and ribotypes detected within *P. egalikensis* and its putative parents is in accordance with the secondary contact model. More detailed analyses are currently in progress to circumscribe glacial refugia, and reconstruct the post-glacial recolonisation routes of the latter complex.

Dik Heg, Nicole Bender & Ian Hamilton, U Bern

Strategic growth decisions in helper cichlids

Recently, it has been shown that group-living subordinate clownfish *Amphiprion percula* increase their growth rate after acquiring the dominant breeder male position in the group. Evidence was found for strategic growth adjustments of subordinate fishes depending on the threat of eviction, i.e. subordinates adjust their growth rates so they remain smaller than the dominant fish and thereby limit the threat of being expelled from the territory. However, it is impossible to exclude several alternative factors that potentially could have influenced the observed changes in growth, owing to the nature of that experiment (removing the second-ranking fish - the breeder male - caused the third-ranking fish to change sex to become breeder male and change rank). We studied strategic growth decisions in the group-living Lake Tanganyika cichlid *Neolamprologus pulcher* under controlled laboratory conditions with ad libitum food availability. First, we show that male breeders grow faster than subordinate male helpers of the same initial size and confirm that *N. pulcher* shows status-dependent growth. Second, we improved on the experimental design by not removing the dominant breeder male in the group; instead we replaced the breeder male with a new breeder male in a full factorial design and measured growth of the subordinate male helpers is a function of the size difference with the old and the new breeder male. As predicted, male helpers showed strategic growth adjustments, i.e. growing faster when the size difference with the breeder male is large. Strategic growth adjustments were less pronounced than status-dependent growth adjustments.

Linda Hollén & Marta Manser, U Zürich

*Age related modification of alarm call response strategies in meerkats (*Suricata suricatta*)*

Because young individuals are highly vulnerable to predators, selection should favor early development of adult-like responses to alarm calls. Meerkats, *Suricata suricatta*, have evolved an alarm call system that combines information about predator type and on the level of response urgency in the acoustic structure of different call types. This allows receivers to respond appropriately to calls emitted in a specific context. The mechanisms underlying the development of alarm call responses were investigated by monitoring the behaviour of free-living meerkats to natural predator encounters and playbacks of conspecific alarm calls from emergence (three weeks old) until adult-hood (one year old). At the time of first foraging with the group (four weeks old), the probability to show adult-like responses was only 50%. Pups typically ran to, or looked towards older group members, when hearing an alarm call. Relying on others increased the probability to show adult-like responses. Pups relied less on others when hearing alarm calls signalling high urgency, where an immediate response may be of crucial importance. The probability to respond independently and adult-like increased as pups grew older and by six months of age was higher than 95%. These results suggest that pups need to learn how to respond appropriately to the different alarm call types and relying on others may be a safe strategy while still learning. Although learning from others may not be necessary to acquire correct alarm call responses, this study emphasizes the importance of social and ecological factors on the development of alarm call responses.

Barbara Holzer, Laurent Keller & Michel Chapuisat, U Lausanne

*Genetic structure and recognition ability in an unicolonial *Formica ant**

Unicoloniality is an extraordinary social organisation found in several ant species. In unicolonial ant populations colony boundaries are absent and individuals are able to move between neighbouring nests without eliciting aggression. Several studies have documented a loss of aggressive behaviour in introduced and invasive ant species. However, the recognition ability and the genetic structure in native unicolonial ant species remain poorly known, particularly at large geographical scales. We therefore investigated the pattern of aggression and the genetic structure of six unicolonial populations of the ant *Formica paralugubris* at four hierarchical levels: within nests, between nests within the same population, between nests of populations within the Alps or Jura mountains and between nests of the two mountain ranges. Ants within populations showed no aggressive behaviour, but recognized non-nestmates as evidenced by longer antennation bouts. Overall, the level of aggression increased with geographic and genetic distance but always remained considerably lower than between species. No distinct behavioural supercolony boundaries were

found. Our study provide evidence that unicoloniality can be maintained in non-invasive ants despite well-developed recognition ability and significant genetic differentiation.

Antonina Internicola, Nicolas Juillet, Ann Smithson & Luc Gigord, U Lausanne

Experimental investigation of density-dependent reproductive success in a rewardless orchid

In sedentary organisms such as plants, intra- and interspecific interactions are strongly density-dependent. For instance, resources availability and acquisition by individuals depend on density. This may imply consequences on individual survivorship, as well as individual reproduction. Moreover, reproduction of most Angiosperms relies on animal pollinators and plant density within a patch may influence its attractiveness to pollinators. Consequently, individual reproduction within a given patch may depend on plant density of the patch through density-dependent attraction of pollinators. In the case of rewardless species, the density may also influence learning abilities of pollinators. In consequence, the reproductive success of rewardless species may strongly depend on density of rewardless plants through learning abilities of pollinators. Also, the species composition and the density of plants that co-flower with the rewardless plants may have an influence on pollinators' behavior and, consequently, on the reproductive success of the rewardless species.; To test the hypothesis that the reproductive success of a rewardless species is affected by densities of both the rewardless and a rewarding co-flowering species, we set up a large-scale artificial metapopulation of 16 sub-populations consisting of two co-flowering species, one rewarding and one rewardless. For each species, two levels of density (high and low) were considered in a full factorial design with four replications. Our results showed that both the densities of the rewardless and rewarding species influenced the reproductive success of the rewardless species. The higher the density of the rewarding or of the rewardless species, the lower was the reproductive success of the rewardless species. To our knowledge, this is the first experimental study showing the importance of density effects both of a rewarding co-flowering species and of a rewardless species on the reproductive success of the rewardless species. We discuss the mechanisms that may lead to such a situation and the importance of the link between density, the proximity and the spatial distribution of the two species.

Julie Jaquiéry, Alexandre Hirzel & Nicolas Perrin, U Lausanne

Effective size and capacity of metapopulations: a simulation approach

Habitat fragmentation poses serious threats to the survival of many populations, by increasing demographic stochasticity and lowering genetic diversity. The minimal size of patches and connectivity among them necessary for population survival are questions that must be considered in terms of both demography and genetics, since both interact to drive fragmented populations into extinction vortices.; Conceptual tools were recently developed to quantify, not only the value of a given landscape, but also that of particular patches in this landscape, in terms of capacity to resist either demographic extinction (models of metapopulation capacity) or genetic drift (models of metapopulation effective size). These two currencies, however, may bear no direct relations. Landscape features favouring the capacity of a metapopulation may poorly affect its effective size, and vice versa. Small and isolated patches, for instance, may contribute negligibly to the ability of a metapopulation to avoid stochastic demographic extinction, but significantly to its effective size by maintaining a large amount of variance among demes.; We investigate these topics through stochastic population-based models, and will show how the value of patches in different currencies (demographic or genetic) correlate, depending on landscape features.

Christopher Kaiser, U Zürich

Facilitative or competitive interactions for pollination between an invasive and a native plant species: an experimental approach

Invasive alien plant species are known to interact with native plants in several ways. There is recent evidence that biotic mutualistic factors, such as facilitative or competitive interactions for pollination can influence plant community composition. In Mauritius, *Psidium cattleianum* is heavily invasive to most parts of the upland rain forest, where it's flowering season corresponds with the flowering phenology of many endemic plant species, e.g. *Bertiera zaluzania*. We proposed that the

presence of *P. cattleianum* flowers will affect the reproductive success of *B. zaluzania* plants in co-occurring communities. A flower removal experiment was conducted in the Black River Gorges National Park in Mauritius between November 2003 and February 2004. We marked out 20 areas of *P. cattleianum* with a 10m radius centred around a single female plant of *B. zaluzania* pre-flowering. In 10 plots, all flowers of the surrounding *P. cattleianum* plants were removed. Pollinator observations and self-pollination experiments were conducted. The most abundant pollinator was the introduced *Apis mellifera* (honeybee). There were no significant differences in visitation rate between the two plant species. Results of fruit and seed set suggest that the reproductive success of *B. zaluzania* was not influenced by the presence or absence of *P. cattleianum*. The introduced pest *Prophantis smaragdina* was shown to have a severe impact on the fruit set of *B. zaluzania*. Although both plant species shared the same pollinator, no indirect or direct competition for pollinator services could be demonstrated with this experiment. We concluded that competition for resources is the primary factor limiting reproductive success of native plant species.

R. Kümmerli, K. Helms & L. Keller, U Lausanne

*Experimental manipulation of queen number affects colony sex ratio investment in the highly polygynous ant *Formica exsecta**

In polygynous (multiple queens per nest) ants queen dispersal is often limited with young queens being recruited within the parental colony. This mode of dispersal leads to local resource competition between nestmate queens and may lead to extremely male biased sex ratios at the population level. The queen replenishment hypothesis has been recently proposed to explain colony sex ratio investment under such conditions. It predicts that colonies containing many queens (subject to high local resource competition) should only produce males, whereas colonies hosting few queens (reduced or no local resource competition) should produce new queens in addition to males. We experimentally tested this hypothesis by manipulating queen number over 2 years in 120 colonies in a highly polygynous population of *Formica exsecta* in the Swiss Jura Mountains. Queens were transferred from 40 colonies into another 40 colonies while queen number was not manipulated in 40 control colonies. Genetic analyses of worker offspring revealed that our treatment was successful. The sex ratio of colonies was significantly different between treatments in the third breeding season following the experiment initiation. As predicted by the queen replenishment hypothesis, queen removal resulted in a significant increase in the proportion of colonies that produced new queens. Our results provide the first experimental evidence for this new hypothesis, which might account for sex ratio specialization in many highly polygynous ant species.

H. P. Kunc, V. Amrhein & M. Naguib, U Bielefeld, D

*Whistles make a difference: male nightingales (*Luscinia megarhynchos*) whistle at night to attract females*

Song is among the most conspicuous bird behaviours, and the main functions of song are mate attraction and territory defence. Nocturnal song is generally thought to be important for attracting nocturnally migrating females, whereas dawn song in nightingales is thought to function mainly in territory defence. Nightingales have large vocal repertoires but one song category stands out acoustically 8211; the whistle songs (WS). WS are best suited for long range transmission, because the acoustic structure of whistle suffers less from degradation than do more complex song features. Thus, WS may be a more effective signal to attract nocturnally migrating females. We predicted that males that are successful in attracting a mate would sing more WS at night, but not at dawn, than males that remain unpaired (so called bachelors). Comparisons between nocturnal and dawn song showed that nocturnal singing behaviour of male nightingales is strongly correlated with mating success and genetic paternity. Males that were able to attract a female sang more WS at night during mate attraction than bachelors. During the dawn chorus, we did not find such differences between mated males and bachelors. Furthermore, playback experiments showed that males significantly reduced the proportion of WS during playback, suggesting that WS are less important in short-range interactions with rival males. These findings suggest that WS are used as long range signals to attract nocturnally migrating females. Our study emphasizes that

time of day can play a critical role in understanding the relationship between song and mating success.

Urs Landergott, Rolf Holderegger, John D. Thompson & J. Jakob Schneller, U Zürich
Is there a female advantage in seed weight in gynodioecious mountain thyme associated with the species' sex ratio change along altitudinal gradients?

The frequency of females in populations of gynodioecious *Thymus praecox* agg. increases with altitude in the Alps. Variation in seed weight along altitudinal gradients has been reported in several plant species, and a female advantage in seed weight has repeatedly been reported in gynodioecious species. Two major sources of variation in seed weight were detected in *T. praecox* agg.: (1) allocation of resources within fruits (one up to four seeds per fruit), with an almost linear decrease in weight with increasing seed number, and (2) altitude, with heavier seeds found at higher elevations. A reciprocal transplant experiment indicated genotypic differentiation for heavier seeds at higher altitudes in *T. praecox* agg. This would provide a template for selection to act on a female advantage in seed weight and thereby on the sex ratio with a female advantage being more important at higher altitudes. Females of *T. praecox* agg. indeed provisioned seeds better than hermaphro; dites in natural populations, but their relative advantage was constant at different altitudes. Moreover, hermaphrodites set less and thus heavier seeds per fruit, whereas females set more and thus lighter seeds per fruit. This counteracted the female advantage gained from better seed provisioning, i.e. no net advantage was detected in natural populations. No correlation between female advantage and current population sex ratio was found. However, given the genotypic differentiation in seed weight along altitudinal gradients, the female advantage in seed provisioning in mountain thyme may nevertheless have played a role in reaching the current population sex ratios.

Sandra Lass & Dieter Ebert, U Basel

The rise and fall: causes of prevalence fluctuation in a parasite with horizontal and vertical transmission

An understanding of epidemiological patterns is crucial to test theory and to be able to control disease. Here, we shed light on the causes of fluctuation in parasite prevalence using the cladoceran *Daphnia magna* and its microsporidian parasite *Octosporea bayeri* as a model system. *O. bayeri* transmits vertically, from infected mothers to their offspring, and horizontally, via spores released from dead infected hosts. Long-term field data reveal that the parasite's prevalence increases quickly and drastically during the host's growing season (summer) but decrease again during the host's diapause (winter). Horizontal transmission is shown to be eminent to the dynamics of parasite prevalence. Exclusion of horizontal transmission in experimental host populations led to a rapid decrease in prevalence. Uninfected *Daphnia* out-competed their infected conspecifics resulting in the extinction of the parasite. Furthermore, an infective spore bank can over-winter in the sediments of rock-pools, thereby providing an additional mechanism that leads to rapid spread of disease during summer. Several factors contributed to the decrease in prevalence during winter. First, the contribution of diapausing eggs from uninfected hosts is disproportionately high: Production of diapausing eggs starts early in the season when prevalence is still low and infected hosts produce less diapausing eggs than their uninfected conspecifics. Second, the parasite fails to maintain its prevalence in diapausing eggs: Vertical transmission into the eggs is imperfect and infected eggs are less likely to survive winter conditions. These results show that particular mechanisms of parasite transmission play a crucial role in explaining the epidemiology of a disease.

Nicolas Margraf, Sabrina Taylor, Carolyn Tepolt & Ian G. Jamieson, U Neuchâtel

Wildlife translocation and inbreeding: the case of two endemic New Zealand bird species

In New Zealand, introduced mammalian predators have driven many endemic birds to the brink of extinction. To save them, one solution has been to transfer part of the menaced populations to offshore islands where predators have been eradicated. For many species this practice has given good results. However, often only a small number of founders are used, which could produce a

population with low genetic variability and trigger high inbreeding that might harm the rescue process.; In this study, we assessed the influence of inbreeding on reproductive success in two recent translocations. Populations of South Island Saddleback and New Zealand Robin were introduced onto Ulva island in 2000. We found a low correlation between inbreeding coefficients estimated using microsatellite markers and fledging success. These results have implications for both wildlife conservation management and evolutionary ecology.

Katrin Maurer, Anne Weyand, Markus Fischer & Jürg Stöcklin, U Basel

*Influence of human land use on genetic diversity of *Poa alpina* L. in the Swiss Alps – a microsatellite study*

The grass species *Poa alpina* L. is widespread in subalpine and alpine grasslands of the Alps. The plant is an indicator of nutrient rich and moist meadows and pastures, but it is also a pioneer species in alpine screes. It is one of the most important fodder grasses for cattle, and therefore *Poa alpina* has been under an agricultural selection pressure for hundreds of years. *Poa alpina* L. reproduces either sexually by seeds or asexually by pseudovivipary producing small plantlets instead of flowers. The species is a highly polyploid complex with common aneuploidy.; To investigate the effects of altitude, cultural traditions and land use on genetic diversity of *Poa alpina* L. we collected plants from 12 villages in the Swiss Alps, from four villages of each of the cultural traditions Romanic, Alemannic and Walser. Eight individuals were sampled at three altitudinal levels, in parcels of land either used as meadows or pastures and either unfertilized or fertilized. Additionally, samples were collected from natural sites. Altogether we sampled 574 individual plants from 74 populations and screened them for alleles in five microsatellite loci. In total we found 209 different alleles, between 25 and 61 per locus. As measures for genetic diversity we calculated the mean number of alleles per plant and the allelic richness per population. There was no difference between populations from natural and agriculturally used sites. Among the used parcels, populations from pastures were more diverse than were those from meadows. Among Walser villages the allelic richness was higher than in Alemannic villages while it was intermediate in Romanic villages. We found that 75 % of the variation in allelic richness was within and 25 % among populations. We conclude that human land use has shaped genetic diversity of *Poa alpina* L. in the Swiss Alps.

Stefan W. Müller, Hans-Peter Rusterholz & Bruno Baur, U Basel

Genetic structure of two relic plant species in the Swiss Jura mountains

Knowledge of the genetic structure of isolated plant populations is a prerequisite for the development of efficient conservation and management strategies. We examined the genetic structure of the arctic-alpine dwarf-shrub *Draba aizoides* and the Mediterranean grass *Melica ciliata* in the Swiss Jura mountains. RAPD-PCR techniques were used to study 15 populations of *Draba aizoides* (with 10 to 16 individuals each) and 13 populations of *Melica ciliata* (with 12 to 18 individuals each). We found high proportions of polymorphic loci ranging from 28 – 60% for *Draba aizoides* and 20 – 63% for *Melica ciliata*. The results of AMOVAs and UPGMA-clustering indicate a discrete genetic reservoir of the plant populations in the Jura mountains and a genetic isolation on the limestone cliffs due to asexual reproduction. The high genetic similarity of populations of *Melica ciliata* situated nearby castles of similar historic origin suggests a considerable anthropogenic impact on the distribution of the species.

Samuel Neuenschwander, Carlo R. Largiadè & Laurent Excoffier, U Bern

*Simulation based estimates of the Bayesian estimation of the colonization history of *Cottus gobio* L. in the Swiss Rhine basin*

After the retreat of glaciers, animals like freshwater fishes colonize newly freed habitats. In order to study the dynamics of this process, we have developed a computer model to simulate the colonization of fishes in a realistic vectorized river system, as well as the resulting genetic diversity at various locations. These simulations were used in an Approximate Bayesian Computations (ABC) setting to obtain estimates of the parameters of the recolonization process of the bullhead (*Cottus gobio* L.) after the last glacial maximum (LGM) in the Swiss Rhine river system. The

analysis of microsatellites and mtDNA data allowed us to obtain estimates of the timing of the colonization, the colonization and current migration rates, or effective population sizes.

Mathieu Perret, Botanical Garden, Geneva

Flower color evolution in Sinningieae (Gesneriaceae): phylogenetic and molecular aspects

Patterns of flower color evolution and the genetic basis of pigment biosynthesis were investigated in the tribe Sinningieae (Neotropical Gesneriaceae). Phylogenetic reconstructions indicate several independent color shifts between red and other colors that reflect light at lower wavelengths (< 600 nm). These color shifts rely on the biosynthesis of different types of flavonoids and correspond with a transition between hummingbird and insect pollination. To gain further insight on molecular changes that underlie evolutionary modifications of this phenotype, we performed a comparative genetic study between two closely related species – *Sinningia sellovii* and *S. tubiflora* – that differ in their floral color (red versus white). The red flowered *S. sellovii* contains mainly pelargonidin glucoside, whereas the white flowered *S. tubiflora* synthesizes only colorless flavones. To understand this difference in flavonoid composition, six structural genes (CHS, CHI, F3H, F3'H, DFR, and ANS) involved in the anthocyanin pathway were characterized. Sequences and expression patterns of these genes were compared between *S. sellovii* and *S. tubiflora* to point out the molecular mechanism responsible for the switch of floral color. Our results showed that structural genes of both species are highly similar and that only a subset of genes differs in their expression patterns. In *S. tubiflora*, the low expression of genes acting late in the pathway (DFR and ANS) prevent the synthesis of anthocyanin whereas in *S. sellovii*, these genes are normally expressed. This result indicates that transcription regulation of a restricted number of genes may cause large phenotypic effects.

Philipp Raab, Annemarie Brennwald & Dirk Redecker, U Basel

Mitochondrial large subunit rDNA sequences as novel marker genes in the Glomeromycota

Partial sequences of the large subunit (LSU) of mitochondrial rDNA were obtained from the arbuscular mycorrhizal (AM) fungi *Glomus proliferum* and *Glomus intraradices* (Glomeromycota) cultivated in root organ cultures. The exon sequences of the two species were 87% identical, showing short regions of strong divergence. There was no evidence of intra-isolate sequence heterogeneity as it is found in variable regions of nuclear ribosomal genes. In *G. intraradices*, but not in *G. proliferum*, two introns were found in the partial LSU sequence. One of them (intron 1) contained an ORF for a putative site-specific endonuclease of the LAGLIDADG family. Phylogenetic analysis of the endonuclease sequence showed its closest known relatives to be hosted in other fungal mitochondrial introns. A specific PCR primer was designed and used to amplify a fragment of the mitochondrial large subunit of *G. intraradices* from colonized roots of a field sample. The apparent absence of intra-individual variation and the gene structure of alternating short conserved and variable regions with strong length variation make the mitochondrial large subunit valuable as a future marker gene for molecular identification purposes. The intronic sequences may be useful as an even more sensitive molecular marker for phylogeography and population studies.

Christophe Randin, Thomas Dirnböck, Antoine Guisan, Niklaus Zimmermann & Stefan Dullinger, U Lausanne

Testing the geographic transposability of predictive plant species distributions models

Predictive habitat distribution models have been increasingly used to assess the impact of climate and other environmental changes on the distribution of species. In this context, developing models that are applicable to a wide range of geographic and environmental situation is highly desirable. These models, based on the theory of the niche, fit a relationship between real field observations of species and a set of environmental predictors, and project it into the geographical space. Due to their very empirical nature, these models can only picture patterns of distributions that already result from possible biotic interactions (competition, symbiosis, facilitation, etc.), and thus they rather fit the realized than the fundamental niche of species. For this reason, it has often been argued that these models have their application limited to the specific regional and also temporal domain of calibration. In order to verify this assumption, we reciprocally fitted habitat distribution

models for more than 100 plant species in two regions of the European Alps: the northern calcareous Alps (Prealps of the Canton de Vaud, Switzerland) and the western calcareous Prealps (Mt Hochschwab-Mt Schneeberg, Austria), and additionally derived climate change scenarios for both sets of models. This study aims at answering the following questions:(1) Do environmental response models of the same species differ between the regions? (2) Can we predict plant species distributions of region 1 using models of region 2 and vice versa under present and future climate conditions?

Heiko Schmaljohann, Felix Liechti & Bruno Bruderer, U Basel

Spring migration of passerines across the Sahara: One large jump or several small hops?

In order to learn whether nocturnal migration over the Sahara stops or continues after sunrise, we carried out radar and ground observations at an oasis in central Mauritania during spring 2003. Birds departing from the Sahel had to cross an ecological barrier of 300 km before reaching this first oasis.; If songbirds migrate non-stop across the Sahara, we expect nocturnal migrants at Ouadâne about 6-8 hours after sunset and to fly across our site until the last birds having left the northern border of the Sahel have passed (i.e. until noon). If they are restricted to night flights, nocturnal migrants should rest in the ecological barrier south of Ouadâne during the day, cross our site just after sunset and nocturnal migration stops around sunrise. If birds adjust flight schedules opportunistically, we expect flight and landing behaviour to vary with environmental conditions.; Density of songbirds varied from day to day and decreased towards sunrise. Under good wind conditions passerine migration continued into the day, landing tendency (sink rates) correlating negatively with tail wind component. Considering the scarcity of diurnal migrants on the ground but high densities of passerine migration during the day, we suggest that nocturnal passerine migrants are responsible for most of the recorded daytime passage (aerial hunters and soaring birds being excluded). Passerine migrants seem to shift gradually between intermittent migration and prolonged migration according to conditions aloft, thus speeding up the Sahara crossing.

Manuel Schweizer, Laurent Excoffier & Gerald Heckel, U Bern

*Dispersal and fine-scale genetic pattern in the common vole *Microtus arvalis**

The rate and scale of dispersal are key parameters for understanding demographic processes in natural populations. Extreme demographic fluctuations are well known from small mammals, but dispersal parameters; and the consequences for populations are difficult to determine and remain often unknown for these organisms. In this study, we investigate dispersal patterns of the probably most abundant European mammal, the common vole (*Microtus arvalis*), from both a spatial and temporal perspective. Voles were studied in six natural populations at distances of 0.4 to 2.5 km over three different seasons corresponding to different life history stages. The analysis of ten microsatellite markers revealed surprisingly high levels of genetic structure among populations given the small geographic scale and high population densities. Despite genetic differentiation among populations, assignment analyses identified a high proportion of individuals as being of immigrant origin in their population of capture. Significantly more males than females were identified as first generation migrants, but the genetic signal of male-biased dispersal was overall relatively weak. Dispersal seems to be less sex-biased in our study than recently shown for gene flow in colonization processes of the common vole. However, this discrepancy as well as the maintenance of genetic differentiation among populations despite many migrants could be explained by a generally low and sex-dependent effective dispersal rate as the consequence of only few immigrants reproducing successfully in the new populations.

Gabriele Soland, Gerald Heckel, Peter Fluri & Laurent Excoffier, U Bern

Consequences of breeding programs on genetic structure and gene flow in the honeybee population in the Alpine region

The different subspecies of the honeybee (*Apis mellifera*) were described based on morphological and ethological traits, and have recently been confirmed by analyses of mitochondrial DNA. The purity of subspecies is of concern in areas where formerly allopatric subspecies now occur sympatrically due to beekeeping practices. Particularly in Switzerland, great efforts have been

made to keep breeding stocks of the native *A.m.mellifera* genetically separate from other subspecies like *A. m. carnica* and *A.m.ligustica*, already introduced 150 years ago from Slovenia and Italy, respectively. The genetic separation of sympatric breeding stocks is complicated by the hardly controllable mating behavior of honeybees. Despite the maintenance of remote mating yards, genetic introgression cannot be excluded fully.; In our study we evaluate the effectiveness of the highly selective breeding programs for *A.m.mellifera* and *A.m.carnica* in Switzerland. We quantify the levels of genetic differentiation between breeding stocks and admixture proportions in populations. We show that there still is a high level of differentiation among the different subspecies but admixture could not be prevented completely. We further show that admixture proportions correlate with the occurrence of different subspecies in an area. This shows that the maintenance of secure mating yards is not sufficient in order to preserve the highly endangered subspecies *A.m.mellifera*. Other measures will have to be taken in order to preserve the unique ecotype of *A.m.mellifera* in the Alpine region.

Anne Streiff, Michelle Price & Nicole Galland, U Lausanne

Phylogeny of Grimmia Hedw. (Grimmiaceae, Bryopsida): reproductive strategies influence evolution rates

The mosses are a very old land plant lineage and their long evolutionary history has been accompanied by a trend of morphological character simplifications. This phenomenon has somewhat complicated morphology based phylogenetic reconstructions. This work investigated the phylogenetic relationships among 33 species of *Grimmia* Hedw., a genus with a worldwide distribution, using a combination of plastid (*trnL-trnF* and *rps4*) DNA sequences and of 52 morphological and anatomical characters. The chosen *Grimmia* species represent the majority of those found in Europe and Asia. The combined analysis of the two plastid DNA sequences and morphology using one *Funariidae* species and 10 *Dicranidae* species as outgroup supports the monophyly of the family *Grimmiaceae*. The results also indicate that *Grimmia*, as currently defined in literature, is paraphyletic. Two main clades were present in the tree, one that contained the species traditionally placed in the subgenus “*Rhabdogrimmia*” Limpr. and one that contained the remaining *Grimmia* species. No geographical and/or ecological traits differ in these two clades. A focused analysis, using 113 sequences of *trnL-trnF* and representing the 33 *Grimmia* species, shows a difference in the intraspecific variability of the two clades: “*Rhabdogrimmia*” contains well-defined species groups with little intraspecific variability compared to *Grimmia* s.l. which has higher intraspecific variability and is composed by species groups less defined. This phenomenon is linked with different reproduction strategies: asexual reproduction in “*Rhabdogrimmia*” and sexual reproduction in *Grimmia* s.l. which may imply two different evolution rates.

Ursina Tobler, U Zürich

Mating behaviour in the common toad: Effects of population density

Recent work suggests that population density can determine the impact of sexual selection and sexual conflict, since high population densities can increase encounter rates between individuals of both sexes. High density thus selects for competitive traits in males that enable access to females. I tested experimentally how population density affects reproduction in the common toad, *Bufo bufo*, an explosively breeding anuran, and found that competition level varied with density. Males adopted a mating tactic with respect to population density and males of different tactics experienced unequal mating success. Furthermore, high population density decreased the probability of oviposition in females during the experiment but did not affect reproductive output. These results suggest that population density affects male and female reproductive behaviour in the common toad and that high population densities alter sexual selection.

Urs A. Treier & Heinz Müller-Schärer, U Fribourg

*The geographical distribution of genetic variation in the toxic pasture weed *Veratrum album* in relation to its colonisation history*

Understanding the colonisation history of noxious plants as well as the selection of efficacious control agents rely on knowledge of the weed’s population genetic structure. We quantified the

genetic structure of *Veratrum album* populations along an east-west transect from the Ural and Caucasus mountains to the western distribution border of the species in Portugal, using AFLP marker. We found a highly significant correlation between the genetic and geographic distances between populations ($R^2 = 0.55$). Furthermore, phylogenetic clustering as well as principal coordinate analysis reveals an east-west orientation in the genetic pattern. There was little evidence supporting the importance of expected glacial refugial areas in Europe such as the Balkan-Carpathians and the South-Western Alps. Population differentiation is significant but rather moderate ($F_{ST} = 0.13$) and the pattern of genetic diversity seems to be shaped by different factors. Genetic diversity, population density, and distances from an assumed Asian origin of *V. album* are all significantly correlated. Although pollen records document the presence of *V. album* in Europe already in the late-glacial period, our results show that the genetic structure of today's populations in Europe are mostly influenced by post-glacial re-colonisation of the Continent from more eastern refugia or from the assumed geographic origin in Asia. Recent factors like human impact on landscapes may have additionally contributed to the amount and distribution of genetic diversity observed today.

Gillianne Vergnerie*, Sophie Hoehn* & Markus Fischer, *U Zurich

Effects of Inter-Population Crosses between Fragmented Populations of the Common Lychnis flos-cuculi: first generation

We use the common but declining *Lychnis flos-cuculi* to evaluate the effect of landscape fragmentation on plant populations. From previous studies (Galeuchet, 2003; Perret, 2003) we know that populations vary in quantitative traits and degree of local adaptation. There is a wide range of selectively neutral genetic distances between populations. Here, we present an experiment on consequences of these mechanisms for inter-population crosses. In spring 2003 we crossed 7 plants of each of 13 populations with a plant from: 1/ the same population, 2/ a small population, 3/ a large population, 4/ an ecologically similar population and 5/ an ecologically dissimilar population. Compared with crosses within populations, crosses between populations yielded 26 % more seeds per fruit ($p < 0.001$), which weighed 7 % less ($p < 0.05$), indicating overall hybrid vigour for early fitness measures of the first generation of outcrossing. The type of interpopulation cross did not affect the early fitness measures. From each of the 281 successful crosses, we have grown up to 7 offspring: 3 in a common garden and 4 transplanted to natural populations (1913 plants in total). We measured fitness components and levels of herbivory and pathogen infection in summer 2004. To assess longer-term consequences of mixing gene pools from different populations, we produced F2 and backcrosses (1260 plants in total) in spring 2004. An evaluation of the extent of local adaptation and of the risks of outbreeding depression will provide guidelines to choose seeds and plants from appropriate source population when reinforcing threatened plant populations.

Christoph Vorburger, U Zürich

*Positive genetic correlations among major life-history traits related to ecological success in the aphid *Myzus persicae**

Life-history theory is based on the assumption that evolution is constrained by trade-offs among different traits that contribute to fitness. Such trade-offs should be evident from negative genetic correlations among major life-history traits. However, this expectation is not always met. Here I report the results of a life-table experiment designed to measure the broad-sense heritabilities of life-history traits and their genetic correlations in 19 different clones of the aphid *Myzus persicae* from Victoria, Australia. Most individual traits, as well as fitness calculated as the finite rate of increase from the life-table, exhibited highly significant heritabilities. The pattern of genetic correlations revealed absolutely no evidence for life-history trade-offs. Rather, life-histories were arranged along an axis from 'better' to 'worse'. Clones with shorter development times tended to have larger body sizes, higher fecundities, and larger offspring. Interestingly, the fitness of clones estimated from the life-table in the laboratory tended to be positively associated with their abundance in the field. Fitness also increased significantly with heterozygosity at the seven microsatellite loci that were used to distinguish clones and estimate their frequencies in the field. I

discuss these findings in the light of a recent proposition that positive genetic correlations among life-history traits for which trade-offs are expected can be explained by genetic variation for resource acquisition ability that is maintained in populations by a 'cost of acquisition', and I propose ways to identify the nature of this cost in *M. persicae*.

H. Wandeler, G. Uehlinger & S. Bacher, U Bern

Compatibility of the creeping thistle and its potential control agent Puccinia punctiformis

The creeping thistle *Cirsium arvense* is considered to be one of the worst weeds in ecological compensation areas. One potential biocontrol agent is *Puccinia punctiformis*, a biotrophic rust fungus that induces local lesions and systemic infections. Systemically infected thistle shoots die before flowering. In recent years, our group demonstrated that females of the weevil *Apion onopordi* transmit *P. punctiformis*, resulting in systemic rust infections in the year following weevil infestation. Both organisms benefit from their interaction (mutualism) [1]. In all probability, the success of the rust transfer depends on the compatibility of rust and thistle populations and the virulence of the rust line used. Thus, we conducted an experiment to examine the compatibility and to isolate virulent rust lines, with local lesions infections as a first step. Potted thistles of five different origins were tested against five different rust lines, whereas two rust lines derived from two of the plant populations used. Of each rust line, a suspension containing urediniospores was made and applied to one leaf of each plant. Likewise, one leaf was treated with a control suspension. The results show that plant and pathogen differ in their general susceptibility resp. virulence rather than showing local adaptations. The degree of rust infection was significantly different between different plant origins, whereas the single plant has also a significant effect. The fact that generally virulent rust lines exist, is an important precondition for the use of the rust fungus *P. punctiformis* for biological control of the creeping thistle. Thus, it should be possible to find a rust line that can successfully infect most of the thistle populations. As a next step, we need to verify these results in experiments including the weevil *A. onopordi* as a vector to induce systemic rust infections. References: [1] Friedli J, Bacher S (2001) Mutualistic interaction between a shoot-base boring weevil and a rust fungus, two parasites of the weed creeping thistle. *Oecologia* 129:571-576

Peter Wandeler, Fridolin Zimmermann & Stephan M. Funk, U Zürich

Inferring Dispersal in a Continuous Population of Red Foxes

Studying dispersal is central to our understanding of the ecology and evolution of species on an individual, population and species level. Yet, gaining reliable information on dispersal in natural populations is considered to be difficult. In an attempt to better understand dispersal in red foxes (*Vulpes vulpes*), individual genetic and accurate spatial data of a continuous and local population in the Swiss Alps were combined to obtain indirect estimates of sex-bias, direction and distance of dispersal. A total of 145 tissue samples were genotyped using 16 microsatellite loci. A strong isolation-by-distance pattern (IBD) was revealed by comparing individual pairwise genetic with spatial distances. Dispersal in red foxes was sex-biased and further altered by the topography of the Alpine landscape. The average gene dispersal distance – inferred from the slope of the IBD regression and an estimate of effective population size – was considerably smaller compared to the; demographic estimate from the literature for an equal population density. This study highlights that effective dispersal in red foxes was spatially restricted. The importance of this findings will be discussed in respect of the fate of dispersed individuals and the general applicability of fine-scale genetic studies to infer dispersal pattern.

Poster presentations

Florian Altermatt & Dieter Ebert, U Basel

Local parasites promote host immigration success

Parasites not only influence life histories of individual hosts but have the potential to shape dynamics within and between host populations. In a structured system parasites might be locally adapted and harm sympatric hosts more than allopatric hosts. As migrating hosts can escape from their sympatric parasites, the influence of parasites on host migration is of importance in a metapopulation. In a natural metapopulation of the freshwater crustacean *Daphnia magna* in Southern Finland we have the unique opportunity to study how a microsporidian parasite (*Octosporea bayeri*) interferes with the immigration success of its host. We show experimentally that a) immigrants are more successful when they arrive uninfected and b) that immigration success is higher when the resident population is highly infected. This success could not only be due to an epidemiological process, but also because of the genetic predisposition of the parasites. Therefore we did a reciprocal common garden experiment to measure the influence of locally adapted parasites on the competitive abilities of their hosts. Indeed, we found that host clones had a higher fitness when the competitor's parasite was present compared to the presence of their own parasite. Even more, the presence of the competitor's parasite gave host clones also an advantage compared a situation when no parasite was present. Our results show that local parasites give immigrating host genotypes a competitive advantage and elevate the success of immigrants above the level expected from neutral models. This mechanism promotes gene flow and maintains genetic diversity in local host populations.

Valentin Amrhein & Nathaline Erne, U Basel

Dawn singing reflects yesterday's territorial challenges in the wren

Intrusions of rivals into the territories of male songbirds have been shown to influence reproductive behaviour of females. Here, we investigated whether intrusions could also have long lasting effects on the territorial song of males. To avoid an immediate influence of reproductive behaviour on song output, we examined autumnal dawn singing in the European wren (*Troglodytes troglodytes*). We used song playback to simulate intrusions shortly after dawn and compared male singing behaviour immediately before and one day after the simulated intrusion. According to what is known for many bird species, unchallenged male wrens tended to sing more songs before than after sunrise. One day after an intrusion, however, this pattern was much more pronounced: Males significantly increased their song output before sunrise, but reduced singing after sunrise. This result suggests that dawn singing is important for territory defence. Interestingly, after the intrusion, males varied less in their start of dawn singing, although the average starting time remained the same. If males form an interactive communication network during the dawn chorus, they might synchronise their start of singing to cooperatively defend their territories against intruders. Taken together, our findings indicate that a territorial challenge can influence singing behaviour almost 24 hours after the intrusion.

Susanne Appoloni, R Bunn, C Zabinski & D Redecker, U Basel

Symbioses in extreme environments: Molecular community analysis of; arbuscular mycorrhizal fungi in roots from geothermal soils in; Yellowstone National Park (USA)

Volcanic activity in Yellowstone National Park in the northwestern USA has caused the formation of geysers and thermal springs. In many geothermal sites, soils show an elevated temperature and altered chemistry. In those sites, plant growth is sparse and restricted to a few species, among them the grass *Dichanthelium lanuginosum*, which shows a particular capability to grow under thermal conditions. Recent studies showed that *Dichanthelium* is consistently well-colonized by arbuscular mycorrhizal fungi (R. Bunn & C. Zabinski, 2003, *Western North American Naturalist* 63:406-415). We sampled roots of *D. lanuginosum* and analyzed the fungal community by molecular identification methods. A previously unknown group of Archaeospora was detected, as well as *Paraglomus* and *Glomus*. Further analysis of the community composition will provide important clues whether especially-adapted arbuscular mycorrhizal fungi contribute to the survival of plants in the thermal environments.

M. Bendel, F. Kienast, H. Bugmann & D. Rigling, WSL

Coarse-scale population structure of Armillaria cepistipes, A.borealis, and A.ostoyae in the mountain pine forests of the Swiss National Park

The root-rot-causing fungi *Armillaria* spp. are known to have an important influence on the mountain pine (*Pinus mugo*) forests of the Swiss National Park. The studied area is situated in the Park at an altitude of 1800-2200 m a.s.l. and extends over roughly 1000 ha. *Armillaria* isolates were obtained from 71 mountain pines that were sampled in 42 forest gaps, and from 105 mountain pines that were sampled in the forests between these gaps. All *Armillaria* isolates were collected from symptomatic or recently dead mountain pines. Isolates were grouped into genets by using somatic incompatibility, the self-nonsel self recognition system in basidiomycetes. A random isolate from each genet was determined to the species level using diploid-haploid pairings. In addition to the more saprophytic *A.borealis* and *A.cepistipes*, which have already been known from the study area, the parasitic *A.ostoyae* was detected for the first time in the Swiss National Park. Most genets of *A.borealis* and *A.cepistipes* are restricted to one or a few trees. These small genets are mainly found along the today's and the former route over the Ofen Pass. The parasitic *A.ostoyae* forms the largest genets (max. 400x800 meters). These genets mostly occur at a larger distance from the pass route. The size and spatial distribution of the *Armillaria* genets suggest that past human forest management dating back to the time before the foundation of the Park in 1914 has favoured the establishment of new genets along the pass route.

Benetollo, C. & Guisan, A., U Lausanne

Using predictive models to monitor and estimate population size of an invasive species

Heracleum mantegazzianum is a potentially troublesome exotic plant species, introduced in Switzerland as a garden curiosity at the beginning of the 20th century. It forms a dense canopy out-competing native riparian species and increasing soil erosion along the stream banks where it occurs. It also represents an increasing public health hazard, because of its clear watery sap that sensitizes the skin to ultraviolet radiation. Therefore, predicting where the species is likely to spread in the future can be seen as a matter of prime importance, for: (i) directing monitoring efforts, and (ii) estimating its current population size in an area of interest. Statistical models based on a quantification of species environmental niche projected into geographical space are powerful tools in this regard, as they can serve both aims. Here, we illustrate this by presenting a predictive distribution model for *H. mantegazzianum* based on important environmental predictors and known occurrences of the species at the regional scale in the Prealps of Canton de Vaud. Three predictive methods were compared: Generalized Linear Model, Generalized Additive Model and Ecological Niche Factor Analysis. A random-stratified adaptive sampling design based on a preliminary model allowed the number of individuals in the region to be estimated: (i) based on the method of Thompson (design based estimation) and (ii) by cumulating predicted values obtained by applying the model onto the whole study area (model based estimation). Our results show that the species could be detected in 23 out of 100 of the squares sampled, totalizing 2590 individuals, whereas it could only be observed in X out of 500 plots from an earlier random-stratified sampling design. The species was mainly observed in disturbed habitats, like river banks and forest edges, but also along roads and railways so as in fallows and house garden, as confirmed by the selection of predictors in the models. ENFA was the most parsimonious predictive method, probably due to the fact that it does not need absence data, and these are ambiguous in the case of an invasive species. Based on our sampling and models, the best design-based estimates of the population size of *H. mantegazzianum* in the whole area was 5 million individuals (corresponding to 25% of the total colonisation of the most favourable habitats), whereas model-based estimates provided values within the range of X.X to X.X million. Hence, even the minimal estimate show the urgency to take phyto-sanitary measures of eradication.

Ralph Bergmüller & Michael Taborsky, U Neuchâtel

Strategic niche specialisation in helpers in a cooperative breeder, Neolamprologus pulcher

Behavioural syndromes, i.e. functionally unrelated behavioural traits that correlate across contexts are a challenge to behavioural ecology as evolutionary theory predicts that animals should behave optimally in each single context. Theories to explain behavioural syndromes propose that

behavioural traits that are beneficial in one context (e.g. aggression in a competition context) carry over into other contexts where they can be detrimental (e.g. aggression in the courtship context) and thus seemingly maladaptive. Alternatively, correlated selection on two functionally independent traits, e.g. due to strategic specialisation or alternative niche picking may result in such behavioural syndromes. Field and lab observations suggest that helpers in the cooperatively breeding Lake Tanganyika cichlid *Neolamprologus pulcher* might specialise for one of two types of different strategies: (a) stay and help in the home territory to eventually inherit the breeding position, or (b) disperse early to acquire an own breeding position in another territory. We tested 14 helpers repeatedly for exploration and two types of helping behaviour, i.e. territory defence (aggression against a conspecific intruder) and territory maintenance behaviour (digging). We found that all three behaviours were highly repeatable and thus are consistent traits. Helpers that were faster in exploring a novel environment engaged more in territory defence and helpers that engaged more in territory maintenance behaviour performed less aggressive displays towards intruders. These results demonstrate that all three behaviours are part of one behavioural syndrome and further suggest that helpers may specialise in different strategies with regards to helping and possibly dispersal behaviour.

E. Chapuis, S. Trouvé & J. Goudet, U Lausanne

Molecular vs. quantitative variation between contrasted habitats in a high selfing species: indirect evidence of selection.

In a randomly mating metapopulation, under the assumption of neutrality, the proportion of ADDITIVE genetic variance among populations for quantitative characters (QST) should be the same as that in allelic frequencies (FST). Several studies have tested this relationship, but no clear pattern has emerged, one possible reason for this lack of pattern being the unaccounted effect of dominance and epistasis. In clonal organisms and under the assumption of neutrality, it is the proportion of TOTAL genetic variance among populations for quantitative characters that should be the same as that in allelic frequencies, since the multi-locus genotypes are transmitted intact from one generation to the next. In order to study this relationship, we used the highly selfing freshwater snail *Galba truncatula*. Because of the high selfing rate, we assume that individuals from a family are clones. If the quantitative traits measured are neutral, we expect FST to be equal to QST. If, on the other hand, diversifying selection is acting, we expect QST to be larger than FST. We sampled 17 populations in Western Switzerland, 10 from permanent and 7 from temporary habitats. We genotyped the sampled individuals and measured in a common garden experiment several quantitative traits. We found a total lack of concordance between FST and QST. Among habitats, we found $QST \gg FST$, suggesting a differential action of selection in the two habitats.

Crémieux L., Bischoff A., Steinger T. & Müller-Schärer H., U Fribourg

Consequences of genetic introgression from foreign provenances into local plant populations: implication for biodiversity restoration in agro-ecosystems

Throughout Europe, conservation and restoration of biodiversity in agro-ecosystems has become a priority. In restoration schemes of ex-arable land, seed mixtures of several plant species are commonly sown to create species-rich communities. However, little is known about the effects of the origin of the seed material used on restoration success. Besides the poor adaptation to local site conditions, one risk of introducing foreign populations is genetic introgression into native populations through hybridisation. Indeed, genetic introgression may have a destabilising effect on the genetic integrity of locally adapted populations and thereby reduce population fitness. In this study, the effects of gene flow from foreign provenances into local plant populations are studied in two species commonly included in commercial seed mixtures for extensive grasslands in Switzerland, *Lotus corniculatus* and *Plantago lanceolata*. Two generations of hybrids (F1 and F2) were made between local Swiss plants and plants of English and Czech origin, as well as plants from a contrasting habitat on a local level. The results of a field experiment, comparing the performance of the progeny of crosses between geographically or environmentally distant populations to that of within-population crosses, will be presented. Resistance of the hybrids to insect herbivores and pathogens will also be discussed.

Aline Dépraz & Jacques Hausser, U Lausanne

Postglacial recolonisation of the Alps at a snail's pace, Trichia villosa (Hygromiidae, Gastropoda).

How did species recolonise the empty spaces left by the retreating quaternary glaciers and where did they come from? Such questions have often been addressed using species with moderate to high dispersal abilities. Nevertheless organisms with low vagility (such as land snails) represent good models to investigate evolutionary processes and phylogeography: indeed their populations tend to keep lasting traces of past events. *Trichia villosa* is a pulmonate land snail that has a limited distribution in Europe, centered on Switzerland and can reach rather high altitudes (above 2000m). This suggests a possible survival of the species within the Alps in regions free of ice (mountain tops rising above the ice sheet). Alternative refugia are expected to be located in Germany or in the Rhône valley in France. In order to test whether *Trichia villosa* might have survived in the Alps, 41 localities were sampled extensively throughout Switzerland with two extra localities in France. A hundred and thirty-nine individuals were sequenced for the 16SrRNA gene resulting in 24 different haplotypes. Based on a haploypete network, 2 to 3 major groups emerge with defined geographic distributions roughly splitting Switzerland into the Jura and the western and eastern Alps. An approach combining Nested Clade Analysis and coalescence suggests a mixed history of recolonisation: both refugia within and outside the Alps are involved. Such a combination of recolonisation pattern is likely to be true for many other species.

René Eschen, Urs Schaffner & Heinz Müller-Schärer, CABI Bioscience Switzerland

Carbon addition alters vegetation development on ex-arable fields

Carbon addition is a poorly known technique to reduce plant-available nitrogen in soils. Carbon amendments are thought to enhance soil microbial activity, causing an increase in soil microbial biomass and a simultaneous fixation of soil nitrogen. We investigated the use of carbon addition as a management tool to facilitate the restoration of species-rich grasslands on fields that have been taken out of intensive cultivation under Agri-Environmental schemes.; In 2002, experimental plots were established on two ex-arable fields each in the United Kingdom and Switzerland. Carbon was applied as mixtures of sugar and sawdust and sawdust and wood chips, respectively, and the soil chemistry and microbial community composition was monitored over the following three seasons. In the treated plots, soil nitrate content was reduced after carbon addition, but ammonium was unaffected. The expected increase of microbial biomass was not found. In 2003, there were significant treatment effects on vegetation composition both in the UK and in Switzerland, with a pronounced reduction in cover by dominant grasses and bryophytes. In 2004, the proportion of grass cover remained significantly lower, while legume cover was increased on the treated plots in Switzerland.; Our data suggest that carbon addition is an interesting management tool to influence the course of secondary succession on ex-arable fields. The effect of carbon amendment on vegetation composition was more pronounced on freshly abandoned sites than on four to six years old fallow sites, suggesting that carbon application should start immediately after taking the land out of cultivation.

Guillaume Evanno, Emmanuel Castella & Jérôme Goudet, U Lausanne

Measuring the genetic structure of populations: an approach using neutral and quantitative markers in the freshwater snail Radix balthica

Neutral molecular markers are useful to infer the genetic structure of populations but they do not provide any information on the selective pressures that can lead populations to local adaptation. A way to detect local adaptation is to calculate Q_{st} , a measure of population structure analogous to F_{st} but based on quantitative traits. Q_{st} higher than F_{st} indicates differential selection between populations and the possible occurrence of local adaptation.; We measured Q_{st} and F_{st} in four populations of the hermaphroditic freshwater snail *Radix balthica*. F_{st} was inferred with AFLP markers and Q_{st} with both morphological and life history traits measured on individuals bred in the laboratory for two generations. Depending on the trait considered, Q_{st} was lower or equal to F_{st} . Overall, our results suggest that the populations of *R. balthica* we studied are very structured for neutral markers, but no sign of local adaptation was detected.

Sabine Fink, Laurent Excoffier & Gerald Heckel, U Berne

The effects of local adaptation and historical divergence on mitochondrial gene diversity in the common vole (Microtus arvalis, Rodentia)

Phylogeographical patterns in the common vole (*Microtus arvalis*) were examined by analyzing mitochondrial DNA sequence variation in 1044 base pairs (bp) of the cytochrome b (cytb) gene among 106 individuals from 58 locations. The geographical distribution of four previously recognized cytb lineages in Europe was refined and an additional lineage was detected in southern Germany. Applying a rodent molecular clock for cytb, divergence between the different lineages appears to date to several glaciation periods ago. A combination of the cytb sequences with 322 bp of the control region revealed a similar pattern of 5 lineages, with a more refined geographic resolution. Except for one sample probably lying in a contact zone, all lineages were distributed allopatrically. The translation of 84 cytb DNA sequences produced 33 distinct protein types. At the protein level, the phylogeographical pattern of the DNA haplotypes was not resolved due to a majority of synonymous mutations. In a structural model of cytb, variability at 29 positions was detected, and among these, evolutionarily conserved and functionally important sites were affected. Neutrality tests did not detect overall evidence for positive selection in comparison with *M. agrestis*, but a new phylogeographical test revealed significant deviations from random accumulation of nonsynonymous mutations in tree lineages. This leads to the conclusion that the molecular diversity of cytb in *M. arvalis* is overall the result of the demographic history of the populations, but that there have been several episodes of local adaptation to peculiar environments.

ECOGENICS GmbH, Zürich-Schlieren

ECOGENICS GmbH molecular marker services

Luc DB Gigord & Ann Smithson, U Lausanne

Is rewardlessness an evolutionary stable strategy?

Many orchids have been found to cheat their pollinators by failing to produce any form of nectar or pollen reward in return for visitation. The ecology and evolution of this phenomenon is fascinating, because it allows us to explore the evolution of normally mutualistic pollination systems where this interaction clearly benefits only the plant. It has been argued that cheating should be difficult to evolve because learned pollinator avoidance should always disadvantage female reproductive success. In this talk, we will describe a recent series of experiments designed to quantify the reproductive advantage accruing to cheating orchids when competing with similar plants manipulated to contain a nectar reward. Individual pollinators foraged along a row of orchids, encountering rewarding or cheating plants in a predefined sequence, allowing us to manipulate precisely the frequency of rewarding and cheating plants encountered. From subsequent estimates of male and female reproductive success, we argue that cheating can be an ESS, irrespective of the initial frequency of cheats in a population, and we will explore the conditions under which we predict this ESS will be achieved.

Mailyn Adriana Gonzalez & Luc Gigord, U Lausanne

Adaptive significance of the heterophyllic polymorphism in a native tree of La Réunion Island (Indian Ocean)

Because of their modular architecture, plants can possess organs that have strictly identical functions but totally different morphologies. When this phenomenon involves leaves, one speaks about heterophylly. Heterophylly can show different aspects: one given individual can bear different kinds of leaves simultaneously, or can bear different kinds of leaves sequentially over time (heteroblasty), or, some individuals can bear one type of leaf and other individuals another type (heterophyllic polymorphism). Whatever the type of heterophylly, studies on the adaptive significance of this life trait history are scarce in the literature. We conducted a study in natural populations of a species that show a discrete and bimodal polymorphism for leaf morphology. The goal of this study is to determine which biotic/abiotic factors are involved in this polymorphism

and explain its geographical distribution. Two main hypotheses could explain the maintenance of this polymorphism according to the first one, individuals with largely jagged leaves would show a higher resistance to xerophytic conditions decreasing the likelihood of evapotranspiration compared to individuals with full leaves. According to the second hypothesis, individuals with largely jagged leaves would show a higher resistance to predation compared to individuals with full leaves. So depending on the habitat quality (dry versus wet, presence of predators versus absence of predators), we would expect a morph to be advantaged compared to the other one. We proposed to present preliminary results of the in situ investigation done in March 2004 and about the genetic determinism of this polymorphism, which has been investigated after within- and among-morphs controlled crossings.

Vittoz P, Guisan A, Buttler A & Rebetez M, U Lausanne

PERMANENT.PLOT.CH: a databank for Swiss vegetation permanent plots

PERMANENT.PLOT.CH is a project aiming at (1) setting up a databank of historical and contemporary permanent vegetation plots in Switzerland, (2) setting up new permanent plots in the field to complement existing data, and (3) defining sub-networks of historical and new permanent plots to quantify and document changes in vegetation caused by landuse and climatic changes.

Gusberti M, Smit C & Müller-Schärer H., U Fribourg

Seedling establishment of Picea abies in relation to nurse structures

Studies on grazed ecosystems document spatial associations of tree saplings with unpalatable plants (avoided by cattle) suggesting nursing effects. However, it is not clear whether this association is only an effect of protection from browsing. Increased seed input by seed trapping or enhanced germination under the canopy of structures could also contribute to higher densities of tree saplings near unpalatable plants. Firstly we tested the hypothesis of seed trapping by comparing seed densities of *Picea abies* under the canopy of the shrub *Crataegus monogyna* with that of controls (1.5m away). Secondly we tested for improved germination of *Picea* seeds by *Crataegus*, *Gentiana lutea*, rocks and tree stumps. Thirdly, we analyzed the effects of the main seed predators (birds, mice and insects) on seed predation, germination and establishment, using selective exclosures in two vegetation types. Firstly, we found no evidence of seed trapping. Secondly, the germination rate of the sown seeds was very low (0.14%), mainly due to seed predation (89%). Predation was in general higher under the canopy of the structures as compared to the controls. Thirdly, we found that insects were the principal seed predators (75% predation). Seedlings establishment was higher in open vegetation, possibly due to increased seed(ling) predation in dense vegetation, as the germination rate of the remaining seeds was equal between open and dense vegetation. Seed predation limits tree establishment in pasture woodlands. Seed trapping and enhanced germination could not explain spatial associations between *Picea* saplings and structures, so, protection from grazing seems to be the main process.

Marcel P. Haesler, Simone Immler & Michael Taborsky, U Bern

*Unusual testes morphology and its implications for the reproductive biology of the lekking cichlid *Ophthalmotilapia ventralis* (Cichlidae, Teleostei)*

Ophthalmotilapia ventralis is a mouthbrooding cichlid from Lake Tanganyika, East Africa. Males build small bowers (sand patches on a rock) and form leks. Females are highly polyandrous. They visit many males before, during and after spawning eggs. The behavioural data suggests that females go "sperm-shopping". We studied the histology of male gonads of wild-caught males. The gonads are unusual in three aspects: (1) they contain enormous numbers of Leydig cells producing steroid hormones, (2) they secrete a mucus in which they pack the sperm and (3) they contain a lot of striated muscles in the spermduct. It is also particularly unusual that these special features are not separated into an accessory gland (in contrast to *Gobius niger*, Gobiidae) but are found in the testes themselves. We show that sperm is very longlived (30 minutes) due to the mucus. We further suggest that the Leydig cells produce a pheromone which functions as a male quality signal. The striated muscle in the spermduct indicates that the males can control ejaculate size and

thus economize on their sperm expenditure. The hypothesized pheromone, economizing on sperm and the high longevity of sperm could have important implications for female mate choice (i.e. male quality, females may be sperm limited etc.). We suggest that the occurrence sperm competition is supported by the available behavioural data as well as the histological data. The hypothesis of sperm competition in the buccal cavity of this mouthbrooding cichlid is currently being tested experimentally.

Hautier. Y, Peverelli. S & Guisan. A, U Lausanne

Effect of provenance on plant fitness along an elevation transect

Currently, models predicting the distribution of species in a climatically changed future provide static projections, which is, they do not incorporate rules of biotic interactions explicitly. Including interspecific competition within species' distribution models is thus a highly desirable development. However, this requires quantifying the fundamental niche of species to those climatic parameters most likely to affect their distribution, such as mean annual temperature (MAT). In this context, a competition study was started along an altitudinal gradient in the Swiss Alps, measuring the growth and fitness of *Poa alpina* and *Cynosurus cristatus* in monoculture and competition at 8 experimental sites along an elevation transect ranging from 425 to 2156 m in the PreAlps of Vaud. Individuals of *Poa alpina* were transplanted from one unique altitude while the *Cynosurus cristatus* specimens were grown from seeds, hence different responses of competition can be expected depending on the altitude of provenance of *Poa alpina*. In this study, we complemented this competition experiment by testing the effect of provenance on growth and fitness of *Poa alpina* grown in monoculture (i.e. without competition) by conducting transplantation experiments along the same elevation transect. *Poa alpina* is an alpine plant found between 1200 and 2650 m in the study area. It survived to the transplantation and was even able to produce tillers and flowering tillers until lowland (425 m). Growth of morphological and phenological traits was maximal at elevations between 1400 and 1700 m, which does not correspond to its elevations of maximum occurrence - between 1800-2400 m - in the study area and let suppose that competition prevents abundance of *Poa alpina* at its optimal altitude of growth. Two pattern of senescence (faster senescence for plants of high altitude provenance) let suppose that there are two ecotypes of *Poa alpina* in the studied transect. Hence, results of competition should not be the same according to the altitude of provenance.

M. Held, C. Schnee, T. Koellner, J. Degenhardt & T. Turlings, U Neuchatel

Studying tritrophic interactions by manipulating the release of terpenoid volatiles with molecular techniques

Parasitoids of herbivorous insects make use of odours emitted by herbivore-infested plants in order to locate their hosts. The odours are made up of blends of volatile organic compounds (VOCs) that show many similarities among plant families and can be roughly divided in "green leaf volatiles" (C6 aldehydes, alcohols and derivatives), terpenoids and aromatic substances. Maize (*Zea mays*) reacts strongly to *Spodoptera littoralis* caterpillar feeding. The resulting odour is highly attractive to females of the parasitic wasp *Cotesia marginiventris* but it remains unclear which are the key compounds mediating the attraction. The application of molecular techniques to this system has allowed modification of the pattern of released terpenoids by manipulating genes involved in terpenoid synthesis. In olfactometer assays we tested the attractiveness of maize knockout-mutants with reduced ability to produce specific terpenoid compounds and transgenic *Arabidopsis thaliana* plants expressing maize terpene synthases. The combination of molecular tools, analytical chemistry and behavioural studies provided new insights in the relative importance of terpenoid VOCs for the attraction of parasitoids.

Elze Hesse, Mark Rees & Heinz Müller-Schärer, U Fribourg

*Life-history traits and population dynamics of the perennial herb *Veratrum album* in contrasting habitats.*

Veratrum album can be found in a wide range of mountain habitats such as grasslands, open woodlands and forests. Plants contain steroid alkaloids and are selectively avoided by life-stock

which may lead to problematic infestations in more extensively grazed areas. In general, plant population dynamics depend on the rate of growth, survival and reproduction of individual plants. External environmental inputs such as density of con-specifics and herbivory, can affect these life-history processes. Hence, life-history traits and population growth rate of the same species may vary in different habitats and between years.; Understanding the selective pressures that shape plant life-histories and developing effective approaches to the management of plant populations require a knowledge of the contribution of various components of life-history to population growth under varying environmental conditions. To achieve this we follow the fate of *Veratrum* seeds, seedlings and adult plants in natural populations occurring in three different habitats (i.e. forests, pastures and meadows). Integral projection models will be used to (a) calculate the population growth in these different habitat types (b) quantify the selection forces that shape the evolution of life-history traits that we observe in these different habitats (c) analyze the effect of density-dependence on population growth and life-history traits under varying environmental conditions and (d) to explore the effect of possible management strategies on population growth and persistence of *Veratrum album*.

Sophie Hoehn, Gillianne Vergnerie & Markus Fischer, U Zürich

What are the consequences of longer-term inbreeding for the fitness of plants from a fragmented landscape ?

We used plants from 19 wild populations of the perennial species *Lychnis flos-cuculi* to study effects of longer-term inbreeding on plant fitness. Since 50 years we observed in these populations, located in the North-East of Switzerland, an increase of isolation and a decrease of population size due to landscape fragmentation, resulting from agricultural and demographical development. Small population size and isolation may lead to a decrease of plant fitness through inbreeding depression, which can result from higher inbreeding rate, lower genetic variation and/or lower gene flow between populations. Moreover, Inbreeding depression may have effects over generations, masking fitness effects of Dominance and Epistasis can be ruled out only in later generations and/or population history of drift and inbreeding may have caused purging of deleterious mutations.; In our experiment we performed self- (inbred) and out-crosses (outbred) on plants during three successive generations. We showed the presence of inbreeding depression (ID) on germination and flowering for plants from the first generation (F1) but in few traits this ID was reduced in plants from smaller and more isolated populations. In the second generation, mass and number of seeds are larger on outbred F1 mothers than on inbred ones. And germination rate of F2 seeds is higher for seeds from outcrossed F1 mother. What could happen for the third (F3) generation ? on going analyses...

Itten, Beatriz & Urmi, Edi, U Zürich

*Genetic diversity in European populations of *Sphagnum fimbriatum**

Sphagnum fimbriatum is a rare species in some areas of Central Europe. In Switzerland it is included in the red list of endangered bryophytes. It usually grows in swampy mesotrophic woodland as loose mats or small cushions. The aim of this study is to test the genetic variability within and among populations in order to assess whether: •There is a positive correlation between population size and genetic variability, •The current distribution in Switzerland is a consequence of fragmentation of populations, •The worldwide differences in frequency correlate with differences in genetic diversity. DNA from twenty two populations were amplified with RAPD markers and the data analysed with hierarchical analysis of molecular variance. The genetic distances/similarities between pairs of populations were calculated. The higher partition of the variation found is within populations. That might be due to large effective population sizes, and hence, the weak effect of genetic drift. Key words: Genetic diversity, RAPD, Bryophytes, *Sphagnum fimbriatum*, red list.

Jaccard Hélène, Randin Christophe & Guisan Antoine, U Lausanne

Importance of land use in predictive habitat modelling of plant species in the Swiss PreAlps

Predictive modelling of the geographic distribution of habitat for plants is a growing discipline in ecology. Over the last years, several models were developed for predicting the distribution of

alpine plant species, using climatic and topographical variables. However, a major and recurrent limitations highlighted by these models was the lack of information about land use.; So far, few studies have taken land use into account, although grazing as well as fertilisation effects on plant species richness has been recognised. At a large spatial scale land use or land cover variables do not improve the predictive accuracy of pure bioclimatic variable whereas at a finer scale land use has been shown to be among the important explanatory variables to predict community distribution.; In this study, we assessed how much can land use data improve the fit of predictive models and get better spatial predictions. LU data were gathered by interviews with agricultural inspectors and farmers for each vegetation plot of a vegetation data base sampled according to a random stratified design across the Prealps of Canton de Vaud.; By regressing presence/absence data of 235 species on climatic and topographic variables (GLM stepwise procedures), land use was shown to improve very significantly the models in 29 times. The inclusion of land use in the models led to a significant decrease of the residuals deviance in 47 cases, although not kept by a stepwise selection procedure. The difference in estimated D2 was on average 0.027. The maximal difference was of 0.108.; Although the amount of explained deviance explained by land use is not high, this factor could play a role at other levels of analyses (model evaluation, spatial prediction), but this remain to be assessed. Also, more accurate information, like the intensity of fertilization and the cattle type, might prove to be better land use predictors.

Gwenaël Jacob, Kurt Bollmann & Felix Gugerli, Swiss Federal Research Institute WSL
*Population structure in the capercaillie (*Tetrao urogallus*) in the Swiss Alps and relevance for the conservation of the species*

The capercaillie is a forest-dwelling grouse species with narrow habitat requirement, making it an umbrella species for age-structured coniferous forests. During the last decades, the size and number of suitable forest stands has decreased, leading the species to the brink of local extinction in several regions of the Swiss Alps and Prealps. Conservation measures were initiated and include the monitoring of the species and the characterization of its habitat requirements. In this study, we used molecular methods to estimate the numbers of individuals and to infer the extant and historical relationship among the remaining populations in the Swiss Alps. The aim of the project is to identify units of relevance for the conservation of the species. Sampling was conducted over the distribution range of the species in the Swiss Alps over four years. DNA extractions were processed from faeces and feathers and the samples were genotyped at twelve nuclear microsatellite loci. The population census sizes were estimated from the number of unique genotypes observed in each local population. Genetic differentiation among three geographically isolated regions was tested using a clustering method and an AMOVA. Genetic diversity was similar in the three regions and generally lower in peripheral than in central populations, which indicates a source/sink population structure. Within regions, both sexes dispersed over large distances in the continuous and patchy habitats. Isolated and suboptimal quality patches may be used during migration events. Thus, conservation measures should aim at maintaining or restoring habitat quality and dispersal corridors among regions.

Ton J., Jourdie V., Jakab, G. & Turlings T.C.J., U Neuchâtel
Herbivory-induced volatiles of maize prime neighbouring plants for defense gene expression

Plants protect themselves against herbivore attack using both direct and indirect defense mechanisms. The release of toxins affecting herbivores constitutes a direct plant defense, whereas the attraction of natural enemies of the herbivore with complex mixtures of volatiles is a common form of indirect defense. Recent evidence suggests that these volatiles, which are released in response to herbivory, can also prime neighbouring plants for defense against herbivore attack.; In this study, we explored the molecular basis for the induced defense response of maize plants infested by *Spodoptera* caterpillars and a possible priming of the genes involved. Using a differential hybridization technique, genes were selected that showed induced or repressed expression at two days after infestation by *S. littoralis*. These differentially expressed genes were sequenced and tested for expression upon treatment with wounding, jasmonic acid and *S. littoralis* saliva. Finally, we tested whether volatiles emitted by podoptera-infested plants could prime other

plants for a faster and/or stronger expression of defense genes upon attack by *S. littoralis*. We found evidence for priming with the B73 lipoxygenase, lipase and serine proteinase inhibitor genes.

Nicolas Juillet, Ann Smithon & Luc Gigord, U Lausanne

*Experimental investigation of the effect of corolla colour polymorphism on the fitness of the food-deceptive orchid *Dactylorhiza sambucina**

In contrast to most flowering plants, approximately one third of orchid species are rewardless to their pollinators, i.e. they produce no nectar or other reward. Rewardlessness has fundamental consequences for orchid ecology, because it greatly modifies pollinator behaviour. Pollinator visitation sequences within populations of rewardless orchids are short, because pollinators learn to avoid empty flowers. Thus rewardless orchids produce on average many fewer fruits per plant than related nectariferous species. Many rewardless orchids are rare, and low fruit set can adversely affect population viability if recruitment is limited by seed availability. Some abundant, rewardless orchid species have comparatively high levels of phenotypic diversity within populations, particularly in corolla colour. Pollinators visit rewardless flower colours disassortatively while searching for nectar-bearing flowers. This causes plants with rare flower colours to receive more visits than those with common colours, which can result in a rare-colour fitness advantage through higher fruit production. My experiments with the rewardless orchid *Dactylorhiza sambucina*, which has populations dimorphic for corolla colour (red and yellow), have shown that pollinator preference favouring rare colours drives populations to a stable equilibrium that maintains plants with both corolla colours in populations. However, we do not know whether the presence of corolla colour variability per se within populations of rewardless orchids can increase average population seed set. This would happen if polymorphic populations attract more pollinators, or retain existing pollinators for more visits. We tested this hypothesis using an experimental investigation with the abundant alpine rewardless orchid *Dactylorhiza sambucina*.

Urs Kamm, Felix Gugerli, Rolf Holderegger, Peter Rotach & Peter J Ewards, ETH Zürich

*Landscape genetics of a rare, naturally scattered temperate forest tree (*Sorbus domestica*)*

The goals of this proposed project are to study how landscape structure influences gene flow and dispersal in plants. For this aim, we will investigate (1) life history characteristics, in particular the reproductive system, of a long-lived plant species with a naturally scattered occurrence, and (2) how landscape features may affect the potential of this species to persist. We have chosen to study the rare tree species *Sorbus domestica*. Its distribution in the study area, a heterogeneous landscape in the Canton of Schaffhausen (Switzerland), is well known and all individuals have been mapped. This allows us to precisely and spatially explicitly evaluate gene flow in a real landscape. Controlled pollination experiments (open, selfing, interspecific crossings) will be conducted in a common garden to identify the principal breeding system of the species. To quantify actual levels of gene flow by pollen, we will carry out paternity analyses of naturally pollinated single-mother progenies using nuclear microsatellites (SSRs). This also requires the genotyping of all potential parents with nSSRs and cpSSRs, which, at the same time, allows us to infer historical gene flow by pollen and seed based on the genetic structure of the adult population. Changes in landscape structure may affect pollen and seed dispersal. We will therefore assess the historical and the actual distribution of selected landscape elements within our study area and relate them to the patterns of gene flow detected. These findings should contribute to a better understanding of how landscape structure influences gene flow and, hence, population structure - a key topic of landscape genetics.

Seraina Klopstein & Laurent Excoffier, U Bern

Surfing mutations

Edmonds et al. (2004) reported that mutations occurring at the front wave of a range expansion can eventually be carried by this wave, reaching a much higher frequency and larger spatial distribution than would be expected for mutations arising in stationary populations. We studied this "mutation surfing phenomenon" further, conducting extensive computer simulations on both a simple rectangular grid and on a digital model of Europe. We find that the proximity of the newly

arising mutation to the wave of advance determines largely its success. Other factors influencing the fate of a new mutation are deme size, migration rate and growth rate, the shape of the experimental grid and the time passed since the end of the colonization.; The ability to infer the origin of a mutation that arose during a range expansion from its current distribution, as suggested in the previous study, is shown here to be only possible for mutations that arose in expansions that are younger than 1,000 generations. Furthermore we found that spatial bottlenecks erase the information of the place of origin, which makes such an inference even more difficult under more realistic settings.; The surfing phenomenon is shown in our analysis to often create clines of allele frequency and could thus provide an explanation for clinal patterns observed in Europe. The wide range and high frequency of some genetic diseases could as well be attributed to the surfing phenomenon.

Albert Kölbener, Dieter Ramseier & Matthias Suter, ETH-Zürich

Competition alters response of three wetland species to zinc and nickel

Heavy metal soil pollution is a global problem. Since contaminated industrial effluent and sewage sludge or ashes were often applied as fertiliser in agriculture - and in many countries still are - heavy metals were transferred to plant tissue and thence to men and animals, causing a health hazard. Heavy metals are also a severe health hazard for plants. This study focused on the influence of zinc and nickel on plant growth and on their competitive behaviour. The main question was, whether competitors change the negative effect of heavy metals on the species investigated.; In a greenhouse experiment, the three wetland species *Carex flava*, *Centaurea angustifolia*, and *Salix caprea* were exposed to nickel and zinc. The concentration levels ranged from 0 to 2500 ppm. The three species were planted pair-wise, each species competing with itself or one of the others at each of the three levels of zinc and nickel. Each treatment was replicated four times in blocks.; *C. angustifolia* and *S. caprea* were able to significantly lower soil pH. Both metals had a considerable negative effect on the growth of all three species, whereby nickel impact was stronger than that of zinc. *C. angustifolia* in particular responded sensitively to metal stress, whereas *C. flava* was relatively tolerant.; The competitors *C. angustifolia* and - to some extent - *S. caprea*, were able to alter effects of heavy metals on all three species, demonstrating that competition can modify the effects of heavy metals on plants.

Daniela Pauli, Irene Künzle & Sylvia Martinez, Swiss Biodiversity Forum, SCNAT Bern

Swiss Biodiversity Forum

Macel M., Buchala A. & Müller-Schärer H., U Fribourg

Does plant provenance affect soil microbial communities?

Restoration programs of biodiversity in agro-ecosystems often include sowing seeds of a target community. These seed mixtures can contain non-local seeds. The deliberate introduction of alien plant genotypes may have consequences at various trophic levels within an ecosystem, which may also feed back on plant communities and, thus, influence the success of restoration. Past research in restoration ecology focused mainly on aboveground trophic interactions while interactions between plants and soil organisms have received far less attention. Here we study the effect of plant provenance on the composition of soil microbial communities. We established monocultures of 5 provenances of *Cichorium intybus*. Soil cores were taken from the rhizosphere and the soil surrounding the monocultures. The microbial community composition and biomass were analyzed using phospholipid fatty acids. Results will be discussed in the context of ecosystem functioning.

Mayor R., Aeschimann D., Lambelet C. & Naciri Y., CJB Genève

Population Biology of Aster amellus L.

Aster amellus L. is an infrequent species in Switzerland. The aim of the study is to determine the state of threat of the species for about 30 populations along the Jura, between Haute-Savoie and Aargau (240 Km distance).; Isolation, fragmentation and lack of land-use are the main causes of population decrease (Fischer M., 1996; Hooftman D., 2001; Lienert J., 2002). To test this parameters, we use microsatellites, germination test, in-situ and ex-situ growing.

Doina Muncaciu & Georg Ribi, U Zürich

The abundance of adult Astropecten (Asteroidea) may have decreased in the western Mediterranean: A good reason to look into the nursery

There is a decline in the population densities of three *Astropecten* species at Costa Colostrai, in the south east of Sardinia. A decrease in population of the two starfish species *Astropecten aranciacus* and *A. bispinosus* was followed recently by reduction in the population of the coexisting species, *A. jonstoni*. Newly settled juveniles of *A. jonstoni* occurred in similar densities during the last 6 years. Oddly, the subadults have been especially rare for the past two years. This hints to higher mortality of juveniles compared to previous years. Newly settled marine invertebrates generally suffer a high mortality, if they settle on an unfavourable substrate. Thus the ability to disperse soon after settlement could strongly influence the survival rate of juveniles. To assess the mobility of juvenile *A. jonstoni*, we removed all juveniles from two sample sites and investigated the immigration during the following two weeks. Our results indicate high juvenile mobility and lead to the conclusion that the distribution pattern of young juveniles is more likely a result of active movements rather than a relict of the settlement pattern.

Russell Naisbit, U Neuchâtel

There's no such thing as a free lunch: the cost of defence chemical sequestration in a leaf beetle

Plant defence chemistry often backfires, when insect herbivores take those compounds for their own protection. Among leaf beetles of the genus *Oreina* (Coleoptera: Chrysomelidae) two types of defence are known: synthesis of cardenolides, and sequestration of pyrrolizidine alkaloids (PAs) from host plants in the Asteraceae. Sequestration, by taking advantage of chemicals already produced by the plant, might provide the cheaper strategy. However, there are also likely to be costs associated with uptake, concentration, and avoidance of toxicity. Here we test for a cost of chemical sequestration in larvae of *Oreina elongata*. This species is able to synthesise cardenolides when feeding on *Cirsium spinosissimum*, but can also sequester PAs from its three hosts in the genus *Adenostyles*. We used individuals from six isolated populations, two of which never encounter *Adenostyles*, and hence PAs, in nature. Larvae were reared on *Cirsium*, with the addition of either a methanolic solution of PAs extracted from *A. alliariae* (at natural concentrations), or methanol alone as a control. Pyrrolizidine alkaloids significantly reduced larval growth rate but left development time unaffected, resulting in a 6% reduction in weight at the start of the fourth instar. The effect was fairly consistent across populations, suggesting that the cost has not been overcome in those populations normally exposed to PAs. Sequestration of PAs therefore does not represent a free source of chemical defence.

Parisod Christian & Galland Nicole, U Lausanne

Postglacial phylogeography of the autotetraploid Biscutella laevigata in the Western Alps revealed by chloroplastic markers.

Biscutella laevigata L. (Brassicaceae) is a perennial herbaceous species supposed to have colonized the Alps before the last glacial maximum in a diploid form ($2n = 18$) and to have recolonized this area after the Würm as an autotetraploid ($4n = 36$). Classically, tetraploids were thought to be derived from the *varia* diploid taxon, but a new one (*B. prealpina*) has been described in Italy and questioned as a putative ancestor of the polyploids. Furthermore, diploid populations are here reported on peripheral glacial refugia. The present study points out the putative parents of the Western Alps tetraploids by counting chromosomes of four individuals in 60 populations and analysing their chloroplastic DNA using new ultrapolymorphic markers. Thirty different haplotypes were revealed and analysed by Median-Joining network to get insights into the evolutionary history of this young polyploid complex.; Most of the $2n$ populations show well differentiated, rare but fixed, haplotypes and are thought to be interglacial depauperate relicts. Furthermore, tetraploids display haplotypes belonging to different lineages. The northern and the southern parts of the western Alps are inhabited by different tetraploids lineages. The northern populations share their haplotype with a relictual diploid population in Jaman that is thus interpreted as the putative origin of those tetraploids. The southern tetraploids should be further divided and linked to different

prealpina haplotypes. The central part of the western Alps presents admixed populations from these lineages.; Post-glacial recolonisation of *B. laevigata* is characterised by polytopic autopolyploidy out of refugia and finally admixture of expending lineages.

Michelle J. Price & Anne Streiff, Conserv. et Jardin Botaniques, Geneva

Index Hepaticarum: a useful tool for global liverwort biodiversity ?

The liverworts, with around 5000 species are the second most speciose group of bryophytes after the mosses. Index Hepaticarum, a series of publications that list effectively published liverwort names, was started by C.E.B. Bonner at Conservatoire et Jardin botaniques – Geneva, in the 1950's and continued by P. Geissler and H. Bischler up until 1990. The philosophy behind Index Hepaticarum was to present all published names for liverworts as accurately as possible, citing the authors, publication, protologue information and nomenclatural status for each name. An effort to finish the last of the second editions of Index Hepaticarum (A-Jubula), begun in CJBG in 2003, is now nearing completion. Our project database, to be made available on-line, now contains 30,000 liverwort names representing all those published during the period 1753-1973. Names published after December 1973 to present are collated in Index Hepaticarum, Supplements by Engel and Crosby. The publication of this final part of Index Hepaticarum and the debut of our searchable database will complement the Index supplements so far. Collectively this work will be an enormous resource for the study of hepatics worldwide in various research domains, specifically floristics, taxonomy and systematics, thus contributing to the study of global liverwort biodiversity. The on-line availability of the database will permit access to this resource by national and international researchers. This is especially important for workers in tropical countries and other regions where financial resources can be limited and where biodiversity is often coincidentally high.

Caetano S, Naciri Y & R Spichiger, U Geneva; Conservatoire et jardin botaniques de Genève

*Genetic differentiation of the Pleistocenic Arc tree *Astronium urundeuva* in South America*

The Pleistocenic Arc, which must have originated from climatic shifts in South America during late Pleistocene, is constituted by 3 major nuclei of distribution: the Caatingas nucleus in north-eastern Brazil; the Misiones nucleus that includes Paraguay-Paraná river system in north-eastern Argentina, east Paraguay and south-western Mato Grosso do Sul (Brazil); and the Piedmont nucleus in south-western Bolivia and north-western Argentina. The tree *Astronium urundeuva* (Allemão) Engl. (Anacardiaceae) is an important member of the woody species list that follows part of the Pleistocenic Arc distribution. We report here a study on the population genetics of *A. urundeuva* in two of its distribution centres, the Misiones and the Piedmont nuclei. The genetic variability and structure of 26 populations are investigated using chloroplast sequence data and microsatellite markers. A preliminary survey of the chloroplast polymorphism in 9 loci, revealed a low variability. The identification of a single haplotype (for 7 of these loci) shared by individuals of both nuclei suggests the same source population at the time of colonization. On the other hand, microsatellite data indicate a relevant genetic differentiation between nuclei, which can be explained, at least at some degree, by some gene flow between the populations of these two groups. The results are interpreted in the light of the colonization history of this species.

Sergio Rasmann, Tobias G. Köllner, Joerg Degenhardt, Ivan Hiltbold, Stefan Töpfer, Ulrich Kuhlmann, Jonathan Gershenzon & Ted C. J. Turlings, U Neuchâtel

Recruitment of entomopathogenic nematodes by insect-damaged maize roots

Plants under attack by arthropod herbivores often employ a strategy of indirect defence, emitting volatile compounds from their leaves to attract natural enemies of the herbivores. Herbivore-damaged plant roots may employ a similar strategy by attracting entomopathogenic nematodes. Here we report on the first identification of a belowground indirect defence signal, (E)-b-caryophyllene. This sesquiterpene was found to be released by maize roots following attack by larvae of the beetle *Diabrotica virgifera virgifera*, an important pest of maize that is currently invading Europe. (E)-b-Caryophyllene strongly attracted the nematode *Heterorhabditis megidis* in a belowground olfactometer. Curiously, *Diabrotica* attack does not induce the release of (E)-b-

caryophyllene in most North American maize lines, whereas European lines and the wild maize ancestor, teosinte, readily emit the signal in response to an attack. This difference was consistent with dramatic differences in the attractiveness of representative lines observed in the laboratory. Subsequent field experiments showed a 5-fold higher nematode infection rate on a maize variety that produces the signal as compared to a variety that does not, whereas spiking the soil near the latter variety with authentic (E)-b-caryophyllene resulted in a more than 2-fold reduction in emergence of adult *Diabrotica*. The ability to emit (E)-b-caryophyllene is likely to have been lost during breeding of North American maize lines. Development of new varieties that release the attractant in adequate amounts should help to enhance the efficacy of nematodes as biological control agents against root pest like *Diabrotica*.

I. Hijri, F. Oehl, K. Ineichen, P. Mäder, A. Wiemken & D. Redecker, U Basel

Molecular characterization of arbuscular mycorrhizal fungal species communities in agriculturally-used soils

We studied species communities of arbuscular mycorrhizal fungi (AMF) in agricultural field sites of different management intensities in the "three country corner" area near Basel. All these sites were on Loess soils, including a long-term field experiment, where organic and conventional agricultural practices have been compared side by side since 1978 ("DOK trial"). We used molecular tools, which allow to detect AMF directly within colonized roots. Roots from a maize monoculture with relatively high pesticide and fertilizer input showed low AMF diversity, in agreement with previous reports on agricultural soils. In contrast, a substantially higher diversity of AMF was found throughout the DOK trial, where a seven-year crop rotation is performed under lower levels of inorganic fertilizer input and chemical pest control. In addition to fungi from *Glomus* group A, we regularly found members of the genera *Scutellospora*, *Paraglomus* and *Acaulospora*. A significant seasonal influence was detected for the genus *Acaulospora*. These data show that the diversity of AMF is not necessarily extremely low in arable soils, and that the active community is influenced by management intensity and crop rotation, as well as seasonality.

Dominik Refardt & Dieter Ebert, U Fribourg

Different views on local adaptation of a microsporidium to its invertebrate host

We examined local adaptation of the microsporidium *Ordospora colligata* to its host *Daphnia magna*. We measured performance of several parasite isolates on host clones from four populations in a reciprocal transplant experiment. Performance was measured both as infection intensity in single host clones and as persistence of the parasites in monoclonal host populations over a three months period. We tested for local adaptation using different criteria: 'local vs. foreign' compares the performance of several parasites on the same host, 'home vs. away' compares the performances of one parasite on several hosts. We show that although there is clear evidence for local adaptation, application of the 'home vs. away' criterion leads to wrong conclusions because strong variation in infection intensity between host populations obscures patterns of local adaptation. Our second dataset on parasite persistence shows a correlation with infection intensity. However, this correlation is weak and patterns of local adaptation are less compelling. Possible reasons for this are discussed. Besides providing a cautionary tale on the inference of local adaptation, our data add to studies on local adaptation of other parasites of *Daphnia magna*. Their comparison yields insight into which traits of host and parasite determine local adaptation and on which level (within or between host populations) local adaptation will be expressed.

Thomas Reichlin, Erich Klansek & Klaus Hackländer, U Bern

*Choosey European hares: Diet selection of *Lepus europaeus* in arable land*

Populations of European hares (*Lepus europaeus*) have experienced a dramatic decline across Europe in the last decades. As European hares are assumed to prefer weeds to arable crops and weed abundance was lowered by the intensification of agriculture, modern agriculture has been blamed as a major factor affecting European hare populations. However, it is still questionable whether European hares select weeds at all as previous studies had major methodological faults. We investigated whether the European hare really feeds selectively on different plants in arable

land by comparing availability and use of plants with Chesson's Electivity Index. Food availability and use was dominated by cultural crops (e.g., winter wheat, summer barley, and sugar beet). Diet selection analysis revealed that in autumn and winter European hares predominantly preferred cultivated crops (winter wheat) and food items (tubers of sugar beet and carrot) provided by hunters. In spring and summer, apart from soy only weeds (e.g. clover and corn poppy) were positively selected, especially after harvesting cereal crops. We discuss that it is likely that the decline of European hare populations across Europe was facilitated by the decrease of weed abundance. Wildlife-friendly set-asides in arable land have the potential to reconcile the Common Agricultural Policy (CAP) of the EU with wildlife conservation.

Gregory Röder, U Neuchâtel

*Interactions between a foliar disease (rust) and the herbivorous leaf beetles *Oreina elongata* and *Oreina cacaliae* (Coleoptera: Chrysomelidae) on their alpine host plant *Adenostyles alliariae**

Individually, both pathogenic fungi and herbivorous insects are known to have important effects on plant populations, reducing reproduction and growth and altering the outcome of competitive interactions with other species. On the other hand, plants also form the focus for interactions between plant pathogenic fungi and phytophagous insects. These three-way interactions may be indirect, whereby the insect or fungus alters the host plant, and thus affects its neighbour: for example fungal infection can alter leaf nutrient content, produce changes in host plant quantity or induce resistance against herbivores. This study focused on the indirect effects of a systemic infection of *Adenostyles alliariae* with the rust *Uromyces cacaliae* on the phytophagous leaf beetles *Oreina elongata* and *Oreina cacaliae*, by examining larval and pupal performance, larval and adult food plant preferences and host plant choice. Experiments were carried out in four populations across the Swiss and Italian Alps. Development time until pupation was significantly longer for larvae fed on infected leaves. The weight of last-instar larvae and pupae was lower and larval mortality was higher when larvae had been fed with infected compared to healthy leaves. In a three-choice experiment, adults and larvae of both species preferred leaf discs from healthy plants over those containing the rust, and also over those infected but without marks from *Uromyces*. In the field, adults and larvae showed avoidance of infected host plants. Thus, rust infection could affect the distribution and population dynamics of *Oreina* beetles, for both species avoided infected host plants for adult and larval feeding, and infection negatively affected larval development and survival.

Saner, Philipson & Hector, U Zürich

How do shadehouse grown dipterocarp saplings develop under different light conditions, is there evidence for an ecological trade-off?

There are several hypotheses that try to explain the maintenance of plant diversity in tropical forests. These range from neutral theories (Hubbell & Foster 1986) to various niche-based models.; The gap-size niche-partitioning hypothesis (Denslow 1980) proposes that different species are; competitively superior under the varying light conditions found in different size gaps and under; closed canopies.; We measured the growth of saplings of twenty-two species of dipterocarp grown under different; light conditions in shadehouses. We present analyses of non-destructive measurements that test; for an ecological trade-off in growth rates along the light-gradient.

Benedikt R. Schmidt & Jérôme Pellet, U Zürich

Population size and site occupancy in two anurans

Conservationists need easy tools to assess the short-term extinction risk of populations of threatened species. We asked whether the size of the chorus of calling males predicts site occupancy in the next year; chorus size is a population index that is easy to determine. We also asked whether chorus size is a better predictor of site occupancy than habitat or metapopulation variables. Model selection showed that population size explains site occupancy much better than habitat or metapopulation variables. Not surprisingly, the model selection analysis showed that large populations are likely to persist whereas small populations are likely to go extinct. More

importantly, we quantify the relationship between chorus size (our population index) and site occupancy in the next year. Our analysis shows the populations of both species are likely to persist if the number of callers is greater than twenty. Such a value may be used by conservationists to identify populations at risk. To be on the safe side, one should probably select a chorus size where the lower limit of the confidence interval for the probability of site occupancy is greater than 95%; i.e. a chorus size greater than 50 for *Hyla arborea* and 40 for *Bufo calamita*. The analysis shows that „empty“ sites have a great probability of being colonized in the next year. This implies that these species are organized into metapopulations.

Rouven Z. Schmidt, Hansjoerg P. Kunc, Valentin Amrhein & Marc Naguib, U Bielefeld

*Does prior information gained during vocal interactions influence subsequent contests in male nightingales (*Luscinia megarhynchos*)?*

Previous studies have shown that songbirds memorize different singing strategies of neighbours. However, territorial males should also benefit by memorizing singing strategies of unfamiliar rivals, with whom repeated encounters can be expected. Here, we investigated how male nightingales (*Luscinia megarhynchos*) use auditory information on a stranger several hours later in territory defence. We first simulated rivals by an overlapping or alternating playback treatment during nocturnal song. In a second non-interactive playback on the following morning, we investigated how the males used the prior information on the rivals' aggressiveness in territory defence during simulated intrusions by the same rivals. Remarkably, the prior experience did not lead to differential territorial responses, but led to a singing strategy, in which songs of one category were used more frequently after playback by males of both treatment groups. Moreover, only those males that had received the overlapping playback tended to increase the proportion of this song category stepwise after playback. This presumably non-aggressive singing strategy may serve to obtain more information on the intruder's identity and motivation by stimulating the rival to sing. Our study provides limited evidence that birds recall a stranger's identity and singing strategy after a prolonged period of time.

Tanja Schwander, Sara Helms-Cahan & Laurent Keller, U Lausanne

Genetic caste determination in harvester ants: a social solution to reduce costs imposed by hybridization?

Eusocial groups are characterized by reproductive division of labor between queens and sterile workers that specialize on non-reproductive tasks. Genetic similarity between queens and workers is supposed to be fundamental for reproductive division of labor as workers pass their genes on indirectly by helping to raise close relatives. Two cases of genetically determined caste differentiation have been described in harvester ants of the genus *Pogonomyrmex*. Populations with genetic caste determination are composed of pairs of interbreeding lineages that are genetically highly differentiated. Workers and gynes differ in genomic composition; queens are almost always pure-lineage individuals while workers are invariably F1 inter-lineage hybrids. Genetic caste determination in *Pogonomyrmex* might have evolved to reduce the costs related to hybridization. If inter-lineage hybrids are intrinsically viable but reproductively unfit, colonies which make hybrids into workers rather than queens should achieve higher reproductive success than those expending resources on low-fitness hybrid queens. Here we show that hybrid queens have low reproductive success relative to pure-lineage females during independent colony founding, the most vulnerable period in the life-cycle when the strongest selection on queens occurs. Hybrid queens raised significantly less brood than pure-lineage queens and lost more weight per offspring produced. Low productivity was due to low survival of eggs and not to a reduction in fecundity of hybrid queens. Hybrid queens thus have a lower probability of survival and establishing new colonies. Genetic caste determination in *Pogonomyrmex* may represent a social solution to the evolutionary challenges imposed by hybridization.

Lisa N.S. Shama & Christopher T. Robinson, ETHZ

Sex-specific life history responses to seasonal time constraints in an alpine caddisfly.

Facultative species that occur in permanent and temporary aquatic habitats can be locally adapted to their habitat of origin or exhibit life history plasticity. Temporary stream populations may be selected to respond to environmental cues signalling stream drying, whereas permanent stream populations may not. Sex-specific selection pressures imposed by seasonal time constraints imply that males should prioritize early maturation whereas females optimize body size at maturity. We used a common garden experiment to test whether males and females of a caddisfly (*Allogamus uncatus*, Trichoptera) inhabiting permanent or temporary alpine streams differed in their response to combined changes in photoperiod (ambient/late) and hydroperiod (constant/drying). Caddisflies exhibited life history plasticity, although responses varied by time-constraint cue and sex. Both sexes shortened development time in late photoperiod treatments, but neither sex showed a stronger response when exposed to both time-constraint cues. Protandrous males did not respond to stream drying, whereas female responses differed by source stream and photoperiod. Temporary stream females increased growth rate and size at emergence in the most stressful treatment (late photoperiod/drying). Permanent stream females responded to stream drying with decreased growth rate and size at emergence, and offset mortality by desiccation with lower fecundity. Our results demonstrate that multiple state variables can interact in determining life history responses to seasonal time constraints. This evidence for life history plasticity and not local adaptation suggests that temporary stream populations of *A. uncatus* likely persist via repeated colonization following local population extinction, inferring source-sink metapopulation dynamics.

F. Sinniger, P. Chevaldonné & J. Pawlowski, U Geneva

Phylogeny of the order Zoantharia (Anthozoa, Hexacorallia) based on mitochondrial genes

Zoantharia is the third largest order of Hexacorallia, characterised by two rows of tentacles, one siphonoglyph (sulcus) and a colonial way of life. Current systematics of Zoantharia is based exclusively on morphology and follows the traditional division of the group into the two suborders Brachycnemina and Macrocnemina. Each suborder comprising several poorly defined genera and species. Indeed the criteria used in species identification are not clearly defined, and are usually related to acute histological preparation and statistics on the different types of nematocysts. Those methods are not easily accessible and the efficiency of such characters was not clearly proved yet. To resolve the phylogenetic relationships among Zoantharia, we have analysed the sequences of mitochondrial 16S rRNA and COI genes obtained from more than 24 specimens of zoanths, representing two suborders and eight genera. All examined genera are monophyletic, except Parazoanthus, which; appears as a complex of several independently branching clades and individual sequences. Some groupings, especially among Parazoanthus, can be defined by particular insertion/deletion patterns. All these clades show specificity to a particular type of substrate, such as sponges or hydrozoans. Such substrate specificity is also observed in zoanths living on gorgonians or anthipatharians, such as genus *Savalia* (*Gerardia*). The combination of substrate specificity (for epizoic zoanths) and molecular markers could provide an efficient tool in species identification.

Christian Smit, Charlotte Vandenberghe, Francois Frelechoux & Heinz Müller-Schärer, U Fribourg

Effects of grazing intensity on facilitation

Recent studies show that unpalatable plants can protect tree seedlings against cattle grazing (associational resistance) and, hence, enhance tree establishment in wooded pastures. However, the effects of the degree of grazing on this facilitative process are unknown, but important for successful management of these endangered ecosystems. Conceptual models show that an increase in stress (drought, consumer pressure, physical stress) may shift interactions between plants from competitive to facilitative. Accordingly, we hypothesised to find a positive relationship between stress, incurred by grazing, and facilitation. We tested this hypothesis by transplanting seedlings of four different tree species (*Fagus sylvatica*, *Abies alba*, *Picea abies*, *Acer pseudoplatanoides*) under and next to nurse shrubs (*Rosa rubiginosa*) in enclosures differing in grazing intensities (no, low and high). Preliminary results show facilitation of the tree seedlings by the nurse shrubs at both low and high grazing intensity compared to the cattle free controls.

However, tree seedling survival under nurse shrubs was lower at the high- as compared to the low grazing intensity and nurse shrubs were heavier damaged. This suggests that facilitation does not infinitely increase with stress (grazing intensity) in grazed ecosystems.

Yi Song, Yong-ming Yuan & Philippe Küpfer, U Neuchâtel

Phylogeny of Balsaminaceae: Evidence from chloroplast DNA sequences

Balsaminaceae comprises two genera, *Hydrocera* (one species) and *Impatiens* (~900 species), distributing primarily in the highlands and mountains of the Old World tropics and subtropics area. Sequences of the trnL-F spacer of chloroplast DNA were acquired from 144 species of Balsaminaceae worldwide and 1 species of its closest relatives Marcgraviaceae. Phylogenetic analyses applying Neighbor-joining (NJ) algorithm confirmed the monophyly of the family Balsaminaceae and genus *Impatiens*. The topology of the trnL-F tree is in principle congruent to that of our earlier ITS tree, both implying that extant *Impatiens* species are of Southeast Asian origin, from where dispersals to boreal Eurasia and North America, to central Asia and eastern Europe via the Himalayas, and to India and Africa have occurred. The Madagascan *Impatiens* shows an African origin.

Thomas Spiegelberger, Urs Schaffner & Heinz Müller-Schärer, CABI Bioscience Switzerland

Increasing spatial scale changes predictors for plant species richness and functional groups

Mountain grasslands below the timberline contain some of the most species-rich ecosystems in Central Europe. The combination of topographic heterogeneity, soil chemistry and selected grazing by cattle has created a mosaic of microhabitats on pastures which are characterised by different plant species assemblages. Cessation or intensification of traditional management is likely to alter species composition, but the effects may vary among different spatial scales.; In an ongoing project, we are studying mountain grasslands with different land-use in Switzerland, Italy and France. On all sites, soil characteristics and vegetation relevés were sampled on different spatial scales ranging from 1m² to 1000 m². PCAs and multiple linear regressions revealed that variables which predict best the total species richness or cover of plant functional groups change from small plots (1 m²) to large scales (1000 m²). On the 1-m² plots, species richness is negatively correlated with cover of unpalatable species, indicating species packing as the driving process. At larger scales, no interaction was found between cover of unpalatable plants and species richness. In contrast, soil parameters such as available nitrogen explain a significant amount of variation in both species richness and unpalatable species cover.; These results highlight the need to apply multiple-scale sampling designs to further our understanding of patterns driving species richness and species composition on mountain grasslands.

Chantal Staehli, Marco Moretti & Jean-Daniel Gallandat, U Neuchâtel

*The role of fire in the dynamics of threatened plants in the Swiss Alps: the *Cistus salviifolius* community as a study case*

Fire regime and land use history are two main drivers of landscape dynamics in Southern Switzerland. Land use has dramatically changed since the 1950s and fire has become a major disturbance factor that maintains open habitats with high value for conservation. *Cistus salviifolius* is a Mediterranean shrub plant that depends on fire for germination. In Switzerland this species lives only in Ticino and it is related to the Gryllo-Callunetum community. Our hypothesis is that fire and land use play an important role in the distribution of the *Cistus salviifolius* community.; During the summer of 2004 we investigated 84 sites randomly selected and stratified due to fire frequency. In each site we sampled the vegetation and different factors related to fire regime, forest management, as well as topographical and geographical components. CCA has been used to relate the species composition and abundance to underlying environmental gradients. The significance of the axes was tested with a Monte Carlo permutation test. The variance of the plant species data has been partitioned into environmental factors and geographical (spatial) components.; Environmental variables account for 19.3%, geographical factors for 5.0%, and their interaction for 4.1% of the species variance. The first axis was related to total solar radiation,

number of fires, and time since the last fire; the second axis to clear-cutting, rocky habitat and altitude.; Our study indicates that site conditions and fire are important factors at local scale for maintaining the *Cistus salviifolius* community in the Southern Swiss Alps.

Claude Steck & Matthias Bürgi, ETH Zürich

Hotspots of common and endangered grasshopper species - differentiation and conservation

The increasing rarity of species and the impoverishment of biodiversity in the European cultural landscape are partially caused by habitat loss. Due to the environmental requirements of the different species, hotspots of endangered grasshopper species (‘rarity hotspots’) should mainly be located in relics of either natural or traditional cultural landscapes, while hotspots of common grasshopper species could be situated in areas with a higher productivity. If rarity hotspots can actually be characterized as elements of either natural or traditional cultural landscapes, they could be affected above average by ongoing human induced landscape change. In this study we investigated, by which environmental factors rarity hotspots and hotspots of common species can be differentiated, and how rarity hotspots are affected by landscape change.; The two hotspot-types were differentiated by means of a logistic regression based on several environmental variables. Landscape change in the surroundings of the hotspots was classified by an expert key.; Rarity hotspots are located in areas where landuse intensity is probably relatively low, and they are significantly more affected by landscape change than hotspots of common species. Most of the landscape changes in the surroundings of the rarity hotspots can be classified as landuse-extensification.; We conclude that the conservation of rarity hotspots should be given top priority, because they are highly affected by landscape change. Reintroduction or imitation of traditional landuse practices may be a strategy to maintain and develop biodiversity.

F. Steinebrunner, F. Schiestl & A. Leuchtmann, ETH Zurich

Odour-communication in a symbiotic fungus-fly interaction

Epichloë fungi (Clavicipitaceae, Ascomycota) are widespread endophytes of temperate grasses. They produce a conspicuous fruiting structure (stroma) on aborted flowering stems (choke disease). The fungus is heterothallic and depends on small dipteran flies of the genus *Botanophila* for the spermatia transfer. The *Botanophila* females forage and oviposit on the stroma. It appears that Epichloë fungi and *Botanophila* flies live in a balanced mutualism in which the fungi benefit from the fly as a reliable vector of spermatia for cross-fertilization, while the fly larvae depend on the stroma as food source.; We investigated the odour-communication in the Epichloë-*Botanophila* system.; Odour-bouquets of Epichloë stroma were sampled in the spermatial stage. To determine which substances are potentially detected by the flies, and are thus biologically active, we conducted GC-EAD (gas chromatography with electroantennographic detection) analyses. GC-EAD analyses detected one compound that triggered electroantennographic responses. The compound was identified as Chokol K. To test its potential to attract flies under field conditions we used synthetic Chokol K on glue traps containing an odour emitting bait. The caught flies were identified to the species level by sequencing the cytochrome oxidase gene (COII). Since *Botanophila* flies were successfully caught on traps with baits that emitted odour in concentrations similar to natural stromata, we suggest that this substance is involved in long range attraction of the *Botanophila* vector.

Zuzana Sykorová, Andres Wiemken & Dirk Redecker, U Basel

Host preferences of arbuscular mycorrhizal fungi?

The aims of this study were to characterise the communities of AMF (arbuscular mycorrhizal fungi) in the roots of different plant species from two natural field sites and to determine whether possible differences can be explained by host preference or spatial heterogeneity. Two field sites were analyzed: Landskron (species rich calcareous grassland close to Basel, CH) and Ramosch (species rich meadow in Engadin, CH). In each site, four and nine plant species were sampled, respectively. The roots were analysed by nested PCR, RFLP analysis and sequencing following the protocol by Redecker (2000). Sequences of AMF were analysed phylogenetically in the program PAUP and used to define monophyletic sequence types. The differences between AMF communities

in different root samples were evaluated using canonical correspondence analysis.; Overall, 14 different sequence types were found. The AMF communities in Ramosch and Landskron were significantly different. Neither in the Landskron nor in the Ramosch meadow, spatial variability was significant. Significant differences between AMF colonising different plant species were observed in the Ramosch field site. However, in order to obtain compelling evidence for host preferences in AMF, more detailed and quantitative analyses of a larger number of root samples are needed.

Conny Thiel-Egenter, Rolf Holderegger & Felix Gugerli, Eidg. Forschungsanstalt WSL

INTRABIODIV – Comparing Biodiversity at Three Levels: Habitats, Plant Species and Genes

Biological diversity implies the variation among organisms and the ecological complexes in which they occur. It is mostly species richness that is used as a representative parameter for total biodiversity. However, intraspecific diversity stands for the evolutionary and adaptive potential of each species and accordingly is of prime importance for the preservation of biodiversity. The EU-project INTRABIODIV tests whether intraspecific diversity correlates with species richness and habitat variation, and which environmental parameters best explain the observed diversity in order to identify surrogates for biodiversity. Vascular plants of the Alps and the Carpathians are used as a model system to test this hypothesis. On 400 cells of 25 x 23 km, covering the entire range of the Alps and the Carpathians, we will produce an integrated database containing data on intraspecific polymorphisms in 30 species (amplified fragment length polymorphisms, AFLPs), on geographic distributions of 1000 high-mountain taxa, and on environmental, biophysical variables. These results will provide information relevant for the best conservation strategy in designing networks of nature reserves that preserve most of the total biodiversity. The data on genetic diversity of 30 common and widespread alpine plant species allows us to ask a suite of both broad and specific questions, exemplified as follows: Do functional traits such as life form, breeding system, reproductive mode or altitudinal range influence genetic diversity? Did *Geum reptans* and *G. montanum*, due to their contrasting life history, react differently to the ice ages, with *G. reptans* surviving in situ and *G. montanum* in peripheral areas?

Britta Tschanz, Louis-Félix Bersier & Sven Bacher, U Bern

Host plant exposure causes interference between predators

Although rarely appreciated, predator interference can critically determine the specific form of functional responses, and thus can fundamentally affect the dynamics of predator-prey systems. The mechanisms creating predator interference in the field are, however, poorly understood. One of them can be natural variation in the vulnerability of prey to predators in a heterogeneous environment. The exposure of the host plant may cause such a variation between herbivorous prey individuals. We assessed the importance of host plant exposure for the predation probability of shield beetle larvae by paper wasps, hypothesizing that prey on exposed plants are more likely to be found and eaten by predators.; In three investigation years, we recorded the predation rates on exposed (i.e. free-standing) and hidden (i.e. surrounded by other vegetation) host plants within natural vegetation patches.; Host plant exposure significantly affected predation probability of shield beetles. Larvae on hidden host plants were less likely to be killed by the wasps than larvae on exposed shoots.; To our knowledge, this study is the first to show experimentally, that plant exposure affects the foraging success of insect predators by causing indirect predator interference. Our finding can explain the sigmoid form of the predator-dependent functional response in paper wasps found in a previous study.

Barbara Tschirren & Heinz Richner, U Bern

Resource allocation trade-off between growth and immunity shapes parasite defence

The evolution of optimal functioning and maintenance of the immune system is thought to be driven by the costs arising from the allocation of resources to immune functions rather than to growth and reproduction, and by the benefits arising from higher defence if an infection occurs. In young animals there is a high premium for fast growth and competitiveness, and a parasite-mediated trade-off is thus predicted between the allocation of resources to growth versus immune function. In a field study on nestling great tits, *Parus major*, we manipulated simultaneously the

level of immune defence and ectoparasite pressure and thereby assessed both the costs and benefits for growth. Nestlings supplied with an age-dependent dose of the immunostimulant methionine grew slower over the first half of the nestling period than controls, independent of infection status. However, thereafter nestlings with an experimentally boosted immune system grew at faster rates under parasite pressure compared to unstimulated birds. It suggests that the evolution of optimum host defence is governed by a parasite-mediated allocation trade-off between growth versus immune system functioning.

Vandenberghé C., Freléchéux F., Moravie M-A. & Buttler A., EPFL

Short-term effects of cattle grazing on tree sapling growth of Norway spruce, Silver fir, Sycamore maple and Beech in grasslands

The influence of livestock on the early stages of tree development in grasslands is of main concern in silvopastoral ecosystems. A field experiment at a site in the Swiss Jura Mountains was performed to investigate the effects of cattle on tree sapling growth. Two different sizes of each 4 species (*Picea abies*, *Abies alba*, *Acer pseudoplatanus* and *Fagus sylvatica*) were transplanted into pastures with varying grazing intensity and in exclosures. We found that the likelihood for a tree sapling of being grazed by cattle depends on its size, the height of the surrounded vegetation and grazing intensity. At the end of the experiment only 1% of the large saplings but 25% of the small saplings had escaped grazing. The small saplings were partially protected when surrounded by taller vegetation. No grazing preferences by cattle between tree species were found. The number of grazed saplings and damage tended to be lower under lower stocking densities. Grazing reduced significantly the biomass production and final biomass of all tree saplings. The evergreen tree saplings lost relatively more biomass due to grazing than broad-leaved species which might be due to different life history traits and different behavioural responses of cattle to the saplings' growth forms. In a following field experiment of longer duration the influence of cattle activity and grazing intensity on tree sapling survival will be investigated.

Elisabetta Vannoni & Alan G. McElligott, U Zürich

Acoustic correlates of male quality in fallow deer and their implications for intrasexual competition

Fallow deer bucks invest time and energy in vocalising and fighting in order to gain matings. Studies of other species suggest that the phonic structure of calls may contain information on body size or condition of the vocalising individual. Therefore, the information content of calls could be used by males to assess the current competitive abilities of their rivals. Previous studies showed that fallow bucks have a vocal signature based on the spectral structure of the groans. However, the relationships between the phonic structure and some male characteristics related to the condition of the male have not yet been elucidated. The aim of this research was to investigate the relationship between the phonic structure of groans and other characteristics of males e.g. body size, reproductive success and dominance rank. We showed that as male body size increases, the frequency of the fourth formant and the formant dispersion decrease. Moreover, males with higher mating success produce calls with significant lower fundamental frequency (F0). No significant relationships between acoustic parameters and dominance rank were found. The phonic structure of groans thus potentially provides information that can be used by the males to assess competitors.

Daniel Wegmann, Mathias Currat & Laurent Excoffier, U Bern

Spatial and temporal heterogeneity during range expansions

Recent range expansions have been quite common in many species, including humans. Reasons for these may include population growth after a speciation event and gaining of suitable habitat following ice ages or through recent introductions of invasive species. It has been shown that range expansions lead to patterns of molecular diversity distinct from these of a pure demographic expansion. In these studies, however, the fact that many species do live in heterogeneous environments has been neglected. We present here a model which includes spatial and temporal heterogeneity of the environment and makes therefore a link between ecological parameters and molecular diversity. We show that spatial and temporal heterogeneity indeed shape the patterns of

molecular diversity, including strong bimodal mismatch distributions and higher F_{ST} values. It seems as if populations having small carrying capacities or being highly fragmented are affected most. Further we show that intr; a-deme and inter-deme molecular diversity are affected differently. It is therefore possible to distinguish effects of heterogeneous environments from those of the carrying capacity or the migration rate. This fact may lead to a procedure to estimate the parameters used to simulate spatial and temporal heterogeneity in a Bayesian manner.

Werth S, Csencsics D, Wagner HH & Scheidegger C, U Bern

Dispersal and persistence of the old forest lichen Lobaria pulmonaria in a dynamic landscape

We quantified the dispersal process in the putatively dispersal-limited old forest lichen *Lobaria pulmonaria* in terms of diaspore densities from snow samples. The following hypotheses were tested: 1. Diaspores are dispersed isotropically (i.e. no directionality). 2. Diaspore densities decrease with distance from the source tree. 3. There is no long-distance dispersal of diaspores, haplotypes and alleles amplified from snow samples are therefore identical to those from *L. pulmonaria* on the source tree. To test these hypotheses, we placed snow traps surrounding an isolated source tree in four directions and six distances up to 40 m. The content of the traps was analysed by a *Lobaria*-specific RealTime-PCR assay, allowing for a discrimination between two ITS haplotypes. The only haplotype present on the isolated source tree was found most frequently, its frequency of occurrence in snow traps declining with distance from source tree, a support of the second hypothesis.; The frequency of positive samples was highest along the North and South snow trap transects, indicating that dispersal was anisotropic. Comparatively many snow traps also contained an ITS haplotype not present on the isolated source tree, rejecting hypothesis three. These results indicate that in the study area, *L. pulmonaria* is probably not dispersal-limited at distances up to 300 m, and that long-distance dispersal may not be rare, allowing the persistence of this species in the dynamic pasture – woodland landscape.

Anne Weyand*, Katrin Maurer, Jürg Stöcklin & Markus Fischer, *U Zurich

Adaptation of Poa alpina L. to the Heterogeneous Landscape of the Swiss Alps

The Alpine Meadow Grass *Poa alpina* L. is widespread in subalpine and alpine habitats, where it occurs in natural sites and in agriculturally used land. We asked how land use and altitude affect the occurrence of *P. alpina* in the field and its performance in the common garden. In summer 2002, we searched for *P. alpina* in 216 parcels of land of different land use and altitude (1000-2400 m a s l), in 12 municipalities in the Swiss Alps. *Poa alpina* rather occurred in fertilized and grazed sites and at higher elevations. In May 2003, we set up a common garden experiment at about 1500 m a s l with two plants of each of 615 genotypes, 905 from grassland parcels and 325 from natural sites. To avoid carry-over effects we clipped plants to a standard size at planting. In summer 2003 and 2004, we harvested reproductive and vegetative biomass and noted the mode of reproduction (via seed or vegetative bulbils). The frequency of reproducing plants differed significantly between plants of the 12 municipalities of origin, indicating regional differences. Nearly 90 % of all plants had reproduced by the end of the experiment. 77 % of these reproductive plants from lower altitudes produced seed, and only 45 % of those from higher altitudes, suggesting adaptation in response to the duration of the growing season. The number of reproductive shoots was highest for genotypes from grazed parcels, whereas vegetative biomass and biomass of the final harvest was highest for plants from mown parcels, suggesting adaptation to land use. The genetic differences between plants originating from parcels of different altitude, land use, and region indicate that phenotypic differentiation of *P. alpina* in the field has a genetic component, which is shaped by adaptation to both natural and anthropogenic influences.

Lena Wilfert, Jürgen Gadau & Paul Schmid-Hempel, ETH Zürich

QTLs for male reproductive investment and immune defense – is there a genetic trade-off?

The investment in reproduction and immune defense are two of the most important factors influencing an individual's fitness. Recently, experiments have shown, that there might be a trade-off between these two factors. To elucidate the genetic basis of these fitness-relevant traits, we performed a QTL (Quantitative Trait Locus) analysis based on a mapping population derived from a

field-caught colony of the bumblebee *Bombus terrestris*. As a measure of reproductive investment, we measured the size of the accessory glands, which produce a mating plug that inhibits further matings in the female, as well as the number and length of sperm. We further looked at three of the main mechanisms of insect immune defense, encapsulation, activation of the prophenoloxidase-cascade and the production of antimicrobial peptides. For each of these traits, we discovered at least one minor QTL in this natural population. On-going analysis points towards interactions between phenotypes and genotypes of these traits.

Lea R. Wirth, Andreas Gigon & Hansjörg Dietz, WSL

*How do aspect and altitude affect age and growth of *Erinus alpinus*?*

Plant growth is affected by many environmental factors, with most species showing maximal growth under a specific range of ecological factors. This also holds true for alpine plants, although it has been suggested that the prostrate habit might partly uncouple them from environmental constraints, i.e. resulting in a less pronounced response to environmental variation. To test this hypothesis, *Erinus alpinus*, a prostrate plant, was used as a model species. In a valley of the Säntis region, 70 individuals of *E. alpinus* were randomly selected along rock walls that varied in both aspect (SE to SW) and altitude (1450 to 1900 m a.s.l.). For all individuals, the diameter of the cushion-like plant was measured, and the age and the growth increments (annual rings) of the roots were determined using herb-chronology. Multiple regression indicated that age of *E. alpinus* was independent of aspect, but that plant diameter, the growth quotient (diameter/age) and the variation in annual growth increments decreased significantly from SE- to SW-exposed slopes. Together the results suggest that plants situated in SE-exposed slopes grow more rapidly than those in the SW-exposed slopes. Age and growth ring variation were not related to altitude. Whereas, weak and negative relationships were found between altitude and both plant diameter and the growth quotient. Overall, growth of *E. alpinus* was surprisingly weakly correlated with changes due to altitude (mainly temperature). However, within the altitudinal range surveyed, the species showed clear responses to environmental variations associated with aspect (mainly insolation and humidity).

Wirtz Sabine, Ribl Georg & Steinmann Patrick, U Bern

*Sperm allocation in a polyandrous, sperm limited fish, the Eurasian perch (*Perca fluviatilis* L.)*

Eurasian perch are polyandrous fish with external fertilization. Sperm resources of perch males are limited and therefore sperm allocation tactics are of high interest. In this study, estimations of ejaculate sizes were done using video stills taken from a spawning site in Lake Zurich. A total of 13 different spawnings were observed. The total number of males ejaculating ranged between 1 and 3. The findings of this study indicate that for perch males involved in a spawning act, the main decision is whether to ejaculate or not. This decision may depend on factors such as number of competitors present, quality of the female, amount of sperm resources left or if the spawning event is at the beginning or towards the end of the spawning season. Mean ejaculate size was 3.3ml per male with a minimum of 2.7ml and a maximum of 5.0ml.

Glenn YANNIC, Patrick BASSET & Jacques HAUSSER, U Lausanne

*Study of hybrids zones between species of the *Sorex araneus* group with sex-specific markers*

A complete understanding of gene flow dynamic in hybrid zones demands an extended understanding of the dynamic of the two sex in the reproductive barrier establishment. Various data suggest that both sex don't play the same role in the progression towards complete reproductive isolation between two 'lines', such that they become 'species'; By the analyse of hybrids zones with molecular markers exhibiting different modes of inheritance the question could be answer. An admixture of autosomes, mtDNA and Y markers would indicate no difference in male and female -mediated gene flows, whereas an admixture of autosomes but not sex-linked markers would indicate that all gene exchange between species will be mediated only by one of the two sex.; The shrew's species of the *Sorex araneus* group show a huge variety of chromosomal polymorphism and presents numerous contact or hybrid zones. The extraordinary variety exhibited (from genetic isolation to almost free gene flow) makes this group an ideal model

to study the impact of chromosome mutations on gene flow.; The main objectives of this study are to investigate more intensively mtDNA and Y chromosome variation across hybrids zones. We will assess if the gene flow is equal in the two sexes between the two genetically and karyotypically well-differentiated species, *Sorex antinorii* and *Sorex araneus* Vaud, meeting in the Swiss Alps (Haslital, Bern). We will examine the location of the mtDNA and Y chromosomes clines and compare the extent of introgression of each genetic marker.

2005-02-23/sylvia martinez