

# Biology10

11-12 February 2010

Participating societies:  
zoology, botany, systematics

## Abstract book

### Invited Speakers

**Avraham Levy,**  
The Weizmann Institute of Sciences, Israel

**Gonzalo Giribet,**  
Harvard University, USA.

**Ian Baldwin,**  
Max Planck Institute for Chemical Ecology, Germany

**Nick Colegrave,**  
Keynote Speaker for the Darwin Party  
University of Edinburgh, UK.

**Institute of Biology  
University of Neuchâtel**

Université  
de Neuchâtel

**unine**

**Sponsors** ..... **3**

**Locations** ..... **4**

**Program** ..... **5**

**Abstracts of talks** ..... **8**

**List of posters** ..... **41**

**Abstracts of posters** ..... **44**

**List of participants** ..... **93**



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Akademie der Naturwissenschaften  
Accademia di scienze naturali  
Académie des sciences naturelles



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Zoological  
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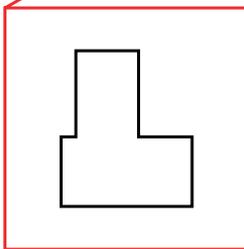
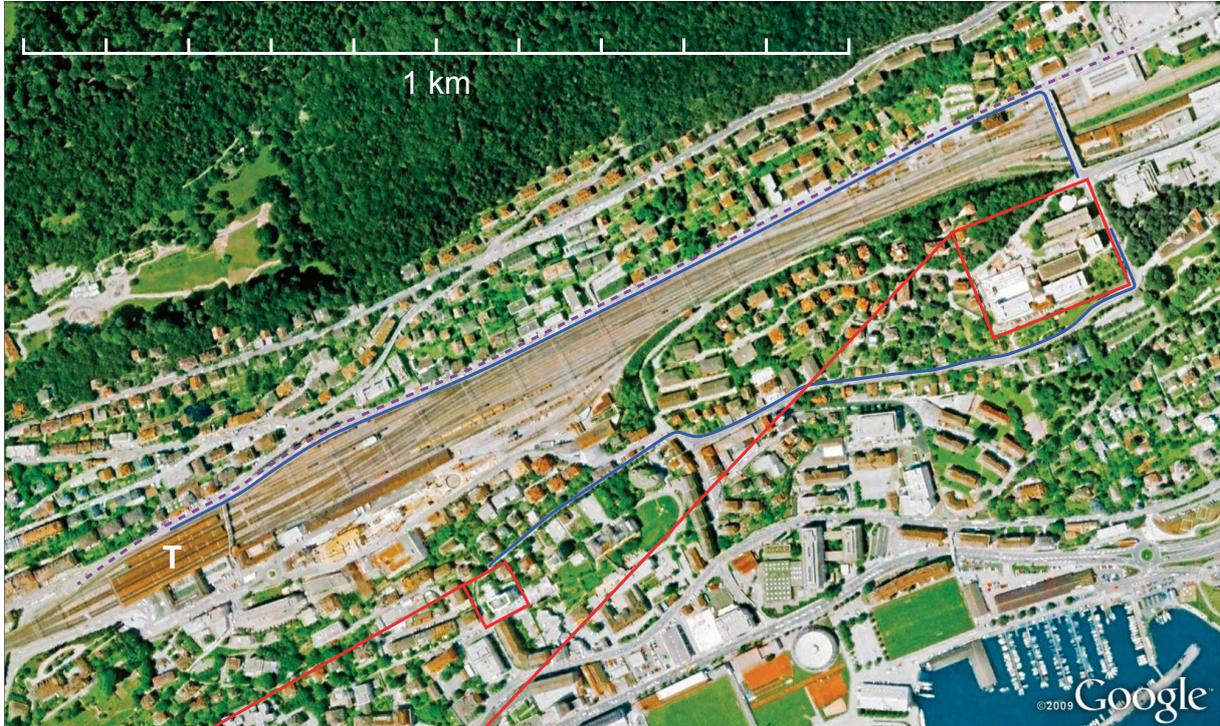
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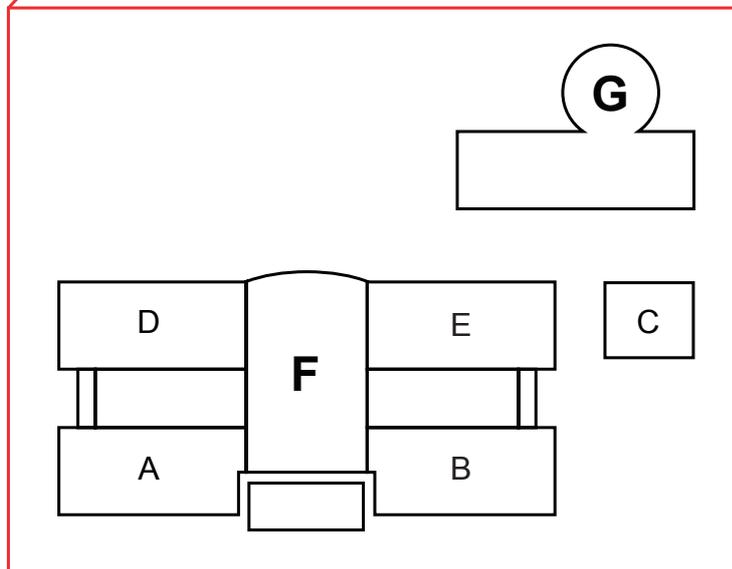
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**Thursday 11 February 2010**

**08:30 registration (UniMail Chemistry building G)**

**09:20 welcome address (UniMail Chemistry building G)**

**09:30 Talks (UniMail Chemistry building G)**

09:30 **Invited speaker - Ian Baldwin**, Hoang Hoa Long, Dorothea G. Sonntag:  
*Eavesdropping on phytohormone signaling as path towards mutualisms: host plant ethylene production and perception structures the culturable root bacterial endophyte community of Nicotiana attenuata*

10:15 **Anne Burkhardt**, Benjamin J. Ridenhour, Lynda F. Delph, Giorgina Bernasconi:  
*The contribution of seed predation to selection on sexually dimorphic traits in a dioecious plant*

10:30 **Michael Coslovsky**, Heinz Richner:  
*Predation risk as a modifier of offspring growth via maternal effects*

**10:45 coffee break (UniMail main building F, first floor)**

**11:15 Talks (UniMail Chemistry building G)**

11:15 **Sarah Kenyon**, Betty Benrey:  
*Hide and seek! The roles of plants and hidden insect hosts in determining the distribution of parasitoids*

11:30 **Romain Libbrecht**, Laurent Keller:  
*Don't forget the King: Males also influence caste allocation and sex ratio in ants*

11:45 **Christophe Lucas**, Laurent Keller, Marla B. Sokolowski:  
*Molecular basis of foraging and defense behaviors in the ant Pheidole pallidula*

12:00 **Miguel dos Santos**, João Rodrigues, Daniel Rankin:  
*Human communication and the scale of competition*

12:15 **Flore Mas**, Mathias Kölliker:  
*Caring or not, the effect of offspring signals on maternal care regulation in the European earwig*

12:30 **Charlène-Aurore Ruppli**, Bettina Almasi, Amélie N. Dreiss, Lukas Jenni, A. Roulin:  
*Corticosterone induces nestlings to switch from vocal signalling to physical competing in the barn owl (Tyto alba)*

**12:45 lunch break (Cité Universitaire)**  
business meeting of the Swiss Systematics Society

**14:15 Talks (UniMail Chemistry building G)**

14:15 **Invited speaker - Avraham A. Levy**:  
*Speciation via hybridization and polyploidization - A molecular view of the opportunities and challenges*

15:00 **Nils Arrigo**, Christian Parisod, Roberto Guadagnuolo, François Felber:  
*Hybridization in the Triticum-Aegilops complex*

15:15 **Natacha Senerchia**, Nils Arrigo, Roberto Guadagnuolo, Christian Parisod, F. Felber:  
*Ecological consequences of introgression of transgenic wheat in a wild relative, Aegilops cylindrica, an open field experiment*

**Thursday 11 February 2010, continued**

**15:30** Posters and coffee break (UniMail main building F, first floor)

**16:30** Talks (UniMail Chemistry building G)

16:30 **Alexandre Antonelli**, Aelys Humphreys, William G. Lee, H. Peter Linder:  
*Ghosts from the past – On plant adaptations to extinct faunas*

16:45 **Blaise Petitpierre**, Christoph Kueffer, Olivier Broennimann, Curt Daehler, A. Guisan:  
*Large-scale test of species niche shifts during biological invasions*

17:00 **Yann Hautier**, Pascal A. Niklaus, Andy Hector:  
*Competition for light as a mechanism of plant biodiversity loss following eutrophication*

17:15 **Anne Kempel**, Thomas Chrobock, Markus Fischer, Mark van Kleunen:  
*Experimental plant introduction: disentangling the roles of propagule pressure, soil disturbance and life-history traits*

**17:30** break

business meeting of the Zoological Society

**18:15** Darwin Party (Cité Universitaire)

18:15 Aperitif

19:00 Dinner and Darwin talk by **Nick Colegrave**:  
*Limits to adaptation: What can microbes in test-tubes tell us?*

**Friday 12 February 2010**

**08:30** registration (UniMail Chemistry building G)

**09:15** Talks (UniMail Chemistry building G)

09:15 **Invited speaker - Gonzalo Giribet**:  
*An integrative approach to the study of metazoan systematics: Assembling the tree*

10:00 **Patrik Mráz**, Barbora Šingliarová:  
*Biosystematic study of the diploid-polyploid *Pilosella alpicola* (Asteraceae) complex with variable breeding systems: patterns and processes*

10:15 **Kay Lucek**, Etienne Bezault, Denis Roy, Arjun Sivasundar, Ole Seehausen:  
*The phylogeography of a successful invasion: Three-spined sticklebacks in Switzerland*

10:30 **Eveline Kindler**, Raphaël Arlettaz, Gerald Heckel:  
*To be or not to be a species: historical separation and contemporary gene flow in the grasshopper *Oedaleus decorus**

10:45 **Benjamin M. Peter**, Laurent Excoffier:  
*Distinguishing between population bottleneck and population subdivision using a Bayesian model choice procedure*

11:00 **Tamara Hofer**:  
*Islands of natural selection in the human genome*

**11:15** coffee break (UniMail main building F, first floor)

**Friday 12 February 2010, continued****11:45 Talks (UniMail Chemistry building G)**

- 11:45 **Andreas Gschwind**, Gerald Heckel:  
*Mating of common voles versus the monogamy gene avpr1a*
- 12:00 **Mélissa Lemoine**, Blandine Doligez, Heinz Richner:  
*Host-parasite interactions between a generalist parasite and its main and alternative hosts: a cross-species infestation experiment*
- 12:15 **Godefroy Devevey**, Luciana Richer, R. S. Ostfeld, M. J. C. Gomes-Solecki, D. R. Brisson:  
*Experimental test of a reservoir-targeting vaccine in order to reduce the tick infection prevalence by the Lyme disease agent*
- 12:30 **Pepijn Luijckx**, Harris Feinberg, David Duneau, Dieter Ebert:  
*Resistance of Daphnia magna to a bacterial pathogen is based on few loci with strong epistasis*

**12:45 lunch break (Cité Universitaire)****14:15 Talks (UniMail Chemistry building G)**

- 14:15 **Sorcha E. Mc Ginty**, Daniel J. Rankin, Sam P. Brown:  
*Horizontal gene transfer and the evolution of bacterial cooperation*
- 14:30 **Valentina Rossetti**, Manuela Filippini, Miroslav Svercel, Homayoun C. Bagheri:  
*Life history traits can produce a length cycle in multicellular filamentous bacteria*
- 14:45 **Martin A. Schäfer**, David Berger, Stephanie S. Bauerfeind, Wolf U. Blanckenhorn:  
*Latitudinal variation and temperature-dependent plasticity of a polymorphic sperm storage organ*

**15:00 Posters and coffee break (UniMail main building F, first floor)****16:00 Talks (UniMail Chemistry building G)**

- 16:00 **Sébastien Nusslé**, Christophe Bornand, Patrick Presi, Tadeusz Kawecki, C. Wedekind:  
*Past and future fishery-induced evolution on growth in an Alpine whitefish*
- 16:15 **Dik Heg**, Susan Rothenberger, Roger Schürch:  
*Habitat saturation, benefits of philopatry, relatedness and cooperative breeding in a cichlid*
- 16:30 **Peter H. W. Biedermann**, Michael Taborsky:  
*Direct and indirect fitness benefits of philopatry and cooperative care in Xyleborina (Curculionidae: Scolytinae)*

**16:45 Award ceremony and end of conference**

## Invited speaker

**Eavesdropping on phytohormone signaling as path towards mutualisms: host plant ethylene production and perception structures the culturable root bacterial endophyte community of *Nicotiana attenuata***

Hoang Hoa Long, Dorothea G. Sonntag, Ian T. Baldwin

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Ethylene (ET) is an important phytohormone that regulates plant-pathogenic microbe interactions, but little is known about how ET influences a plant's ability to recruit bacterial endophyte communities from the rhizosphere, particularly in native plants growing in native soils. The use of plants that are "deaf" and "mute" in either phytohormone production or perception have proved useful in dissecting complicated ecological interactions, such as in between-plant signaling (1) and here we assess ET's role in the recruitment of culturable endophytic bacteria from native soils with a similar experimental strategy. We grew wild type-WT *Nicotiana attenuata* plants and isogenic transformed plants deficient in ET biosynthesis-(*ir-aco1*) or perception-(*35S-etr1*) in four native soils and quantified the extent of culturable bacterial endophyte colonization (by plate counting) and diversity (by amplified rDNA restriction analysis and 16S rDNA sequencing). The endophyte community composition was influenced by soil type and ET signaling. Plants grown in organic-(vs. mineral) soils harbored a more diverse community and plants impaired in ET homeostasis harbored a less diverse community compared to WT plants. WT and ET-signaling-impaired plants fostered distinct bacteria in addition to common ones. *In vitro* re-colonization by common and genotype-specific isolates demonstrated the specificity of some associations and the susceptibility of *35S-etr1* seedlings to all tested bacterial isolates, suggesting an active process of colonization driven by plant-and microbe-specific genes (2). We propose that soil composition and ET homeostasis play central roles in structuring the bacterial endophyte community in *N. attenuata* roots and we discuss these results in a functional context of how endophytes might be recruited to increase a plant's fitness under particular environments (3).

## References:

1. Baldwin, I. T., R. Halitschke, A. Paschold, C. C. von Dahl, and C. A. Preston. 2006. Volatile signaling in plant-plant interactions: "talking trees" in the genomic era. **Science** 311: 812–815
2. Hoang, L. H., D. Sonntag, D. D. Schmidt, and I. T. Baldwin. 2009. The structure of the culturable root bacterial endophyte 1 community of *Nicotiana attenuata* grown in native soils is organized by host plant ethylene production and perception. **New Phytologist** (in press)
3. Hoang, H. L., D. D. Schmidt, and I. T. Baldwin. 2008. Native bacterial endophytes promote host growth in a species-specific manner; phytohormone manipulations do not result in common growth responses. **PlosOne** 3 (7): e2702.

## The contribution of seed predation to selection on sexually dimorphic traits in a dioecious plant

Anne Burkhardt, Benjamin J. Ridenhour, Lynda F. Delph, Giorgina Bernasconi

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In dioecious plants, pollinator-mediated selection can favour the evolution of sexually dimorphic traits. We explore the role of a pollinating seed predator as selective agent on dimorphic traits. We used *Silene latifolia* selection lines varying for dimorphic traits (flower number and size) and exposed them in a common garden to the specialist moth *Hadena bicruris*. We expected Small-Flowered plants (SF) to suffer from higher predation rate than Large-Flowered plants (LF), and that interaction with the moth would favour plants with few, large flowers as a pre-oviposition « defence ». We found positive total selection but no significant moth selection on flower number. Selection lines did not differ significantly in predation rate, but SF plants reared significantly more larvae, tended to have a larger parasite load, and lost more fruits as a consequence of predation and abortion than LF plants. Overall abortion was selected against, and moths contributed to the selection against abortion in SF but not in LF plants. Abortion was significantly more common in plants with a high parasite load. Thus the observed difference between selection lines was more indirect than expected and was mediated by differential effects of selection against fruit abortion (i.e., by a post-oviposition response) presumably resulting from differences in fruit-abortion costs. These results suggest that the fitness of female *S. latifolia* may be maximized by producing fewer flowers that decrease the cost of rearing parasite larvae. Because male siring success may increase with flower number, this may have contributed to evolution of sexual dimorphism.

## Predation risk as a modifier of offspring growth via maternal effects

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Breeding animals are locally confined and hence especially sensitive to predation risk. Higher predation risk increases the level of circulating stress hormones in mothers, which can lead to higher levels also in the eggs. Stress hormones during embryogenesis affect growth and development. Here we test for this maternal effect via manipulation of perceived predation risk by presenting great tits during ovulation with stuffed models of birds of prey (sparrowhawk) or of controls (song thrush). The offspring of mothers under the experimental manipulation were then raised by foster parents subjected to no treatment. Nestlings of mothers under increased predator density were smaller than those of control mothers and showed higher growth rates of the wings. Hen-fleas feeding on nestlings of mothers under increased predator density survived longer and had lower mortality than those feeding on control nestlings. While the maternal-effect stress hormones may be a passive consequence of higher circulating stress hormone levels in mothers, it may alternatively represent an adaptive response since lower weight and bigger wings are a selective advantage for predator evasion. We show for the first time that the predation risk in the environment may elicit maternal effects in birds.

## Hide and seek! The roles of plants and hidden insect hosts in determining the distribution of parasitoids

Sarah Kenyon, Betty Benrey

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In Mexico, wild bean seeds of the genus *Phaseolus* are attacked by bruchid beetles and these beetles are attacked by three species of *Horismenus* parasitoids. The objectives of this study are to 1) determine the abiotic and biotic factors that are associated with the temporal and spatial distribution of insects in this tritrophic system and 2) to determine how genetic diversity varies between related parasitoid species sharing a common resource. Additionally we hope to identify the factors responsible for these differences. Emerging *H. depressus*, *H. missouriensis*, and *H. butcheri* wasps were collected every 2-4 days from infested beans in 10 populations over a period of two years. Nuclear (28SD2 and ITS2) and mitochondrial (cytB) regions were amplified from representative individuals for phylogenetic analyses and all extracted individuals were screened for infection by *Wolbachia* and *Cardinium*. Individuals morphologically identified as *H. butcheri* exhibited far greater genetic polymorphism than either *H. depressus* or *H. missouriensis* and clustered into three groups. In contrast, *H. depressus* and *H. missouriensis* each had limited variability these gene regions. While infection by *Wolbachia* may explain lower levels of variation in mitochondrial markers in *H. missouriensis* (where it was present though not fixed), that of *H. depressus* may be due to other factors. The greater genetic diversity found in *H. butcheri* argues for increased genetic drift, either due to decreased dispersal ability between populations (perhaps due to a more limited altitudinal range), and/or an earlier establishment.

**Don't forget the King: Males also influence caste allocation and sex ratio in ants**

Romain Libbrecht, Laurent Keller

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Individuals in animal societies may differ in their reproductive output. In social insects, differences in reproductive success between queens may also stem from differences in their relative contribution to the three castes (new queens, males and workers). Such a partitioning of reproduction occurs between queens in colonies of the Argentine ant *Linepithema humile*. We conducted controlled crossings and established colonies headed by a single queen to investigate the genetic factors underlying these differences. The biomass produced was only influenced by the genetic background of queens. By contrast the caste fate of the female offspring was only affected by the genome of the male the queen mated with. Finally, the sex ratio was influenced both by the maternal and paternal genomes with a significant interaction between the parental genomes. The finding of complex interactions between the genomes of parents on sex allocation has important implications for life-history evolution and conflict resolution in social insects.

**Molecular basis of foraging and defense behaviors in the ant *Pheidole pallidula***

**Christophe Lucas**, Laurent Keller, Marla B. Sokolowski

*Department of Ecology and Evolution, University of Lausanne*

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Social insects are spectacular examples of behavioral adaptations with sterile sisters performing specialized work in the colony. However, little is known about the molecular basis of their behavioral specialization and flexibility. The ant *Pheidole pallidula* has two sub-castes of workers, majors and minors, which are specialized in defense and foraging respectively. However, majors are able to help minors in foraging activities depending on the needs of the colony. Thus, there is plasticity in the subcaste behavioral repertoires. Here we investigate the molecular underpinnings of subcaste specialization and plasticity in foraging and defense by studying the foraging (for) gene. The behavioral effects of for which encodes a cGMP dependent protein kinase (PKG) were first described in *Drosophila melanogaster*, where for allelic variation affects foraging behaviors (Osborne et al. 1997). In *Apis mellifera*, for expression is different between foragers and nurses (Ben-Shahar et al. 2002). Here we show that for is involved in behavioral flexibility and specialization of *P. pallidula*'s sub-caste. Specifically, majors have higher PKG enzyme activities than minors, their PKG activities are lower in the presence of a foraging stimulus and higher in the presence of an alien intruder. Furthermore, pharmacological activation of PKG decreases foraging and increases defense behaviors. Finally, both the number and localization of neuron clusters in which FOR-PKG is expressed differ between the brains of majors and minors. Together these results suggest that the foraging gene modulates responses to task-related stimuli in the ant colony.

## Human communication and the scale of competition

Miguel dos Santos, João Rodrigues, Daniel Rankin

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The evolution of communication is tightly linked with the evolution of cooperation as it requires that individuals cooperate by signaling reliable information, and by perpetuating received signals. Previous experiments on the evolution of communication in humans usually tested whether communication can arise when individuals have common interests. However, it is predicted that whether individuals have conflicting or common interests (i.e. when the scale of competition changes) can hinder or foster the emergence of communication systems. Here, we tested whether changing the scale of competition (i.e. global or local) had an influence on the emergence of communication. In groups of three, students could learn to acquire a resource through a learning task in a computer game. They could then decide to transmit a signal (a colour) to one of their group member, who then played the same learning task. We varied the scale of competition (either global or local) and the cost of transmitting a signal (either costly or non-costly). We found that when competition was global, players signaled more often and associated a signal with the correct resource, thus developing a communication system. Groups with a better communication system finished with higher payoffs. However, under local competition, fewer signals were sent and no communication system developed. Our results demonstrate that communication involves both a coordination and a cooperative dilemma, and is thus likely to arise under group structure.

## Caring or not, the effect of offspring signals on maternal care regulation in the European earwig

Flore Mas, Mathias Kölliker

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Interactions between mothers and newly hatched offspring set the stage for potential conflict of interests over maternal investment between and within broods. Models of parent-offspring conflict resolution predicted the evolution of offspring signals that regulate the amount and/or duration of parental investment. In our studying species, the European earwig *Forficula auricularia*, mothers display maternal care behaviours toward their nymphs and provide food through trophallaxis. In a first experiment, we demonstrated that earwig offspring produce condition-dependent chemical signals that influence maternal food provisioning. Mothers exposed to chemical extract from high-fed brood (HFB) foraged and later provisioned significantly more food to their brood compared with extract from low-fed brood (LFB). This first result suggests that earwig mothers prefer providing food to offspring of higher reproductive value and thus may select for an offspring chemical signal of quality. In a second experiment, mothers isolated from their brood were continuously exposed to chemical extract from HFB, LFB or a solvent Control. We found that mothers exposed to HFB groomed significantly more than mothers exposed to LFB, which in turn displayed significantly more aggressive behaviours. When we investigated the within brood maternal food distribution, we found an opposite effect of offspring condition, where individuals of low nutritional state received significantly more food than individual of high nutritional state. In the light of these results, we propose a schematic model of maternal care regulation in the European earwig integrating the between-brood effect of offspring chemical signals and the within-brood outcome of offspring competition/cooperation.

## **Corticosterone induces nestlings to switch from vocal signalling to physical competing in the barn owl (*Tyto alba*)**

**Charlène-Aurore Ruppli**, Bettina Almasi, Amélie N. Dreiss, Lukas Jenni, Alexandre Roulin

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In altricial birds, nestlings are in competition for the food brought back by parents. Brood mates are known to resolve conflicts over food share by vocally signalling their level of need and physically jostling for the position in the nest where parents deliver food. However, the way nestlings adjust these behaviours to their own and to their siblings' body condition remains poorly documented. Here, we tested whether body condition, reflecting chicks' level of need and resource holding potential, affected physical and vocal behavioural strategies to obtain food in barn owl nestlings during parent-offspring and sib-sib interactions. In 34 experimental two-chick broods, we manipulated the relative difference in condition between sibs by implanting one of them with corticosterone (CORT) and the other with placebo (PLAC). After the stress response, we video-recorded chicks' call rate and relative positioning both before and during the first feeding event of the night. The CORT treatment did not affect the probability of prey monopolization. However, when they obtained food, PLAC had mainly vocally signalled their motivation to their sib whereas CORT relied mostly on physical competing for the best nest location both before and during the parent's arrival. Corticosterone might then be an important mediator of the trade-off between vocal signalling and physical competing in nestlings. This also raises the question of the evolution of sib-sib communication across different broods and environments.

**Invited speaker****Speciation via hybridization and polyploidization - A molecular view of the opportunities and challenges****Avraham A. Levy***Department of Plant Sciences, Weizmann Institute of Science, Rehovot, Israel**avi.levy@weizmann.ac.il*

Hybridization and polyploidization play an important role in the formation of new species, particularly in plants. Genome merging, in interspecific hybrids and allopolyploids, is associated with novel patterns of gene expression. We have analyzed the genetic and epigenetic basis for this rewiring in two model systems, namely a yeast hybrid between *Saccharomyces cerevisiae* and *S. paradoxus*, and a synthetic wheat hybrid and allopolyploid analogous to bread wheat. In yeast, we have analyzed how hybrid-specific gene expression patterns are generated from the divergence in regulatory components between the parental species. We have distinguished changes in regulatory sequences of the gene itself (cis) from changes in upstream factors (trans). Expression divergence was mostly due to changes in cis. Changes in trans were condition-specific and reflected mostly differences in environmental sensing. In the hybrid, over-dominance in gene expression occurred through novel cis-trans interactions or, more often, through modified trans regulation associated with environmental sensing. In wheat, we also expect gene expression rewiring as a result of new genetic interactions, however, another level of complexity exists through epigenetic regulation. We have investigated the role of small RNAs in the genetic and epigenetic changes that were reported in wheat hybrids and polyploids. We performed a high-throughput screen of small RNAs expression in parental tetraploid *Triticum turgidum durum* and diploid *Aegilops tauschii* species, in their synthetic triploid hybrid and their derived hexaploid, using the Illumina Genome Analyzer. We then compared the average number of hits corresponding to a given RNA, between the two parental libraries (the mid parent value (MPV)) to the number of hits in the hybrid or the polyploid. Micro RNAs represented 30-45% of the total hits, depending on the library. On average, micro RNAs expression in the hybrid and in the polyploid was similar to the mid-parent value, with a few exceptions. Conversely, small RNAs that match repeats and transposons are about 6.5-fold down regulated in the polyploid compared to the mid-parent value. This major decrease is consistent with the previously described transcriptional activation of the Wis2-1 retroelements in the first generation following polyploid formation. It is also consistent with CpG hypomethylation in the LTRs of the Veju1 retrotransposon observed in the polyploid compared to the parents, as shown by bisulfite sequencing. These data support the role of siRNAs as mediators of epigenetic changes that occur upon polyploidization, and in particular, in the activation of transposons.

## Hybridization in the *Triticum-Aegilops* complex

Nils Arrigo, Christian Parisod, Roberto Guadagnuolo, François Felber

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The domestication of wheat (*Triticum* sp.), one of the major crop presently cultivated, results from allo-polyploidization events involving several *Aegilops* species. The reproductive isolation between both genera is incomplete: *Aegilops* species are traditionally used in wheat breeding and intergeneric hybrids are regularly reported along wheat cultivations. Despite these observations, natural genetic introgressions involving wheat and *Aegilops* are poorly documented. This topic is however of great concern for risk assessment studies associated to the potential release of transgenic wheat.

The present study investigates three European *Aegilops* species (*Ae. geniculata*, *Ae. neglecta* and *Ae. triuncialis*) and surveys natural Mediterranean populations. Samples collected along wheat field borders are compared to samples originating in areas isolated from agriculture. AFLP genotyping and sequencing of TE insertion sites are used to assess the presence of wheat genetic markers in *Aegilops* populations.

Various levels of introgression are revealed: *Ae. geniculata*, the most autogamous species, shows no clear evidence of gene flow from wheat, except for one *Ae. geniculata* x *Triticum* F1 hybrid discovered in a Spanish population. In contrast, numerous wheat genetic markers are observed in *Ae. neglecta* and *Ae. triuncialis*. Most introgressed samples originate from populations collected near to crop cultivations. In contrast, agriculture-isolated populations show little evidences of gene flow from wheat. Finally, *Triticum turgidum* (the pasta wheat) appears as the most likely wheat parent of introgressed *Aegilops*. Our study thus suggests that the release of commercial transgenic wheat in southern Europe should consider the possible introgression of transgenes within wild *Aegilops* populations.

## Ecological consequences of introgression of transgenic wheat in a wild relative, *Aegilops cylindrica*, an open field experiment

Natacha Senerchia, Nils Arrigo, Roberto Guadagnuolo, Christian Parisod, François Felber

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Cultivated plants derive from wild species through domestication, involving cross-pollination artificial selection and recently genetic engineering (Genetically Modified Organism, GMO). When cultivated plants grow in contact with their wild relatives, they can potentially exchange genes. Such gene flow from GMOs may be crucial for biodiversity, as it could offer important advantages to wild species (including increased weediness) or it may lead to the extinction of rare taxa by competition. In particular, gene flow has been documented investigating wheat, a worldwide-cultivated crop, and *Aegilops cylindrica*, a European wild relative.

Our study estimates the establishment potential of hybrids between *Ae. cylindrica* and GMO wheat, by estimating fitness of F1 hybrids in an open field experiment. Survival and reproductive potential of hybrids with wild type wheat and GMO wheat was measured and compared with parental species as well as between hybrids. Hybrids showed significantly lower survival and reproductive potential than the parental species, indicating that hybridization is costly. Hybrids should thus generally be eliminated by natural selection under our conditions. Although the different types of hybrids show similar fitness at the beginning and at the end of our experiment, hybrids with GMO wheat grow more slowly, suggesting that genetic transformation is further costly. Some hybrids presented much higher fitness values than others, even higher than wild *Ae. cylindrica*. Although the minority, these individuals may establish in natural populations. Consequently, depending on the fitness and the fertility of hybrids, risk of introgression of wheat to natural populations of *Ae. cylindrica* exists.

This project is funded by the National Research Program 59, Benefits and Risks of the Deliberate Release of Genetically Modified Plants, a research program of the Swiss National Science Foundation.

## Ghosts from the past – On plant adaptations to extinct faunas

Alexandre Antonelli, Aelys Humphreys, William G. Lee, H. Peter Linder

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Most plant species are in some way adapted to animal interactions: they may have thorns and poisonous compounds as a protection against herbivores, flowers that fit their pollinators, empty stems that house ants or fruits that require an animal vector for effective dispersal. Although we now understand many such associations, in some cases it is difficult to establish the animal counterpart of a plant adaptation. Extinct mega-mammals in tropical America have been claimed 'responsible' for the production of large-seeded fruits in several plant families, in the same way as the disappearance of dodos in Mauritius has been linked to a drastic decrease in the population of the calvaria tree (*Sideroxylon grandiflorum*). However, appealing as these hypotheses of the influence of a 'ghost fauna' on plant adaptations seen today may be, they both lack solid evidence. Here we present preliminary results showing that a disproportionate number of New Zealand grasses (Poaceae:Danthonioideae) have evolved the ability to shed their old leaves, as compared to their relatives in all other continents. This adaptation most likely evolved during a time when mammals were absent from New Zealand, i.e. during a time when the dominant herbivores in New Zealand were the now-extinct Moas.

## Large-scale test of species niche shifts during biological invasions

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The worldwide increase of biological invasions puts biodiversity at threat. Robust tools are required to better anticipate and manage ongoing and future invasions. Species Distribution Modeling (SDM) is commonly used to predict potential species distribution but its efficiency may be lowered if changes in the realized niche take place between the native and invaded ranges. These changes may be due to different biotic interactions, rapid evolution or dispersal limitation. Here, we present a new multivariate analytical framework in a gridded climatic space to quantify niche change during biological invasions. We test for niche changes in the large scale climatic niche of 43 plant species native to Eurasia (EU) or North America (NA) and invasive in EU, NA or Australia (AU). Seventeen species present niche similarity between their native and invaded ranges and seven species tend to move into new environments during the invasion process. Native species' niche is far more conserved in AU. We then investigated whether the adaptations to new environments are correlated to specific traits. Our study underlines how changes in the observed realized niche of species can strongly bias SDM predictions and possibly affect the management of biological invasions.

## Competition for light as a mechanism of plant biodiversity loss following eutrophication

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The earth is undergoing rapid changes in biodiversity because of human activities. Specifically, humans have dramatically increased the availability of nutrients in terrestrial and aquatic ecosystems. In grasslands this eutrophication causes loss of plant species diversity. Surprisingly, we lack a mechanistic understanding of how nutrient enrichment decreases plant diversity even though alternative hypotheses were suggested decades ago.

We used a novel manipulation of experimental grassland plant communities that restores light to the species in the lower canopy that are thought to decrease in diversity due to deeper shading following the increase in aboveground productivity caused by eutrophication.

We found that addition of light to the grassland understory reduced competition for light, sustained seedling establishment and maintained plant diversity despite the additional nutrient inputs. While other processes such as competition for soil resources, acidification or accumulation of plant litter can also contribute to diversity loss they played no detectable role in our study.

Our results advance a long running debate in community ecology by providing a direct experimental demonstration of the importance of competition for light as a mechanism of plant diversity loss. Although our results reveal that there is no easy remedy to counteract the negative impact of fertilization, they suggest that the importance of competition for light can be manipulated and used as a tool for restoring plant diversity to eutrophized grassland ecosystems. Our conclusions have implications for grassland management and conservation policy and emphasize the need to control nutrient enrichment if plant diversity is to be preserved.

## Experimental plant introduction: disentangling the roles of propagule pressure, soil disturbance and life-history traits

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Identifying factors promoting invasiveness of plants is one of the main goals for invasion biologists. However, in nature these factors might frequently be confounded. Therefore, to disentangle the roles of species traits and environmental factors we experimentally introduced 46 ornamental non-native and 45 native herbaceous plant species at different propagule pressures in 16 grassland sites with and without soil tilling and will determine the establishment success over three years. In greenhouse experiments we assessed a variety of plant characteristics. Results from the first and second year show that propagule pressure, seed mass, proportion of germination in the greenhouse and the ability to produce induced resistance against herbivores determine early establishment success in the field. This project will be the first one to experimentally quantify and disentangle the influence of life-history traits, soil disturbance and propagule pressure on establishment success while controlling for time since introduction. These types of introduction experiments might be also useful for unambiguously assessing factors promoting invasiveness of other organisms.

**Invited speaker - Darwin talk****Limits to adaptation: What can microbes in test-tubes tell us?****Nick Colegrave***School of Biological Sciences, University of Edinburgh, UK**n.colegrave@ed.ac.uk*

When Darwin first proposed his theory of evolution by Natural selection, he assumed that the process would generally be too slow to observe directly. In “The Origin” he brought together an impressive array of comparative data from diverse taxa, and combined this with evidence from animal breeding to provide a compelling case for his theory. He did not, even once, mention experimental evolution in microbes. This snub has left those of us that work in this field hurt and bitter, unable to say “Method Approved by Darwin” at the beginning of our talks!

In my talk I will attempt to finally heal these wounds. I will begin by outlining the approach of experimental evolution for those of you, like Darwin, that have chosen to ignore it! I will then try to persuade you, using examples from my group, that microbes in test-tubes can provide compelling, direct evidence in support of Darwin’s ideas. Becoming increasingly pompous and grandiose, I will then go on to argue that microbial experimental evolution has the potential to move evolution from being a largely historical science to a predictive experimental science with implications for the future of humanity. I may also mention sex and dinosaurs!

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**Invited speaker****An integrative approach to the study of metazoan systematics: Assembling the tree****Gonzalo Giribet***Harvard University, Department of Organismic and Evolutionary Biology**ggiribet@oeb.harvard.edu*

A vexing issue in evolutionary biology has been the reaching of a stable Animal Tree of Life. The use of numerical methods to study morphology in a systematic context and the advent of molecular data in the form of target-gene approaches have revitalized the field of animal phylogenetics and have contributed to many rearrangements in the Tree of Life. More recently, the study of full genomes or significant fractions through Expressed Sequence Tags (ESTs) have led to unprecedented amounts of molecular data available to study relationships. The use of these data in an integrative fashion with morphology and development has yielded stable hypotheses in what we now considered a modern Animal Tree of Life.

## Biosystematic study of the diploid-polyploid *Pilosella alpicola* (Asteraceae) complex with variable breeding systems: patterns and processes

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Members of the *Pilosella alpicola* group are distributed throughout the alpine region of the European mountains (Alps, Balkan, Carpathians). Like other *Pilosella* species groups (*Hieracium* subgen. *Pilosella*), the taxonomy and species' relationships are poorly understood mostly due to widespread facultative apomixis, frequent hybridization and polyploidization – the most important phenomena substantially involved in the evolutionary history of the genus. We assessed morphology, ploidy level, variation in breeding system and molecular variation within the *P. alpicola* group to provide a new taxonomic concept and to clarify evolutionary relationships and origin of polyploids. Our combined methodological approach enabled us to provide a new circumscription of the *P. alpicola* group and revealed auto- and allopolyploidization events operating within the group. The group consists of four morphologically well differentiated and geographically vicariant species with contrasting cytotype pattern. Interestingly, the mode of reproduction of polyploid cytotypes reflects their origin: *P. rhodopea* autopolyploids reproduce strictly sexually, while allopolyploid cytotypes of *P. alpicola* s.str. reproduce apomictically. Our data also revealed frequent mixed-ploidy populations indicating a primary contact zone between diploid and polyploid cytotypes of *P. rhodopea*. In spite of clear morphological separation the molecular data suggest recent diversification of the group. We hypothesize that fragmentation of more continuous ranges, range's shifts connected with interspecific hybridization (as in the case *P. alpicola* s.str.) and adaptation to different climates were the main speciation drivers in the group. Our data suggest that the *Pilosella alpicola* group is promising model for studying plant speciation, adaptation and recent polyploidization.

## The phylogeography of a successful invasion: Three-spined sticklebacks in Switzerland

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Three-spined sticklebacks (*Gasterosteus aculeatus*) are a widespread Holarctic species complex that radiated into freshwaters from the sea in the past 15,000 years. Sticklebacks invaded Switzerland within 140 years, now occupying a very wide range of ecological different habitats. We investigated the phylogeography and admixture of this recent invasion using mtDNA, AFLPs and their lateral plate phenotypes. We found only 5 different mitochondrial haplotypes originating from 3 different European regions, which are spread throughout the European haplotype network. In contrast to the mtDNA phylogeny, the Swiss populations are monophyletic for 481 polymorphic AFLP loci. This suggests that these lineages are admixed in variable proportions in the western central part of the country. Regions of genetic admixture are associated with elevated ecological functional phenotypic diversity. This is shown by the number of lateral plates, which are important for different predation regimes. The observed diversity covers the whole range of known phenotypes across Europe. We are currently investigating to what extent admixture has contributed to the ecological success of the stickleback invasion in Switzerland. Furthermore, our system provides a unique opportunity to study the evolutionary processes of ecological speciation at its beginning, combining theories of invasion biology and adaptive radiations.

## To be or not to be a species: historical separation and contemporary gene flow in the grasshopper *Oedaleus decorus*

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The extent of evolutionary divergence between organisms limits their future trajectories and is key to their past. Molecular methods provide straightforward access to estimates of evolutionary divergence between individuals and populations but it is often difficult to assess their biological relevance particularly when information on interbreeding is lacking. In this study, we analyzed the extent of genetic divergence and the recent evolutionary history of *Oedaleus decorus*, a thermophilic grasshopper with extremely large distribution range spanning the southern regions of Europe, Asia and parts of Africa. Maternally inherited mitochondrial sequences revealed a surprisingly deep genetic split in European *O. decorus* into an Eastern and a Western lineage which come together in the region of the Alps. These lineages probably pre-date the last glacial maximum and genetic divergence among them was similar to differences between established grasshopper species. However, population-based analyses of microsatellite data (nucDNA) provided evidence that gene flow was considerably higher than genetic divergence between mtDNA lineages indicated. Remarkably, individuals from a population in northern Italy were all exclusively part of the Eastern mtDNA lineage but clustered for nucDNA with individuals from populations containing only Western mtDNA. Taken together these results provide evidence of an ancient separation within *Oedaleus* and either historical introgression of mtDNA among lineages and/or ongoing sex-specific gene flow in this grasshopper. Our results highlight further the importance of multilocus approaches for unraveling the history of populations and species of uncertain evolutionary divergence.

## Distinguishing between population bottleneck and population subdivision using a Bayesian model choice procedure

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Although most natural populations are genetically subdivided, they are often analyzed as if they were panmictic units. In particular, signals of past demographic size changes are often inferred from genetic data by assuming that the analyzed sample is drawn from a population without any internal subdivision, but it has been shown that a bottleneck signal can result from the presence of some recent immigrants in a population. It thus appears important to contrast these two alternative scenarios in a model choice procedure to prevent wrong conclusions to be made. We use here an Approximate Bayesian Computation (ABC) approach to infer whether observed patterns of genetic diversity in a given sample are more compatible with it being drawn from a panmictic population having gone through some size change, or from one or several demes belonging to a recent finite island model. Simulations show that we can correctly identify samples drawn from a subdivided population in up to 95% of the cases for a wide range of parameters. We apply our model choice procedure to the case of the chimpanzee (*Pan troglodytes*) and find good evidence that Western and Eastern chimpanzee samples are likely drawn from spatially subdivided populations.

## Islands of Natural Selection in the Human Genome

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Humans are living in rather diverse environments all over the world. Adaptations to different environmental conditions as well as maintenance of diversity should be reflected in the genome. Therefore, genomic regions with high or low population differentiation are of special interest as surrogates for selection. We have examined two datasets to identify such regions in the human genome. On one hand there are 660,664 SNPs typed by the Human Genome Diversity Panel (HGDP) in 53 populations worldwide, and on the other hand there are 1,455,775 SNPs typed in only 7 populations of the HapMapIII dataset. We applied a newly developed method to test for population differentiation using a realistic demographic model. Overall we detected less evidence for selection than previous studies, but significant loci are non-randomly distributed in the genome. Dealing with large genomic datasets makes it necessary to explicitly model correlations between linked sites and to control for multiple testing. Therefore we apply a Hidden Markov Model to pinpoint genomic islands under selection. Genes overlapping with these regions as well as patterns of linkage disequilibrium and recombination are examined more closely. This study aims at deepening our understanding of the selective history of humans.

## Mating of common voles versus the monogamy gene *avpr1a*

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Genetic determinism of behavior is a central theme of modern life sciences. Innate components of behavior are evident at all evolutionary levels but the complexity and interdependence of behavioral traits makes it difficult to assess the contribution of particular genes. An exception is the arginine vasopressin 1a receptor gene (*avpr1a*) which has been associated with individual variation in social behavior of several mammalian species. Length variation of a short tandem repeat (STR) element in the 5' regulatory region *avpr1a* was linked in several studies with sexual fidelity and pair-bonding in voles and humans. Here we tested for an association of STR polymorphisms with social parameters such as the number of mating partners or offspring in male and female common voles under quasi-natural conditions. We detected considerable variation both in *avpr1a* polymorphism and social parameters but no significant associations despite very large sample sizes. However, there was a strong dependency of the results on the statistical treatment of the complex data. We were able to generate various erroneous associations between STR polymorphisms and social traits that were remarkably similar to previous reports on the *avpr1a* system. Our results show that the impact of *avpr1a* STRs on the social behavior of common voles is - at best - very weak in natural populations, and it is questionable whether the effects of the *avpr1a* system are stronger in other mammalian species.

## Host-parasite interactions between a generalist parasite and its main and alternative hosts: a cross-species infestation experiment

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In host-parasite interactions, the host provides a combination of resources and micro-habitat conditions for a parasite. Since many ectoparasites exploit both a main host species and some alternatives, the speed and magnitude of the adaptive process thus results from the reproductive success on several host species and their combined micro-habitats. Here we experimentally disentangled the effects of host profitability (i.e. host species) and micro-habitat (i.e. nest material) on the fitness of hen fleas exploiting a main host species, the great tit and an alternative host, the collared flycatcher. Their reproductive timing is synchronised with the fleas' reproduction, and fleas feed mainly on offspring. In a 2 x 2 x 2 design, we manipulated both flea infestation (absence or presence) and nest material (great tit or flycatcher nest) in two sympatric host species (great tit or flycatcher offspring). Flea reproductive success was similar on both host species when hosts bred in nests of their own species, suggesting that fleas did not specialise on great tits. Nevertheless, flea reproductive success was lower on flycatcher broods reared in great tit nests than on all other combinations. In flea-infested nests, the fledging success of both host species was higher on great tit nests, suggesting that the micro-habitat in a great tit nest may partly alleviate the cost of parasitism. The study illustrates how the host-engineered abiotic conditions modulate host-parasite interactions.

## Experimental test of a reservoir-targeting vaccine in order to reduce the tick infection prevalence by the Lyme disease agent

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The bacteria *Borrelia burgdorferi* is the agent responsible for Lyme disease, a zoonotic infectious disease emerging in Europe and North America. *B. burgdorferi* is hosted by multiple reservoir species including the white-footed mouse *Peromyscus leucopus* and is transmitted by the black-legged tick, *Ixodes scapularis*, that occasionally feeds upon and infects susceptible human hosts. To remain extant, the bacterium requires a continual cycle between ticks and vertebrates. We have developed a bait-vaccine to inhibit the transmission of the bacteria from the tick to the vertebrate on which the tick feeds to ultimately reduce the proportion of infected ticks, and subsequent human Lyme disease risk, in treated areas. During the spring and summer of 2009, we experimentally distributed the vaccines or the control baits in 10 plots in North-Eastern and Mid-Atlantic forests. To assess the efficiency of the vaccine at each step, we measured the titres of specific antibodies, the transmission rate of the bacteria from mice to ticks, and we monitored the infection prevalence of the bacteria in ticks from the experimental plots. Vaccinated mice show a level of antibody correlated to the number of vaccine doses eaten. Further analyses will be presented and discussed. In addition to its importance in reducing the risk of Lyme disease in tick-infected habitats, this vaccine is one of the first examples of a host-targeted vaccine. This system also provides an efficient tool to experimentally answer ecological and evolutionary questions related to multi-host pathogens transmitted by vectors in the wild.

## Resistance of *Daphnia magna* to a bacterial pathogen is based on few loci with strong epistasis

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*Daphnia magna* and its bacterial pathogen *Pasteuria ramosa* show strong genetic interactions for infectivity, which is consistent with the idea of antagonistic coevolution by negative frequency dependent selection. Evidence is so far based on phenotypic patterns, but the genetic basis is not yet understood. We investigated the genetics behind patterns of susceptibility and resistance in the *D. magna* host. We crossed two inbred hosts to obtain F1 which was selfed to produce F2. F2 were backcrossed and eight of the backcrossed hosts and both parents were selfed. In total 637 recombinant crosses were tested for resistance against *P. ramosa* clones C1 and C19. Segregation for resistance against C1 and C19 was found in two separate crosses and was consistent with Mendelian segregation at one locus with 2 alleles. Resistance is dominant for both *P. ramosa* clones. However, backcrossed hosts did not show expected Mendelian frequencies: double resistant hosts were totally absent and single resistance hosts over represented. Epistasis between both resistance loci could explain the observed frequencies. We tested for and confirmed epistasis by selfing of the backcrossed hosts. In addition, these crosses revealed that the two resistance loci were closely linked. Thus, inheritance of resistance for tested clones of *P. ramosa* in *D. magna* is consistent with Mendelian segregation with dominant resistance and epistasis between 2 closely linked loci. Such a genetic system can lead to coevolution by negative frequency dependent selection, which is believed to be important for the maintenance of genetic diversity and sexual reproduction.

## Horizontal gene transfer and the evolution of bacterial cooperation

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Bacteria frequently exhibit cooperative behaviours but cooperative strains are vulnerable to invasion by cheater strains which reap the benefits of cooperation but do not perform the cooperative behaviour themselves. Bacterial genomes often contain mobile genetic elements such as plasmids. When a gene for cooperative behaviour exists on a plasmid, cheaters can be forced to cooperate by infection with this plasmid, rescuing cooperation in a population where mutation or migration has allowed cheaters to arise. Here we introduce a second plasmid which does not code for cooperation and show that the social dilemma repeats itself at the plasmid level in both within-patch and metapopulation scenarios, under various scenarios of plasmid incompatibility. Our results suggest that while plasmid carriage of cooperative genes can provide a transient defence against defection, plasmid and chromosomal defection remain the only stable strategies in an unstructured environment. We discuss our results in the light of recent bioinformatic evidence that cooperative genes are over-represented on mobile elements.

## Life history traits can produce a length cycle in multicellular filamentous bacteria

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Multicellular filamentous bacteria exhibit varying lengths in the environment. We study the role of cell density dependent birth and death rates on the distribution of filament lengths during growth and stationary phases. We simulate the dynamics of populations of filamentous bacteria, assuming only birth and death rates of the cells as the main parameters. The theoretical model shows a common cyclic pattern of the mean filament length. Furthermore, different life history traits produce different distributions of lengths, although providing the same fitness. We compare the predictions of the theory by culturing species of multicellular filamentous bacteria that are either heterotrophs or photoautotrophs. The experimental results support the theoretical predictions, showing a tendency of filamentous bacteria to be short in the beginning, longer during transient growth phase and shorter again when the population is at the carrying capacity. Furthermore, the theory predicts that species with longer generation times should have longer filaments, which is also validated empirically. The systematic characterization of a morphological property such as length in filamentous bacteria has implications on understanding the pre-existing conditions for the evolution of developmental cycles in simple multicellular organisms. Moreover, the fact that strains with the same fitness evolve to different morphologies indicates that fitness does not necessarily have to determine evolution towards multicellular or unicellular forms.

## Latitudinal variation and temperature-dependent plasticity of a polymorphic sperm storage organ

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Female sperm storage organs are highly diverse between species. Explanations for this diversity typically invoke sexual selection, although alternative hypotheses such as drift and pleiotropy have been proposed. The yellow dung fly *Scatophaga stercoraria* is highly suited to test these hypotheses because females exhibit significant intraspecific variation in sperm storage morphology in that they possess either three or four spermathecae. Here, we report on a study in which flies collected over a broad geographical range were raised at three different temperatures. Our results not only show that populations lacking genetic structure at 'neutral' markers are significantly differentiated regarding the polymorphism, but also that the development of a fourth spermatheca strongly increases with rearing temperature. Rather than being favored by sexual selection as previously hypothesized, we suggest that the four spermatheca phenotype reflects a developmental distortion, which increases in frequency in northern climates as a pleiotropic side effect through selection on faster growth rates.

## Past and future fishery-induced evolution on growth in an Alpine whitefish

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Size-selective fishing, i.e. the systematic removal of larger individuals from a population, is predicted to affect the evolution of individual growth rates. Current management plans mostly ignore this potential problem. We analyzed a 25-year long monitoring survey of an isolated population of the whitefish *Coregonus palaea* to determine (i) the actual change of growth rate over time, and (ii) the selection differentials on growth rate that can be linked to size-selective gill-net fishing. We then used individual-based modeling to predict the potential effects of different kinds of mesh-size regulations. We found no change in juvenile growth, but a marked decline in adult growth rate over the last 25 years. We also found significant selection differentials that suggest that about a third of the observed decline in growth rate is linked to fishery-induced evolution. Size-selective fishing seems to affect the genetics of individual growth in our study population. Our model shows that simple changes in the mesh size regulations have the potential to not only prevent this kind of fishery-induced evolution, but they may even help the population to recover from previous deleterious effects of fishing.

## Habitat saturation, benefits of philopatry, relatedness and cooperative breeding in a cichlid

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Cooperative breeding in vertebrates may emerge due to subordinates delaying dispersal when free breeding habitat is not available ('habitat saturation' hypothesis, HS). However, delayed dispersal might also be due to younger individuals postponing dispersal to when they are more competitively able or have more to gain from breeding independently ('benefits-of-philopatry' hypothesis, BP), or to when inclusive fitness benefits no longer outweigh the benefits from independent breeding ('kin selection' hypothesis, KS). Here we show in three experiments that both HS and BP determine the extent of cooperative breeding in the cichlid *Neolamprologus pulcher*. Contrary to the KS, individuals significantly avoided settlement with related individuals, and an additional settlement experiment confirmed this result. Our results suggest that kin structure in these cichlids emerges from limits on dispersal, but if such barriers are absent, cichlids prefer to settle with unrelated individuals to maximise the benefits of direct reproductive participation.

## Direct and indirect fitness benefits of philopatry and cooperative care in *Xyleborina* (Curculionidae: Scolytinae)

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Reproduction of ambrosia beetles is characterized by parental care and colonial breeding, and eusociality has been described for one species. Social behaviour has not been studied in this group, however, despite its outstanding suitability to serve as model system for the study of genetic and environmental factors in the evolution of cooperation and advanced sociality. We studied the parental and alloparental behaviour of two species of the haplodiploid *Xyleborina* and estimated fitness effects to distinguish between the potential importance of individual and kin selection. We show experimentally that philopatric females gain direct fitness benefits from pre-emergence feeding in their natal gallery, which leads to a higher reproductive output after dispersal and foundation of an own nest. Sometimes philopatric females even breed within their natal gallery. Indirect fitness benefits of alloparental care seem to be important as well. All colony members cooperate in gallery maintenance, brood care and fungus farming, with various task specializations among individuals of different status and age. This polyethism is reminiscent of the behaviour of the socially most highly-developed hymenoptera and represents an advanced level of sociality in Coleoptera.

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## Power analysis of tests for reproductive fitness in two fish populations

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The stocking of hatchery fish in the natural environments are aimed at conservation as well as supplementation. Studies have documented the evidence of fitness decline of hatchery fish in the wild but a lack of statistical power of the existing test of fitness is obvious and leaves much to be desired.

Different statistical tools were used to analyse a set of absolute fitness values randomly generated for hatchery and wild fish based on the Poisson and negative binomial distribution. The power of each test was calculated to determine the most robust test. Our preliminary data suggest: Student t –test and Wilcoxon Ranked test showed power greater than 0.80 at a sample size of 200 - 3000 at relative fitness decline of 10 - 40%. One way analysis of variance and Chi square test showed power greater than 0.80 at sample size of 50 - 1000 at relative fitness decline of 10 - 40%. However, the Chi square test uses paired data and it was unable to analyse unequal sample sizes between the two populations.

### Conclusion

According to the preliminary results, one way analysis of variance has statistical advantages to analyse the fitness difference in different groups. Reliability of the statistical significance of these tests will be further investigated and discussed.

## Impact of genetically modified wheat with improved powdery mildew resistance on insect herbivores

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One of the risks associated with the growing of genetically modified (GM) disease-resistant crops is their potential to adversely affect non-target organisms, either due to the expression of the trait itself or due to transformation-related effects. In this context, alterations in the metabolism of mildew-resistant GM wheat plants could affect insects of ecological relevance, like herbivores, such as aphids (Homoptera: Aphididae) and the cereal leaf beetle *Oulema melanopus* (L.) (Coleoptera: Chrysomelidae), both naturally occurring in wheat fields.

To test our hypothesis, two GM spring wheat lines with enhanced resistance to powdery mildew (Pm3b1- and glucanase/chitinase-transgenic wheat), their non-transformed near isolines, and the Swiss spring variety Rubli were used. Plants were tested in an open glasshouse under near field conditions while simultaneously ensuring a high level of biological containment, in two growing seasons (2008 and 2009). Abundance of aphids and larvae of *O. melanopus* was estimated by visual counts. Moreover, the typical feeding damage caused by the larvae of *O. melanopus* was determined using several scores based on the percentage of the leaf surface damaged.

Our results revealed that the number of *O. melanopus* as well as the damage caused by the larvae did not differ among treatments. However, the intensity of the mildew infection was negatively correlated to the number of aphids present on the plants. The reasons for this effect are unclear and are currently under investigation.

## Evolution of host resistance and trade-offs between virulence and transmission potential in an obligately killing parasite

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Standard epidemiological theory predicts that parasites, which continuously release propagules during infection, face a trade-off between virulence and transmission. However, little is known how host resistance and parasite virulence change during co-evolution with obligate killers. To address this question we have set up a coevolution experiment evolving *Nosema whitei* on eight distinct lines of *Tribolium castaneum*. After 11 generations we conducted a time-shift experiment infecting both the co-evolved and the replicate control host lines with the original parasite source, and coevolved parasites from generation 8 and 11. We found higher survival in the coevolved host lines than in the matching control lines. In the parasite populations, virulence measured as host mortality decreased during co-evolution, while sporeload stayed constant. Both patterns are compatible with adaptive evolution by selection for resistance in the host and by trade-offs between virulence and transmission potential in the parasite.

## Effects of litter diversity and identity on leaf decomposition in a Mediterranean stream under simulated intermittency

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Effects of biodiversity on ecosystem functioning have been studied intensively in the last two decades. Most work on litter decomposition in this context has focused on the effects of mixing litter of different quality as food for leaf-shredding detritivores, whereas knowledge of other mechanisms behind mixture effects is poor. Several studies highlighted the importance of considering the environmental context when addressing these research questions. The present study aimed at detecting mechanisms of diversity effects that could be important for litter decomposition in intermittent streams. We carried out a field experiment in a Mediterranean headwater stream and hypothesized that litter species traits influence the rate of drying and residual moisture in litter accumulations until flow resumes. We expected this mechanism to affect decomposers and consequently decomposition rate. To test this hypothesis, we submerged litter of two indigenous litter species (alder and holm oak) in monospecific and mixed-litter bags in the stream. We then simulated a drought event by transferring part of the bags to dry positions on the stream bank and submerging them again after one week. Rates of litter mass loss did not reveal significant mixture effects, independent of the drying treatments. Similarly, fungal biomass associated with decomposing litter (which was at the base of the hypothesized mechanism) was also unaffected by litter mixing. However, the patterns observed in both response variables (i.e. litter mass loss and fungal biomass) reflect the consequences of vastly different litter traits of the two litter species, when analyzed separately. Our study therefore did not suggest the presence or importance of the hypothesized mechanism of diversity effects. However, the findings highlight the importance of considering functional traits of the species relevant to a given process when assessing the stability of ecosystem functioning under changing environmental conditions.

## The role of vegetation structure and plant diversity in an *Argiope bruennichi* - prey system in wildflower strips

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In this study we were interested in the role of plant diversity and vegetation structure for the abundance and trapping efficiency of *Argiope bruennichi*.

The experiment was conducted in artificially-established wildflower strips in Swiss ecological compensation areas, situated in a region of intensive farmland. Spider webs were observed in 9 different wildflower strips. Each strip was composed of twelve subplots differing in plant diversity (2, 6, 12, 20 sown species). Webs of *A. bruennichi* were counted and measured along transects through the wildflower strips, all prey items collected, and plant cover, diversity and vegetation height measured in all subplots.

Plant diversity neither had an effect on the number of *A. bruennichi* webs nor on trapped prey diversity and abundance. Our results highlight, however, the importance of vegetation structure. More spider webs could be observed with increasing vegetation cover, while vegetation height had a negative effect. These factors did not influence the abundance and diversity of prey items caught, but interestingly, the size of trapped prey species decreased with increasing vegetation cover.

Our experiment shows that the choice of sites for web construction by the spider *A. bruennichi* in wildflower strips is largely determined by plant architecture. This indicates that trophic interactions between higher trophic levels can be mediated by the architecture of the first trophic level (plants). Moreover, *A. bruennichi* seems to face a trade-off between the optimal site for web construction and the prey biomass available.

## Adaptive divergence of ancient gene duplicates in the avian MHC

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Gene duplication and neofunctionalization account for important evolutionary novelties that confer ecological adaptation. These processes are particularly relevant to explain the evolution of the MHC, a multigene family crucial to the vertebrate immune system. In birds, recent analyses showed that MHC class II $\beta$  (MHCII $\beta$ ) genes from within owls were more similar to genes from other orders than among each other, suggesting the presence of two MHCII $\beta$  lineages. These lineages could have arisen by (i) a single duplication in an avian ancestor and subsequent divergence of paralogs, or (ii) independent duplications in recent avian orders followed by functional convergence. We compiled a data set consisting of 63 MHCII $\beta$  sequences from 6 avian orders to distinguish between these hypotheses and clarify the role of selection in the divergent evolution of avian MHCII $\beta$  lineages. Phylogenetic analyses suggest that a unique duplication event preceding the major avian radiations gave rise to two ancestral MHCII $\beta$  lineages. Following duplication, positive selection drove the divergent evolution of the paralogs. This divergence involved a radical shift from basic to acidic amino acid composition of a protein domain facing the  $\alpha$ -chain in the MHCII $\alpha\beta$ -heterodimer. Structural analyses of the MHCII $\alpha\beta$ -heterodimer highlight that three of the divergent amino acid residues are potentially involved in interaction with the  $\alpha$ -chain, suggesting that the shift following duplication may have been accompanied by coevolution of the interacting  $\alpha$ - and  $\beta$ -chains. These results provide new insights into the long-term relationships among avian MHC genes and open interesting perspectives for population genomic studies of avian MHC evolution.

## Getting to know the ancestry of the gentian decorating Swiss butter

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This study addresses the phylogenetic position of *G. acaulis* in comparison with three other *Gentiana* species within the *Ciminalis* group: *G. alpina*, *G. angustifolia* and *G. clusii*. These species that occur in the mountains of central and southern Europe are morphologically well recognizable and share some ecological features: *G. acaulis* and *G. alpina* are calcifugous whereas *G. angustifolia* and *G. clusii* are calcicolous. In the present study a total of 185 individuals (10-20 populations per species, and three individuals per population) were analysed with three chloroplast loci (*trnH-psbA*, *rpoC1* and *rpoB*), whose combination identified eight haplotypes. *G. angustifolia* displays three haplotypes, among which one is shared with *G. acaulis*, and both *G. alpina* and *G. clusii* have private haplotypes (one and four, respectively). The haplotype network separated the species into two groups: *G. acaulis* and *G. angustifolia* on the one side and *G. alpina* and *G. clusii* on the other. Previous studies analysing very few individuals with ITS and *trnL* intron sequences have shown that these species are separated into the same groups. However, a RAPD analysis suggested a different position for *G. acaulis*. While confirming the position of *G. acaulis* as closer to *G. angustifolia*, these preliminary results will be discussed, in light of their ecological features and in terms of biogeographical hypotheses, together with the occurrence of potential hybridization among some of these species. This study helps shed light on intraspecific genetic variability for the four species, in the context of the "DNA Barcoding" to which this project belongs.

## **Introduction bias and human-mediated selection leads to differences in germination characteristics between native and introduced alien plant species**

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A major aim in invasion biology is to find traits that confer invasiveness. To this aim most studies compare invasive alien and native species. However, trait differences between invasive alien and native species could simply reflect an introduction bias towards species with certain traits. Moreover, in the case of ornamental species such traits might even have been bred into cultivars. We tested whether this is the case for germination characteristics that are frequently associated with invasive species.

In a multi-species greenhouse experiment we compared germination characteristics between 43 plant species native to Switzerland and 46 related ornamental alien species that have been introduced to Switzerland but have not become invasive yet. To test for potential effects of human-mediated selection, we included among the alien species 26 cultivars. To test whether differences in germination characteristics between these groups of species depend on an ecologically important environmental factor, we used two different light levels.

Averaged over all 89 species, germination occurred earlier and proportions of germinated seeds were higher under shaded conditions than under unshaded conditions. Ornamental alien plant species germinated earlier and with higher proportions than related native plant species. Among ornamental alien species, cultivars germinated earlier and with higher proportions than non-cultivars.

Our results show that non-invasive ornamental alien species, and particularly cultivars, differ from native species in germination characteristics. This indicates that reported trait differences between invasive alien and native species might simply reflect introduction bias and human-mediated selection for certain traits. Nevertheless, because fast and profuse germination are frequently associated with invasiveness among alien species, our results suggest that biased introduction and human-mediated selection of ornamental plants with these characteristics increase the risk that these species might ultimately become invasive.

## Adapting conservation to climate change: the case of the otter in Europe

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In the last five decades the Eurasian otter *Lutra lutra*, has declined dramatically throughout all of Europe. Nowadays, the otter seems to be thriving in some European countries, but populations are still fragmented and the species is almost absent of central Europe. Promoting population expansion and reconnection is crucial to ensure the long-term maintenance of genetic diversity and the long-term persistence of the species. In this regard, habitat suitability models (HSM) represent powerful tools to evaluate habitat quality and produce maps of potential distribution and natural dispersion of the species. This study aims at determining which factors influence the otter distribution and use them to predict the potential distribution of the species in Europe, under current and future climate. The environmental variables used are related to water availability, food supply, resting site and human disturbance using six different modelling approaches. Future projections are derived by running the CCM3 climate model under a 2 x CO<sub>2</sub> increase scenario. At the European scale, the otter is mostly influenced by water availability. The current potential distribution reveals large gaps of unsuitable habitats limiting connectivity between otter populations in Europe. Climate change would have different effects on otter habitat suitability in Europe. In the Western part, the model predicts losses of suitable habitats, whereas gains are predicted in central Europe and Eastern Europe shows equal rates of losses and increases of suitable habitat. Our results are important in helping setting up conservation actions and promote otter recovery in Europe.

**Divergent selection and local adaptation in the cyprinid fish *Phoxinus phoxinus*****Hélène Collin***University of Lausanne - Department of Ecology and Evolution**helene.collin@unil.ch*

Natural selection is an important evolutionary process shaping variation in nature. At small temporal and spatial scales, geographically localized natural selection can drive local adaptation, especially in heterogeneous and fragmented habitats. The types of phenotypic and genetic changes involved in adaptation to changing environments remains a less-explored aspect of the study of local adaptation. We investigated this issue using the European minnow (*Phoxinus phoxinus*), an endemic fish in the Alps and the Pyrenees. This species occupies a wide range of altitudes and habitats, such as lakes versus streams. We adopted a multifaceted approach based on the quantification of genetic and morphological variation within and among populations. Habitat-associated body shape divergence was detected with a geometric morphometrics approach. An AFLP genome scan allowed us to: (1) quantify the proportion of the genome subject to divergent selection, and (2) examine patterns of neutral genetic divergence among populations due to genetic drift and gene flow. The genome scan revealed that a low proportion of genes displays genetic divergence to different selective pressures. Thus, geography and habitat shaped patterns of genetic divergence at most (i.e., neutral) loci, as well as body shape divergence highlighted by the geometric morphometrics results.

Overall, the results support local adaptation of *Phoxinus phoxinus* to fragmented and ecologically different environments, particularly to lake versus stream habitats.

## Is fast growth really a correlate of alien plant invasiveness?

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An emerging consensus in invasion ecology is that faster growing alien plant species tend to be more invasive than slower-growing species. However, phylogenetic non-independence and precision of growth measures often remain unaccounted for in comparative studies. We tested whether invasiveness was related to relative growth rate (RGR) of over 100 plant species occurring in the UK and invasive elsewhere, using an existing dataset of measurements made under standardized experimental conditions. We also weighted species according to the variance in growth rate, and accounted for potential phylogenetic non-independence. Inclusion of phylogenetic structure in generalized linear mixed models did not improve the quality of model fit, suggesting that RGR had little phylogenetic signal. There was a weak positive relationship between invasiveness and maximum RGR among the species considered. Further global investigation into the relationship between alien plant invasiveness and growth rates will be discussed.

## Differential attraction of parasitoid wasps to cultivated maize and its wild ancestor, teosinte

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Artificial selection of crop plants for increased yield and quality has had a cost for other potentially useful traits, including resistance to herbivores. Restoring defense traits in cultivated plants could be an effective way to combat pests. Besides direct defenses, such as the production of toxic compounds, plants may also indirectly protect themselves by emitting volatile organic compounds (VOCs) that attract the natural enemies of their attackers, like parasitoids and predators. Artificial selection of crops can also lead to the loss of these indirect defense signals, as is the case for a maize root volatile that is emitted upon feeding by a coleopteran larva and is attractive to entomopathogenic nematodes. This root signal can be restored to improve the efficacy of nematodes as biological control agents.

We investigated a possible signal loss for aboveground interactions by comparing the capacity to attract parasitoids between cultivated maize and teosinte, the wild ancestor of maize. Results from an olfactometer experiment show that the two most common teosintes, *Zea mays* ssp. *parviglumis* and ssp. *mexicana*, when induced with caterpillar regurgitant, are more attractive to the parasitoid wasp *Cotesia marginiventris* than a cultivated maize, *Z. mays* ssp. *mays* var. Delprim. Another common parasitoid of caterpillars that occur on wild and cultivated maize, *Campoletis sonorensis*, did not distinguish between the three plants. We are currently analyzing the volatiles that we collected from the plants to see whether a difference in VOC emission could account for the differential wasp attraction. This information will not only provide new insights into plant-mediated tritrophic interactions, but may also help in the development of novel crop-protection methods.

## Kin selected siblicide and cannibalism in the European earwig

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Aggression levels among individuals can severely increase under high density or shortage of crucial resources, sometimes resulting in individuals killing conspecifics. This is not uncommon in family-groups of diverse taxa where the dependent offspring compete for the limited resources provided by their parents. Killing a nest mate can relax the competition level and cannibalism provide a direct nutritional benefit. However, nest-mate killing bears the risk of reducing indirect fitness if the victim is related (i.e., siblicide) and siblicide may impose selection on kin-recognition abilities. Based on this hypothesis, we predicted that first instar larvae (nymphs) of the European earwig (*Forficula auricularia*) kill and cannibalize unrelated nest mates earlier and more often than related nest mates, and that cannibalism has a direct nutritional benefit in terms of survival. We tested these predictions experimentally by establishing related and unrelated pairs of nymphs and recorded survival, aggregation behavior and cannibalistic outcomes in the absence of alternative food sources. In order to obtain expected survival probabilities of victims and survivors in the absence of any interaction we simulated virtual pairs based on the data of singly held control nymphs. As predicted, victims lived for less time than expected and survivor lived longer than expected, demonstrating nest-mate killing and cannibalism. Furthermore, unrelated individuals were killed significantly earlier and were more often cannibalized than related individuals. The survival patterns of victims and survivors were quantitatively consistent with the expectations of Hamilton's rule. Our study shows that earwig nymphs recognize kin and adjust their nest-mate killing and cannibalistic behavior as predicted under the hypothesis of kin-selected siblicide and filial cannibalism.

## Pheasants, phenotypes, and the preservation of genetic divergence on island populations

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Evolutionary change occurs through the accumulation of morphological and genetic variation over time but it is rarely known to which extent morphology and genetics co-segregate or what their causal links are. Additionally, environmental change has the potential to deeply impact on these processes through the separation of populations and the action of selection. Here we investigate the evolutionary history of a plumage-polymorphic bird and examine the extent of morphological and genetic change associated with environmental perturbations and physical separation of populations. The silver pheasant *Lophura nycthemera* is widely distributed in Southeast Asia with clinal morphological variation among continental populations in China but distinguishing plumage patterns and body size for populations on Hainan Island off the coast. Phylogenetic analyses of mitochondrial DNA revealed a pattern of genetic subdivision in the species inconsistent with subspecies taxonomy but consistent with geographical distribution. Mismatch analyses date the population expansion of the Hainan Island population to about 0.15Mya ago, clearly before the last connection of the island to the continent. Population-level and individual-centered approaches based on microsatellites demonstrated deep genetic divergence between Hainan pheasants and continental clades but comparatively little genetic structure among continental populations, a pattern strikingly similar to morphology but not to mtDNA. We conclude that the discordant phylogenetic pattern may be due to a relative reduction of genetic and morphological divergence among continental populations after secondary contact through sex-specific gene flow, and a preservation of ancient levels of subdivision in mtDNA, nuclear DNA and morphology for Hainan pheasants relative to the continent.

## Sex-specific adaptation of the parasite *Pasteuria ramosa* to its host *Daphnia magna*

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Several studies reported that prevalence and intensity of parasitic infections is higher in males than females. In organisms with a parthenogenesis cycle, females are more common than males. Thus, in such organisms, parasites should be more adapted to the females. Using the parthenogenetic cladoceran *Daphnia magna* and its horizontally transmitted parasite *Pasteuria ramosa*, we investigated how host sex affects the host-parasite relationship. In our experiment we exposed 120 female and 120 male *Daphnia* of the same clone to one parasite clone. *Daphnia* females were 3.5 times more susceptible than males. This might be linked to a female immune deficiency to this parasite. In females, *Pasteuria* had a higher fitness than in males because of the double amount of spores produced. Furthermore, in this system, infected females are fully castrated by a chemical way, while infected males still produce half of the normal sperm quantity. Therefore, because of their smaller size and their energy allocation in reproduction, males provide a poorer environment for the parasite. Thus, the bacterium *Pasteuria* seems to be better adapted to exploit the “female environment” compared to the “male environment” which is reflected in high spore production and higher infectivity in females. This result is consistent with our assumption that parasite should be more adapted to the common sex.

## The role of plant diversity, plant structure and biomass on Gastropods - an experiment with two trophic exclusions

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Wildflower strips are nowadays often used to increase natural enemies of crop pests and to conserve insect diversity on farmland. Gastropods, especially slugs, can affect the vegetation development in these strips considerably. While recent theoretical frameworks describe more diverse communities exhibiting greater resistance against herbivore pressure, empirical examinations are scarce and much debated.

We conducted a semi-natural experiment in wildflower strips manipulating trophic structure (exclusion of major herbivores and predators; exclusion of major predators) and plant richness (2, 6, 12, 20 and 24 sown species). With Generalized linear mixed models and partial Canonical Correspondence Analysis, we compare the importance of plant structure, plant species composition, and plant diversity on the abundance of gastropods to answer the questions: Which plant species influences the gastropod abundances in Wildflower strips most? Are species-rich communities more resistant to gastropod grazing than species-poor communities? Is plant diversity or plant identity more important to understand the structure of gastropod communities?

We found 9 species of gastropods under experimental tile plates, with the slugs *Arion lusitanicus*, *Deroceras reticulatum* and *D. agreste* being most frequent. The Control treatment had a higher number of gastropods than the exclusion. The vegetation cover and height positively affected slug abundance and plant diversity had a negative impact on gastropod abundance. Moreover plant identity has a much higher importance than plant diversity as determinant of gastropod community composition.

## Legs of deception: disagreement between molecular markers and morphology (Diptera, Dolichopodidae)

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Conflicting hypotheses in phylogenetics and systematics, generated by different data sets (e.g. morphological vs. molecular) are not uncommon in biology. The clarification of such instances may allow understanding general mechanisms involved in the speciation process in an evolutionary light. Here, we present and discuss the case of the *Dolichopus plumipes* species group in the long-legged flies, Dolichopodidae. A phylogenetic survey was performed based on both morphological and molecular data. The full data set comprises 31 morphological characters and 2'252 molecular characters (COI: 810; 12S: 343; 16S: 514; ITS2: 585) of 49 different species, represented by 82 specimens. The molecular phylogenetic analysis revealed a clade (composed by the species *D. plumipes*, *D. wahlbergi*, *D. polleti*, *D. simplex*, and *D. nigricornis*) that disagrees with the traditional morphological view, based on external characters. In particular, specimens of the species *D. plumipes* and *D. simplex* were indistinguishable with the molecular markers used here. However, we still consider *D. simplex* and *D. plumipes* as two distinct taxa and provide explanatory hypotheses on the evolutionary background. The conspicuous male secondary sexual characters (present in *plumipes* but not in *simplex*) are key factors in sexual selection and their presumably rapid reduction in *D. simplex* is thought to be of main importance for the explanation of the speciation process. The *plumipes-simplex* case may therefore be viewed as a paradigmatic illustration showing that a better integration of the molecular and morphological approaches is needed to understand and clarify the, in some case, complex taxonomy, systematics, and phylogeny of organisms.

## Tritrophic interactions and crop protection: going one step further

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When attacked by insects, plants emit volatiles that can serve as cues for parasitoids searching for host. It has been proposed that the emissions of these signals can be manipulated to improve crop protection. We demonstrated the full potential of this strategy by restoring a specific belowground signal emitted by insect-damaged-maize roots. This signal, the sesquiterpene (E)-BETA-caryophyllene, is highly attractive to the entomopathogenic nematode *Heterorhabditis megidis* and is emitted by ancestral maize and European lines, but not by most American varieties. The loss of the signal was previously found to strongly reduce the effectiveness of the nematode as a control agent of the larvae of the western corn rootworm (WCR), a ferocious root pest. To restore nematode attraction, a non-producing maize line was transformed, resulting in constitutive emissions of (E)-BETA-caryophyllene. In WCR-infested field plots in which we released nematodes, transformed lines received significantly less WCR damage and had fewer adult beetles emerge than isogenic lines.

(E)-BETA-caryophyllene is only weakly attractive to *Heterorhabditis bacteriophora*, one of the most infectious nematodes against WCR. To overcome this drawback, we used a six-arm belowground olfactometer to manipulate the third trophic level by selecting for a strain of *H. bacteriophora* that is more responsive to (E)-BETA-caryophyllene. The selected strain responded better and moved faster towards a (E)-BETA-caryophyllene source than the original strain. In subsequent field tests, the selected strain was significantly more effective than the original strain in reducing WCR populations in plots with a maize variety that releases (E)-BETA-caryophyllene, but not in plots with a maize variety that does not emit this alarm signal. These results illustrate the great potential of manipulating natural enemies of herbivores to improve biological pest control.

These two examples are the first demonstrations that, in order to enhance its applicability in crop protection, manipulation of tritrophic systems is feasible.

## Life-stage specific environmental cues can induce adaptive maternal effects in natural populations

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Environmental cues allow parents, via epigenetic effects, to fine-tune their offspring's phenotype to the conditions offspring are likely to encounter after birth. If juvenile and adult ecologies differ, conditions mothers experienced as juveniles may better predict their offspring's environment than ambient conditions. The evolution of maternal effects that are induced by the environment experienced by mothers during early ontogeny should be favoured when three general, ecological conditions are fulfilled. (i) Adult ecology does not predict the postnatal environmental conditions experienced by offspring. (ii) The environment offspring encounter is heterogeneous in space or time favouring a plastic adjustment of offspring phenotype by maternal effects, but (iii) on average conditions across successive juvenile generations are still correlated and hence predictable. By combining size-structured population counts, ecological surveys and genetic analysis of population structure we provide evidence that all three conditions hold for *Simochromis pleurospilus*, a cichlid fish in which mothers adjust offspring quality to their own juvenile ecology. As in many species adults cannot predict their offspring's environment from ambient cues, we propose that life-stage specific maternal effects should be common in animals, and it will be important to incorporate parental ontogeny in the study parental effects.

## Functional connectivity among populations? Landscape genetics of the European tree frog in Switzerland

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Landscape composition and structure have been demonstrated as major factors impacting metapopulation processes. By facilitating or impeding individual movement, landscape connectivity has a direct influence on the population genetic structure of species. In this study, we addressed the relative effects of geographical distance and landscape features on the genetic structure of several populations of an endangered species, the European Tree Frog (*Hyla arborea*). We focused on 36 populations in a lowland area near Zürich, Switzerland. Besides roads and settlements, agricultural land occupies a large part of the study landscape. We sampled individuals from all these populations and genetically characterized them using microsatellite markers. We described the landcover of the study area using public data supplemented with field data. Using expert knowledge, landcover classes were merged into three or four classes that were thought to support, inhibit, or have no effect on the tree frogs movements. We tested different cost values to contrast landscape elements and used the resulting maps to feed least-cost path models. These models find the optimal paths that minimize the cost of individual movement. We compared Euclidian distances with least-cost paths using Mantel tests. Genetic data revealed four clusters of populations. A river situated in the study area appeared to be the strongest barrier to individual movement. Except these elements, frogs seem to easily cross the landscape. Our results are of interest for conservation management. They will support a project aimed in reconnecting the tree frog populations by creating new ponds as stepping stones to dispersal between populations.

**Assured fitness returns and drifting in the tropical wasp, *Polistes canadensis***

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A noticeable feature of eusocial insects is the variety of their reproductive strategies. One such strategy is nest-drifting behaviour, which occurs in several species of eusocial Hymenoptera (bees and wasps). Drifters, usually workers (non-reproductives), visit non-natal nests of the same or different species. Explanations for this particular behaviour include mistakes in nest identity and social parasitism where drifters infiltrate colonies in order to reproduce. In the Panamanian paper wasp *Polistes canadensis*, however, drifting wasps appear to gain indirect fitness benefits by helping raise related brood on several different nests instead of focusing help solely on their natal nest, to which they are most closely related. But when helpers drift to another nest, or die, what happens to the effort they have already invested in that nest? Assured fitness returns models predict that the offspring a helper has only part-reared can be raised through adulthood by remaining nestmates after the helper dies. Previous studies have suggested that the loss of a helper may be compensated by several ways: helpers recruitment from emerging hatched pupae, increased foraging rates, brood recycling or slower brood development time. We propose a new hypothesis in which drifting may insure these fitness returns through direct recruitment of drifters. The evolution of drifting behaviour and its importance remain poorly investigated because of the difficulties of quantifying drifting with traditional methods (paintmarking, numbered tags). Thus, we will use an innovative monitoring technology (radio frequency identification, RFID), to provide accurate, real-time, continuous data on nest-drifting.

## Range-wide population structure of *Aythya fuligula*: an avian influenza vector with long distance dispersal ability

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Animal migrations have the potential to spread zoonotic pathogens such as avian influenza (AI) at local and intercontinental scales. Long-distance migrants like the tufted duck *Aythya fuligula* have been demonstrated to be frequent carriers of AI viruses but their role in the spread of the epidemic between East Asia and Europe remains unclear. Here we provide the first range-wide analysis of migration patterns in *A. fuligula* covering breeding and wintering grounds across the entire Palearctic. We used phylogeographic and population genetics approaches based on mitochondrial and nuclear DNA markers to delimit population boundaries and regions of admixture between European and Asian ducks. Our results showed significant genetic differentiation between breeding populations suggesting relative fidelity of individuals to the region of origin. However, samples from wintering grounds displayed almost no differentiation across Eurasia. This is consistent with the mixing of ducks from different breeding populations and at odds with scenarios based on ringing data. Higher genetic population structure in maternally inherited mtDNA than in biparentally inherited nuclear DNA provided also evidence that dispersal in *A. fuligula* is biased towards males. We conclude that extensive contacts between European and Asian ducks are particularly plausible on wintering grounds - a situation which provides frequent opportunities for the transmission of associated pathogens.

## **Resistance to oxidative stress and body condition in relation to plumage colour, brood size manipulation and carotenoid supplementation**

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Oxidative stress has recently been considered as a proximate cost of reproduction and hence a major constraint in the evolution of life history traits. Additionally, carotenoid-based sexually selected ornaments have been proposed to mirror male ability to resist oxidative stress. However, despite increasing interest in the role of oxidative stress in shaping life-histories, no studies have yet addressed this issue in a natural, free-ranging population of vertebrates using an experimental approach. We performed a full factorial design experiment in a natural population of great tits, which display carotenoid-based yellow colouration. We manipulated brood size, aimed at increasing male reproductive effort, and supplemented males with carotenoids. We then assessed the effects on male condition and resistance to oxidative stress during the nestling rearing period. Enlarging broods size impaired male resistance to oxidative stress after 5 days of increased workload. Carotenoid-supplementation enhanced body condition, but did not affect male resistance to oxidative stress, suggesting a secondary role for carotenoids as antioxidants. Brighter males were more resistant to oxidative stress 15 days post-hatch. This study on a natural population supports the hypotheses that oxidative stress is a proximate cost of reproduction, and that carotenoid-based plumage traits signal resistance to oxidative stress.

## Characterization of $\alpha$ -amylase activity of bruchids and their natural enemies and their in vitro susceptibility to *Phaseolus vulgaris* $\alpha$ -amylase inhibitor

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Starchy leguminous seeds are an important staple food and source of nutrition in many countries. Bruchid larvae (Coleoptera: Bruchidae) are responsible for the greatest post-harvest losses to stored legumes. Genetic engineering has been used to transfer an  $\alpha$ -amylase inhibitor ( $\alpha$ -AI) from the common bean (*Phaseolus vulgaris*) to other leguminous plants and several studies have confirmed its potential to protect the seeds from bruchids. However, there are concerns regarding the effect that expressed insecticidal proteins might have on non-target organisms. Although previous studies have suggested that bruchid parasitoids might get in contact with the  $\alpha$ -AI, this risk on the third trophic level has so far never been assessed.

We have characterized the  $\alpha$ -amylase activity of selected bruchid larvae, as well as host-feeding parasitoid females and larvae, based on their in vitro characteristics: the pH range of maximum activity, their sensitivity to specific inhibitors and their ability to hydrolyze starch from potato, a specific substrate for this activity. Using different relative concentrations of the purified  $\alpha$ -AI, we have constructed dose response curves to determine the dose at which 50% of inhibition occurs (ID<sub>50</sub>) for each species.  $\alpha$ -amylase activity and sensitivity to  $\alpha$ -AI is present in all tested parasitoids, but varies between species and between females and larvae, respectively. Accordingly, all species are potentially affected by  $\alpha$ -AI, but not to the same extent. Based on these results, we will select the most susceptible bruchid parasitoids for subsequent in vivo studies.

## Special procedures for research with biological samples from abroad

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Whenever scientists intend to use organisms or parts thereof from abroad for research purposes, they have to adhere to the access and benefit sharing regulations of the Convention on Biological Diversity CBD. This convention aims at conserving and sustainably using biodiversity. Its less known third fundamental objective consists of the fair and equitable sharing of benefits that arise from the use of genetic resources. This includes the use by academic non-commercial science.

The historical 'free' use of genetic resources of plants, animals and microorganisms has in many cases led to the development of important drugs for the improvement of society's well being. However, this 'free' use of genetic resources is nowadays being perceived as a form of bio-colonialism: Biodiversity rich countries are used as treasure chest for genetic resources and related traditional knowledge. But commercial products are mostly produced in industrialized countries due to technological advantages but without the participation, remuneration or acknowledgment of the country of origin of the genetic resources. The CBD countries have agreed to take measures to regulate and control research on genetic resources. Regardless of a commercial or a non-commercial research purpose, scientists have to adhere to specific guidelines on correct access to biodiversity resources and the fair sharing of benefits.

With a view to help scientists in Switzerland carry out research in an ethically and legally best way, the Swiss Academy of Sciences has elaborated tools on Good Practice. The paper illustrates the Convention's background and illustrates the necessary steps researchers have to take in order to correctly access genetic resources and how to share benefits resulting from non-commercial research.

## Dating the notothenioid radiation

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The radiation of notothenioid fishes in Antarctic waters provides a prime example of an adaptive radiation in the marine environment. During this radiation, notothenioid fishes have evolved a number of exceptional adaptations to the polar environment, including antifreeze glycoproteins and the loss of the heat shock response. A reliable dating of the onset of the notothenioid radiation is essential for the determination of its causes, given that the Antarctic environment underwent substantial climatic changes throughout the Miocene. However, the paucity of fossils in Antarctica has led to very different datings of the radiation that range from 7 - 24 Ma. These estimates are based either on putative, and highly debated, fossils, or on molecular clock estimates alone. Here, we present a multi-marker phylogeny of notothenioid and related teleost fishes that allows the dating of the radiation on the basis of a relaxed molecular clock, non-notothenioid fossils, and phylogeographic separations.

## Effects of an invasive pathogen on distribution and extinction of amphibian populations

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Emergent diseases are a major threat on biological diversity and are proposed as one of the major factors causing world wide decline of amphibians. We used field surveys over two time periods (2004 and 2008) in combination of model comparison approach to investigate the potential impact of the chytrid fungus, *Batrachochytrium dendrobatidis* (Bd), on amphibian species in Switzerland. We asked two main questions: First, does Bd affect the distribution and extinction of amphibian populations in Switzerland? Second, what is the relative role of Bd and other environmental factors (such as habitat characteristics, isolation, temperature and precipitation) influencing amphibian distribution patterns? Here we will present first set of results from these analyses.

## One clutch or two clutches? Alternative reproductive strategies in the European earwig *Forficula auricularia*

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Alternative reproductive strategies may have profound effects on individual fitness and the evolution of behavioural phenotypes. Females of the common earwig *Forficula auricularia* display two reproductive strategies: some individuals lay a single clutch during their lifetime, whereas others produce a second clutch a few weeks after the first one. The aim of this study was to explore phenotypic and behavioural pathways to fitness returns for females producing one or two clutches. Using an experimental population of 580 females, we first investigated the link between the number of clutches produced and female life-history traits such as clutch size, survival of the nymphs and their developmental rate. Then, we investigated which proximate factors relate to clutch number by looking for associations between the strategy adopted by each female and their physical and behavioural (maternal care) traits. Preliminary results indicated that females producing a single clutch had significantly more eggs and offspring in their first clutch than females producing two clutches. Similarly, one-clutch females provided significantly less food to their nymphs (maternal care) and gained less fresh weight during the two weeks following eggs' hatching. Hence, these preliminary results suggest that reproductive strategies are linked with variation in life-history parameters and phenotypic traits of the mothers. Further analyses are currently carried out to gain further insight on reciprocal interactions between alternative reproductive strategies, female fitness returns and behavioural and phenotypic traits of breeding females in the European earwig *F. auricularia*.

## Accounting for a dominant species in habitat distribution models improves predictions on a regional scale

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Species distribution models (SDMs) provide a powerful tool to investigate niche characteristics and dynamics. However, very few SDM studies explicitly include predictors describing biological interactions, even if their importance has been demonstrated. Here, we provide new evidence that biotic interactions play a significant role in defining the niche of species as captured by SDMs. We modelled the occurrence of subordinate species in the low arctic of northern Norway, both with and without a biotic predictor, based on the abundance of a dominant species, *Empetrum nigrum hermaphroditum*. We showed that by incorporating the additional biotic predictor into the SDM of the species, the model performance increased significantly. Furthermore, we linked the results of the improvement brought by the biotic predictor to several plant traits and to the observed co-occurrence pattern of the species. This permitted us to better understand the biotic processes behind the effect of the biotic predictor in the SDM. This study emphasises the need for the more frequent inclusion of biotic predictors in SDMs even at relatively coarse resolutions.

## **In the footsteps of Darwin's son: Using surnames to infer inbreeding and population structure in modern-day Switzerland**

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George Darwin, the second son of Charles Darwin and his cousin Emma, was one of the first to use surnames as a means to infer inbreeding (i.e. mating among relatives) and its potentially negative consequences (inbreeding depression) in humans. Although George then went on to pursue a career in astronomy, population geneticists have further exploited the fact that, at least until recently, surnames behave in a manner that is similar to a Y-linked genetic marker. Using this analogy, they developed a range of tools that allow for the estimation of population structure, migration rates and inbreeding from surname data alone. Here we use the distribution of surnames across all Swiss cantons to estimate the mean level of inbreeding in each of the cantons, and correlate this with a range of other variables. Furthermore, we estimate the level of differentiation among all of the cantons, and test for an effect of both geographic distance and language. Thereby we show how the phonebook can provide a unique insight into the lives and loves of modern-day Switzerland, and how these are being shaped by culture and geography.

## Possible manipulation of maize plant physiology by the Western Corn Rootworm

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Upon herbivory, plants mobilize systemic defenses and may reallocate resources to undamaged parts. The defense responses and resource reallocation can lead to plant-mediated interactions between herbivores that share a common host. Such effects are usually studied in the context of one herbivore species affecting the performance of another species. Here we report on a strong positive plant-mediated intraspecific interaction among spatially and temporally separated western corn rootworms (WCR), *Diabrotica virgifera virgifera*. Using a split-root approach, two parts of the root system of individual maize seedlings were potted in two separated glass vials. WCR larvae were placed on roots from either healthy plants or from plants that had already been infested for four days with WCR larvae on the other half of the roots. We measured larval weight gain after six hours and found it to be considerably higher for larvae fed on previously infested plants compared to larvae fed on healthy plants. As possible mechanisms underlying this improved performance we propose that WCR feeding suppresses the plant defense efficiency or that WCR larvae manipulate the resource allocation of their host and improve the nutritional quality of the roots. We are currently investigating these possible mechanisms by assessing defense gene expression, hormone levels and resource allocation. Elucidating the physiological processes that allow WCR to perform so well on maize will not only contribute to our fundamental understanding of insect-plant interactions, but should also help in the development of novel varieties that can resist the pest.

## To stink or not to stink...

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Human perception is dominated by auditory and visual information. Nevertheless, like other animals, humans emit secretions from several skin glands leading us to expect that these secretions can play a role in the human ability to identify cues, sexual signals or even health indicators. We can therefore raise the question of the importance of body odours in human communication and perception.

Analyzing the axillary sweat of male and female volunteers, we tested here for sex discrimination and recognition of individual odour patterns of six young adults, as well as for gender, age, and individual odour pattern discrimination between four members of a same family. Sweat was sampled using PDMS stir bars placed in the armpit. Each participant was sampled twice, one week apart. Samples were analyzed using GC-MS.

Overall, our results showed that hundreds of components can be found in a single sample. Based on this finding, principal component analysis (PCA) carried out on selected compounds allowed a coherent distinction between unrelated individuals. Similar analysis underlines the possibility of discerning gender, age, and individuals between closely related family members.

Much like fingerprints, odours provide identifying information for humans. Due to genetic, hormonal, metabolic, dietary, psychological, social and environmental influences, the biochemical composition of human skin secretions, resulting in body odours, is very likely an individual signature. Understanding these phenomena may help the cosmetic industry to formulate perfumes that are optimally attractive or even medicine to diagnose human diseases.

## Linking coexistence with genetic distance in arbuscular mycorrhizal fungi

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Ecological interactions within AMF communities is a poorly known topic. Moreover, such interactions at the intraspecific level have probably never been studied. *Glomus intraradices* is an exciting model to conduct this kind of experiments, as it shows large variation between isolates at the genetic, morphologic and ecological level.

We propose a green house experiment using *G. intraradices* that should shed light on the interactions of isolates from one population. We suggest to use three different host plant species (*Allium porum*, *Oryza sativa* and *Plantago lanceolata*). Based on real-time PCR, we aim to measure the relative abundance of each isolate in the plant roots. The main question is whether genetically closely related isolates are more likely to co-exist or whether they strongly compete similar to different species competing for the same niche.

Our experimental design should also give information on several additional points such as: Existence of host preference, dynamic of the colonization and correlation between plant growth and genetic diversity of AMF. The way in which genetic distance between isolates alter their coexistence and plant growth, should provide new insight into AMF diversity and its consequences for ecosystems.

## From food-web architecture to ecological niche

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Food webs are networks that describe who eats whom in a natural system. Despite their complexity and variability, several simple models are able to reproduce their structure. A prominent one is the niche model of Williams and Martinez (2000), which postulates that each species is characterized by: (1) a niche value, (2) a diet centre, and (3) a diet range. All parameters are drawn at random according to some rules. Using these properties, the model produces simulated food webs that are constructed with the constraint that a species consumes all species lying in its diet range.

Here we propose a statistical version of this model that allows a quantitative estimation of all three parameters for each species of an observed food web. This approach results in two innovations: (1) it allows the interpretation of the model parameters with biological information; (2) it sheds new light on the understanding of the ecological niche by providing an operational definition.

## Access to the cleaner wrasse *Labroides dimidiatus* affects indicators of stress and health in resident reef fishes in the Red Sea

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Interactions between the bluestreak cleaner wrasse *Labroides dimidiatus* and its client reef fish are a textbook example of interspecific mutualism. The fact that clients actively visit cleaners and invite inspection, together with evidence that cleaners eat many client ectoparasites per day indeed strongly suggests a mutualistic relationship. What remains unknown is how parasite removal affects the physiology of clients and thereby their body condition, health and immune function. Here we addressed these issues in a field study in Ras Mohammed National Park, Egypt. In our study area, small reef patches are inter-spaced with areas of sandy substrate, thereby preventing many species (i.e. residents, including cleaner wrasses) to travel between the reef patches. This habitat structure leads to a mosaic of resident clients with and without access to cleaners, on which we focussed our study. We found that residents from patches with a cleaner wrasse had higher body condition than residents of patches without a cleaner. However, indicators of stress like cortisol levels and various immune parameters were apparently unaffected by the presence or absence of cleaners. In fact antibody responses were higher in fish without access to cleaners. This suggest that exposure to cleaners decreases the need for active immunity and that this releases resources that might be used for other traits like increased body condition.

## Plant Biomass in a multitrophic diversity experiment

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Productivity as a measure of ecosystem functioning is still widely discussed. Several experimental studies demonstrate positive relationships between plant diversity and plant biomass. Contrary to these findings, our preliminary results from a multitrophic experiment in wildflower strips show a negative effect of species richness on plant biomass. We discuss these results in light of recent theory and their implications for the diversity debate.

## Effect of maternal and offspring growing conditions on life-history traits of four populations of the yellow dung fly

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Climate is a dominant factor affecting many aspects of ectotherms' life. Two-level responses to climate are often evident – local adaptation and phenotypic plasticity. In this study, we raised yellow dung flies from four populations along the European latitudinal gradient in four climatic treatments differing in temperature and photoperiod. To study the interplay between the effects of climate experienced during the maternal and offspring growth as well as local adaptations, the emerging offspring were split into the same climatic treatments, resulting in a full-block design. There was a gradual decrease in the diapause tendency from north to south, and a clear effect of maternal and offspring growing conditions. Higher maternal temperature decreased the diapause tendency in southern populations but increased it in northern populations, a result probably related to the short summer in the north. Furthermore, the combination of long maternal and short offspring photoperiods induced the highest frequency of diapause. This result is supported by the longer development time and higher growth rate of offspring of the northernmost population, which their mothers were raised under the higher temperature, in contrary to other populations. Higher growing temperature of the offspring mitigated to some extent the effects of photoperiod. For example, body size increased with maternal photoperiod in all populations when offspring grew under the lower temperature, but there was no clear effect when offspring were grown under the higher temperature. Finally, egg size and content had little effect on development pointing on the high plasticity levels exhibited by this species.

## Interspecific female mate choice in Lake Victoria cichlids: the role of male nuptial hue

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Sexual selection through female choice based on male nuptial hue has been suggested as a driving force behind speciation in the species flock of Lake Victoria cichlid.

Several experimental studies have addressed the importance of female mate choice in the reproductive isolation between the sympatric species pair of *Pundamilia pundamilia* and *P. nyererei*. This work showed that behavioral mating preferences for conspecific males broke down, when color signals were masked by light conditions, and that female mating decisions, when choosing between hybrid males, were significantly predicted by male coloration. It had so far not been tested experimentally if assortative mating between the two species breaks down, when the interspecific difference in male nuptial hue is masked. We tested this by giving females of both species the choice to spawn either with a con- or heterospecific male in a two-way choice experiment. First, we found that females of both species spent significantly more time near the conspecific male when interspecific differences in hue were visible, whereas this positional preference was lost in females of both species when the differences in hue were masked. Second, we demonstrate that females of both species mated assortatively, preferring con- over heterospecific mates, when interspecific colour differences between males were visible. We further show that once hue was masked between males of the two species assortative mating becomes asymmetric, resulting in a break down of assortative mating in the females of *P. nyererei* but not in *P. pundamilia*.

Our results suggest that divergent female mate choice is instrumental in maintaining reproductive isolation between the sister species; that the species differences in male nuptial hue are required for this, but that other cues are used in ultimate mating decisions by females of one species and that behavioural mating preference and female mate choice do not necessarily match.

## Phenotypic divergence in reproductive traits of three-spine stickleback inhabiting contrasting temperatures

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Parental effects can have important consequences on adaptive divergence and emergence of biological diversity, but are little studied in this context. Parental effects, the effects of a mother's or father's phenotype on offspring phenotype or performance can arise via diverse mechanisms, such as egg size and parental care. Three-spine stickleback, provide an excellent study system for studies on phenotypic divergence in reproductive traits (e.g. maternal investment in egg size and paternal investment in offspring care) and subsequent parental effects. We present the first set of results from a common garden experiment where we studied the effects of environmental temperature and maternal investment on male parental care between stickleback inhabiting cold (13C) and warm (23C) habitats in Lake Myvatn, Iceland.

## Accessing small scale population divergences in the threespine stickleback

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Rapid adaptive radiations are divergences in related lineages, often in response to different ecological habitats, which occur over a short period of time, and rely greatly on standing genetic variation and phenotypic plasticity. The most readily method for individuals and populations to acclimate to changing or new environments is through phenotypic plasticity. However, recent studies also suggest, standing genetic variation plays an important role in species divergence. Whereas mutation relies on new alleles arising and fixating within a population, standing genetic variation utilizes existing allelic variation. This allelic reserve allows for rapid adaptation radiation to ecological changes. Using a known adaptive radiated species, coupled with ecological recordings we can assess relationship between ecological variation, adaptation and other evolutionary processes. Threespine sticklebacks are a model species for studying adaptive radiation based on their ability to rapidly acclimate and adapt to new environments over a wide geographical range. The Belgjaskógur woodlands northeast of Lake Mývatn, Iceland includes over a hundred lakes and ponds of various sizes from a few square meters to over 520 m<sup>2</sup> within 7.5 km<sup>2</sup>. The main objective of this study is to assess the effects of environmental factors on intraspecific diversity. This study is divided into three main parts. We will 1) determine phenotypic diversity of sticklebacks over a small spatial scale in Belgjaskógur woodland using morphometrics techniques 2) develop a genetic structuring comparison of nineteen ponds using neutral genetic markers 3) compare our phenotypic and genetic findings with ecological data to infer potential links to evolutionary processes, including phenotypic plasticity, parallel adaptation, gene flow, and genetic drift

**Biodiversity and systematics of the genus *Macrocarpaea* (Gentianaceae) in southeastern Brazil**

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*Macrocarpaea* is a genus of tropical gentians (herbs, shrubs, and small trees) that occur in the rainforests of the neotropics. There are presently 105 species recognized in this genus and at least six species occur in one of the most botanically rich regions of the world, the Mata Atlântica of Southeastern Brazil. This group of poorly known species is monophyletic and represents the basal most clade of the genus. This study aims to prepare a monograph of these species in addition to studies on the anatomy, micro- and macro-morphology, molecular systematics, karyology, biogeography, and pollination of the group.

## Mate-choice of *Gammarus pulex* and *Gammarus fossarum*

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*Gammarus pulex* and *Gammarus fossarum* are abundant crustaceans in Switzerland, sometimes coexisting within the same streams. Despite large genetic differentiation, the species are morphologically similar.

The mating system of *G. pulex* and *G. fossarum* includes a precopulatory guarding phase during which the male grasps the female and carries her around for some days until she moults. Precopulatory phase and competition to find mates are energetically costly. Therefore choosing a heterospecific partner will result in substantial fitness loss, and there should be strong selection for the ability to distinguish conspecific from heterospecific individuals.

To test this, we conducted mate choice experiments between the two species under laboratory conditions. We showed that heterospecific pairs between *G. pulex* and *G. fossarum* were formed, but conspecific pairing was more frequent. In addition, we found that *G. fossarum* males engaged in more heterospecific pairings than *G. pulex* males. This result could be produced if males generally prefer large females, as *G. pulex* is the larger species. Our findings suggest that *G. fossarum* and *G. pulex* are able to distinguish conspecific from heterospecific individuals, but that other, possibly confounding factors like size also play a role in mate choice.

## Melanic colouration-dependent anti-predator strategies in the barn owl

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Predators might exert an influence on the evolution of a variety of traits involved in predator avoidance and defence. These traits might have co-evolved and thus be correlated with each other. Different selection pressures in different habitats might allow polymorphism in behavioural responses to predators to evolve. It will be interesting to investigate if such behaviour correlates with a trait that is also known to be under pressure from predators, such as colouration. The barn owl (*Tyto alba*) is a suitable study species for this investigation, because it exhibits polymorphism in melanin-based coloration, which is thought to be correlated to a suite of behavioural traits. It is also known that in different habitats, with varying predator pressures, the degree of colouration varies.

Here we investigate anti-predatory behaviour by Barn owl chicks, in relation to spot diameter, a melanin-based colouration trait. The behaviour consists of hissing, to scare a potential predator away, feigning death and aggression towards the observers (potential predators).

We find that broods with larger spot diameter spots hiss more and feign death longer than broods with less spots. At the same time these broods display less aggressive behaviour towards observers at the time of fledging. Thus it seems that chicks with larger spots invest more in signalling than do the chicks with smaller spots, which seem to invest more in direct aggression. Such behaviour might represent different strategies or it could be involved in communication and/or competition between chicks in the nest.

## Effects of anthropogenic pollution on the dynamic and outcome of host parasite interactions

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In nature, organisms experience simultaneously multiple biotic and/or abiotic stressors. One line of thinking is that organisms exposed to chemical stressors lack energy for mounting up defense against parasite attack and therefore become more susceptible to infection (Holmes 1996). However, interactions between stress and disease may be much more complex. Outside stressors may reduce host density and/or host quality having negative effects on parasite transmission and/or parasite reproduction respectively (Lafferty and Holt 2003). Furthermore, genotypic variation of both host and parasite plays a role in the outcome of the interaction. The host parasite model system we work with is a freshwater diatom *Asterionella formosa* and the obligatory, host specific chytrid parasite *Zygoryzidium planktonicum*. Our main question is whether anthropogenic pollution, that specifically affects the host, increases the negative impact of parasitism on host populations. We set up a cross-infection experiment with a 5 x 3 x 2 factorial design: 5 host strains, 3 parasite strains and 2 treatments (control and herbicide). We followed up infection dynamics and calculated the increase of infected host cells over time to estimate parasite impact on the host population. The elemental composition of the 5 host strains under control and herbicide treatment was determined to gain information on host quality. Host strains had higher N:P ratios and lower C:N ratios in the herbicide treatment compared to the controls, which could point to an increased production of detoxification enzymes. Preliminary results indicate that parasite fitness is enhanced when the host is exposed to a herbicide.

## Why are *Oreina* leaf beetles polymorphic?

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Chrysomelid beetles of the genus *Oreina* show remarkable colour polymorphism within and across populations throughout Europe. Often as many as four or five species occur sympatrically within their moist sub-alpine high-forb habitats. Most species are brightly coloured and are able to excrete defensive compounds. The project aims to uncover the selective forces that maintain colour polymorphism despite the expectation of purifying selection by visual predators.

## Stressed surgeonfish like to be cleaned, a manipulation study of mutualistic interactions using a cortisol receptor blocker

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One major challenge in behavioural ecology remains to understand why some animals are more cooperative than others and which mechanism could underlie such variation. Recent studies have indicated that steroid hormones like corticosteroid and testosterone may modulate tendencies that play a role in cooperation like the sensitivities to punishment and reward. Cleaning interactions between the bluestreak cleaner wrasse (*Labroides dimidiatus*) and its client is a textbook example of mutualism and offer the opportunity to test cooperation experimentally. Here we make a start in analysing the effects of the teleost stress hormone on mutualistic interactions between *Labroides dimidiatus* and one of its client, resident to reef patches, the lined bristletooth, *Acanthurus striatus*. In the present study we went to Mersa Bareika in the Red Sea. We captured lined bristletooth that were assigned to either treatment with a slow release implant containing a cortisol receptor blocker (RU-486 in castor oil, N=5) or control (castor oil only, N=6). Fishes were released in their original reef patch and their behaviour in interaction with cleaners was observed at day 2 and 7 after manipulation. RU-486 implanted fish did not differ from control fish in normal social behaviour but showed a tendency to have less and shorter cleaning interactions. This result could not be contributed to less initiative of the cleaner wrasse in engaging interactions with RU-486 implanted fish. Since ectoparasites have been shown to increase cortisol release, a possible interpretation would be that this effect on cortisol may motivate reef fish to seek for cleaner interactions. We currently test this hypothesis further in the field.

## **Strong impact of metapopulation structure on genetic diversity and differentiation in *Daphnia magna***

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Theory predicts that metapopulation turnover with periodic events of local extinction and recolonization will strongly reduce genetic diversity and increase genetic differentiation compared to populations without turnover. However, only rarely has the genetic structure been compared between turnover and non-turnover populations within the same species. In most of its range *Daphnia magna*, a freshwater crustacean, occurs in medium-sized ponds with stable population dynamics, but in the region of the Baltic Sea, it occurs in small ponds with strong turnover dynamics. Here we compare the genetic structure and genetic diversity between samples from seven metapopulation ponds with five non-metapopulation ponds sampled widely across Europe. Using both sequence and microsatellite data from 71 individuals, we find, as expected, significantly lower genetic diversity and significantly higher genetic differentiation in the metapopulation compared to the non-metapopulation samples. This was true despite the fact that metapopulation samples were obtained from a much smaller geographic area, and implies that population structure may be more important than vicinity in space in respect of genetic differentiation and diversity. The discrete demes can be very different in metapopulations and only species with a high dispersal capacity are able to exist in such systems.

## Species distribution and host specificity of acanthocephalan parasites infecting *Gammarus spec.* in Switzerland

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Acanthocephalan parasites have a large effect on host fitness through their ability to castrate and behaviorally manipulate their hosts. In Switzerland, acanthocephala infect gammarids (Crustacea, Amphipoda), ecologically important stream macroinvertebrates.

In this study, we identify acanthocephalan species in Switzerland and describe their geographical distribution and host specificity. We sampled infected *Gammarus spec.* from 18 sites throughout Switzerland and identified parasite species by sequencing a part of the internal transcribed spacer 1 (ITS) of ribosomal DNA. We detected four species of acanthocephala in amphipod hosts. Two of them were common, *Pomphorhynchus tereticollis* which uses fishes as final hosts and *Polymorphus minutus* with bird final hosts. Both parasite species are widespread throughout Switzerland and sometimes co-occur within the same host population.

We found that *Gammarus fossarum* was more frequently infected in the field than *G. pulex*. To experimentally confirm this finding, we conducted an infection experiment. We kept individuals from multiple populations of both host species at a field site with high parasite abundance (*P. tereticollis*). We found that *G. fossarum* was infected much more frequently than *G. pulex*. This finding suggests that the parasites are adapted to the more common host species in Switzerland, *G. fossarum*.

### Signals for selection in different predator regimes of closely related three- spined stickleback, *Gasterosteus aculeatus*, populations

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Predation has the potential to shift morphological traits in different direction which can cause divergent selection, this can lead to speciation. The three-spined stickleback (*Gasterosteus aculeatus*) is an ideally suited system to study ecological speciation, showing a surprisingly large variation in phenotypic traits. Phenotypic traits, which are possibly under selection, were measured from different age classes in two habitats differing in their predator regimes. By analyzing morphological traits such as dorsal and pelvic spine length, standard length (SL) and lateral plate number of different age classes, a shift towards longer spines in older fish in the habitat with high fish predation pressure was detected. As spines are effective in the defence against fish and bird predators, this can be seen as a signal for selection. I also found shifts in plate distribution between the age classes of the high predation habitats. To have lateral plates can be advantageous because it minimizes injuries caused by predators, but it can be also unfavourable, because lateral plates may provide holds for aquatic insects. Accordingly, in a habitat with both high fish and insect predation, sticklebacks with intermediate numbers of plates appear to have a selective disadvantage, as fewer partial plated fish were found in age class two than in age class one. Additionally I found, that spines are more strongly correlated with standard length in the habitat with higher predation indicating the importance of spines as defence traits. Further, the ratio of young fish in the high predation regime was higher. This is another sign for strong selection, which has the potential to change life history strategies.

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