

Interuniversity Doctoral Program in Organismal Biology

Annual PhD Meeting

When?

19 April 2010

Where?

University of Neuchâtel
Faculté des Sciences, UniMail
Rue Emile-Argand 11, Neuchâtel
Aula Louis-Guillaume (F200) (Second floor between D and E-wing)

Registration?

We will have a small desk set-up in front of Aula Louis-Guillaume (F200) (Second floor between D and E-wing). This aula is also the place where we will have our presentations during the day. You will receive a name tag and have time to upload your talk or hang your poster. IF YOU WISH TO HAVE A COPY OF THE PROGRAM ON PAPER PLEASE PRINT IT YOURSELF. WE WILL NOT PROVIDE THEM.

Posters?

A0 portrait (841 × 1189 mm). Our poster sessions will take place in the area in front room T100 (First floor between A and B-wing)

How to get there from the train station by bus?

From the train station you can get bus 7. Please get out at 'Portes-Rouges' and follow the crowd across the bridge and take a right turn when at the end of it. After 100m you will reach UniMail.

How to get there from the trainstation by foot?

If you feel energetic and the weather is good enough for your liking you can walk from the train station to the university, it takes about 10 minutes. Take the stairs at the back of the train station (also the place where the busses depart). This is the Rue des Fahys, go right here (direction Mitsubishi car dealer) and keep following the train track until you come to a viaduct. Go right here and take the little steep road 'up' on the left side when you exit the viaduct. Go left at the crossing on top of the hill and walk 100m until you reach UniMail.

Do I have to take my own lunch?

No, we will prepare a simple lunch (bread, salads) for all participants which is free of charge. Obviously, you can also bring your own lunch or have lunch in the cafeteria of the university at your own expense.

Details?

For more details please see **program**, **talk abstracts**, **poster abstracts** and **participants list** below.

By whom?

The meeting is organized by Jérôme Frei, Tom van Noort and Christiane Bobillier but you have already guessed that after our four-month spam avalanche.

Annual PhD Meeting 2010

Program

08h30	Registration, uploading presentations and hanging posters Open area in front of Room F200 (Aula Louis-Guillaume) (Second floor between D and E- wing)
09h00	PhD presentation: Kevin Farnier Attraction of the parasitoid wasp (<i>Cotesia marginiventris</i>) to herbivore damaged maize plants
09h20	PhD presentation: Therese Pluess Species traits associated with environmental and economic impact of plant pests
09h40	Invited speaker: Dik Heg General and generalized linear models: tips and tricks
10h30-11h05	Poster Session with Coffee (Even numbers) Open area in front of Room T100 (First floor between A and B-wing)
11h10	PhD presentation: Renate Zindel Endosymbionts in a wide range of mite species
11h30	PhD presentation: Caroline Joris Tsetse fly responses to volatile plant compounds
11h50	Invited speaker: Woodbridge A. Foster Has the African Malaria vector <i>Anopheles gambiae</i> become plant-host independent?
12h40-13h55	Lunch break (including lake view) Room T100 (First floor between A and B-wing)
14h00	PhD presentation: Anne Kempel Experimental plant introduction: disentangling the roles of propagule pressure, soil disturbance and life-history traits
14h20	PhD presentation: Shanmugabalaji Venkatasalam Plastoglobules : new destination for molecular farming
14h40	PhD presentation: Leonore Lovis Identification of resistance of the cattle tick (<i>Boophilus microplus</i>) against acaricides
15h00-15h35	Poster Session with Coffee (Odd numbers) Open area in front of Room T100 (First floor between A and B-wing)
15h40	Invited speaker: Jean-Luc Perret Industrial research, a productive ecosystem with complex interaction network and ecological niche switches
16h30-18h00	Apéro Open area in front of Room T100 (First floor between A and B-wing)

Talk Abstracts (in order of appearance)

1. Kevin Farnier

Attraction of the parasitoid wasp (*Cotesia marginiventris*) to herbivore damaged maize plants

FARCE lab, Institute of Biology, Neuchâtel University, Neuchâtel, Switzerland

Maize is the most cultivated cereal throughout the world just before rice and wheat. In 2007, its production was as high as 800 million tons. Although weeds are the first cause of losses in maize crop ($\approx 40\%$), insects also deliver a great contribution, from 10% loss in Western Europe up to 29% in hotspots in Africa. The intensive use of pesticides frequently resulted in the emergence of more resistant insects. Alternatively, integrative pest management strategies consisting of boosting population densities of naturally occurring beneficial organisms, such as predators and parasitoids, are now envisaged. It has been shown that upon herbivore attack, maize plants emit volatile organic compounds (VOCs) into the air able to attract parasitoid wasps, their invaders' natural enemies, to rescue them. However, which are the actual wasp attracting compounds in this extensive blend has not been identified to date.

In this project, we propose to isolate and identify active compounds mediating the attraction of the generalist parasitoid wasps *Cotesia marginiventris* and *Campoletis sonorensis*, emitted by maize plants attacked by *Spodoptera littoralis* caterpillars. The complete odour blend will be fractionated by UPLC, after which bioassays will answer the question which fractions are the attractive ones.

Eventually, finding the attractants would offer a number of possibilities for new pest control methods aiming at artificially attracting parasitoids in the field to protect the crop. In addition, the attractants could be used to trap and monitor wasps in their natural habitat, which would provide new insights in their extraordinary biology.

2. Therese Pluess

Species traits associated with environmental and economic impact of plant pests

Therese Pluess¹, Marc Kenis², Marten Winter¹, Sven Bacher¹

¹ University of Fribourg, Department of Biology, Ecology & Evolution Unit, Ch. du Musée 10, CH-1700 Fribourg, Switzerland,

² CABI Europe-Switzerland, CH-2800 Delémont, Switzerland

Assessing the future impact of alien plant pests is a major challenge in a Pest Risk Analysis (PRA). In the present study we looked for the first time at species traits associated with impact of alien insect pests. Such traits could be used as predictors for economic and environmental impact in PRAs. We collected data describing environmental and economic impact of plant pests. These reports were categorized and scored for each pest. We hypothesized that two sets of species traits, related to i) the individual feeding behavior or to ii) high population densities would be associated with the overall impact level. The two data sets for environmental and economic impact were analyzed with General Linear Mixed Models. We found that environmental impact was higher for insects with asexual reproduction and for insects with a low number of generations per year. For the economic impact level, different traits relating to feeding behavior or population density were relevant in the five different economic sectors that we investigated (agricultural, forestry, orchard, ornamental or storage pests). Our findings will be integrated in the PRA scheme currently being developed in the EU-wide project PRATIQUE (<https://secure.csl.gov.uk/pratique/index.cfm>).

3. Dik Heg

General and generalized linear models: tips and tricks.

Department of Behavioural Ecology, Institute of Ecology and Evolution, University of Bern, Wohlenstrasse 50a, CH-3032 Hinterkappelen, Switzerland

General (GLM) and generalized linear models (GzLM) are widely used in biology, but the interpretation and (graphical) representation of results remains confusing for students starting to use GLM and GzLM. In GLM the response variable follows a normal distribution, in GzLM the response variable follows another parametric distribution (often poisson, binomial or weighted binomial distribution). The model function and appropriate link-functions can be found in excellent recent textbooks, like Norusis (2007: SPSS) and Crawley (2007: R), including elaborate material and examples complementing this lecture. I use an example to show the relationship between GLM and simpler tests like the t-test, essentially showing they are the same, but they follow a slightly different notation and have a different statistical results output format. This is because GLM and GzLM always involve at least two steps (in contrast to e.g. a t-test), which you need to tell the statistical software to show as output: (1) model statement and the fit (e.g. ANOVA or Chisquare Deviance table), (2) parameter (= coefficient) estimates (e.g. intercept, factors and covariates effects estimates). Additionally, (3) you should check the residuals for over-dispersion (similar to the Levene's F-test for unequal variances in the t-test, if significant you use the Welch's t-test - t-test with unequal variances) and (4) might need to adjust the scaling parameter accordingly or chose a different link-function. Finally, I show how you can use (2) to generate appropriate model curve fits to be implemented in your graphics (e.g. by using Excel, R or SPSS).

4. Renate Zindel

Endosymbionts in a wide range of mite species

Renate Zindel and Alexandre Aebi

Agroscope Reckenholz-Tänikon, Research station ART, Reckenholzstrasse 191, 8046 Zürich, Switzerland.

Mites play an important role in biological control: either as control agents or as pests. The reproduction strategy of many arthropods can be manipulated by maternally-inherited intracellular bacteria (e.g. *Wolbachia*, *Cardinium*). Manipulations such as parthenogenesis induction, cytoplasmic incompatibility, feminization or male-killing evolved to ensure infection spread in the host's populations. Endosymbionts can also have effects on longevity and fertility and induce changes in the susceptibility/resistance to natural enemies and chemicals use as pesticides. These bacteria-host interactions can be used to optimize existing control strategies or even to develop new control strategies of pests or disease vectors. We molecularly screened a wide range of mite species of different life styles (phytophagous, predatory and parasitic) for 7 different bacteria (*Wolbachia*, *Cardinium*, *Flavobacterium*, *Rickettsia*, *Arsenophonus*, *Spiroplasma* and *Midichloria*). *Cardinium* and *Wolbachia* were the most common bacteria. *Cardinium* was found to be frequent in mites (60% of species). Infection rates among populations varied from 3 to 83 %. *Wolbachia* infection was rather rare (20% of species), infection rates among populations varied from 7 to 17 %. The aim of this project is identify endosymbiont-host associations to be integrated or used in existing biological control or new strategies respectively.

5. Caroline Joris

Tsetse fly responses to volatile plant compounds

Caroline Joris, Patrick Guerin

Institute of Biology, University of Neuchâtel, CH-2009 Neuchâtel, Switzerland

Tsetse flies are obligate blood feeders transmitting the sleeping sickness in humans and nagana in animals. To survive under unfavourable conditions of Africa between blood meals they seek cover from the sun under vegetation. In recent decades man-made vegetation zones such as conifer, coffee and banana plantations and thickets of the invasive bush *Lantana camara* have been largely colonized by riverine tsetse species as habitats. Flies from such refugia are implicated in sleeping sickness epidemics due to their association with human settlements. Foliage and plant extracts from *Lantana camara* have been proven attractive to three tsetse spp. from different habitats. Plant products provide important resource signals for tsetse flies not only signalling suitable habitats but during host finding as by-products of the metabolism of host animals, mainly ruminants. Gas chromatography analysis of essential oils coupled to electroantennogram recordings have shown how tsetse fly antennae respond to terpenes, aromatic compounds and other volatiles derived from major biosynthetic pathways of plants. Some 35 tsetse chemostimuli were identified from 16 plant spp. consisting mainly of monoterpenes, sesquiterpenes, oxygenated long-chain hydrocarbons and phenols. In the behavioural context monoterpenes are of major interest due to their relatively high volatility. The behavioural responses of tsetse fly spp. of different physiological status and from different habitats to plant compounds and their mixtures are being quantified in a wind-tunnel using video recording in 3D. First results show that monoterpenes on their own and in mixtures both activate and induce upwind flight in tsetse flies.

6. Woodbridge A. Foster

Has the African Malaria Vector *Anopheles gambiae* Become Plant-Host Independent?

Department of Evolution, Ecology, and Organismal Biology, The Ohio State University

The adult females of most mosquito species engage in mixed-diet foraging, obtaining sugar from plant hosts and blood from animal hosts. This makes life complex, because it requires a sequence of feeding decisions and trade-offs that affect fitness. A possible simplifying exception is *Anopheles gambiae*, a strongly anthropophilic mosquito and the most important vector of malaria in Africa. This species is reputed to feed on plants only rarely or not at all, and it can thrive on a diet of human blood alone. If so, attempts to crush malaria by manipulating plant hosts, or by deploying plant volatile chemicals as lures, will be useless. Yet, in the laboratory, it is well known that these mosquitoes feed on sugar, and we have found that sugar has important effects on biting frequency, egg production, and survival. Contrary to general impressions, our recent field study in Kenya demonstrates that sugar-feeding is common in *An. gambiae*, though much more so in males than in females. And in mesocosms allowing extensive flight and nightly blood meals, but lacking sugar sources, mosquitoes of both sexes suffer higher mortalities, and relatively few females become inseminated, despite daily emergence of more mosquitoes. Models based on our data suggest that field populations will crash in the absence of sugar. The identity of the plant species providing the sugar is under investigation.

7. Anne Kempel

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

Anne Kempel, Thomas Chrobock, Markus Fischer & Mark van Kleunen

Institute of Plant Sciences, Altenbergrain 21, 3013 Bern, Switzerland

An important question in ecology is which factors determine successful population establishment of plant species. Identification of these factors is particularly relevant for biological invasions (and also for restoration ecology). It has been hypothesized that the ideal invasive plant should possess life-history characteristics such as fast and profuse germination, rapid growth, adaptive phenotypic plasticity and high competitive ability. Empirical evidence for the role of species traits in invasiveness, however, is still scarce. Moreover, the importance of species traits may depend on environmental factors such as soil disturbance and might be overwhelmed by the introduction history of species, including time since introduction and propagule pressure. These factors are often not known for natural invasions, and therefore their importance can only be assessed by controlled introduction experiments.

We present results of the first experiment that quantifies and disentangles the roles of species traits, soil disturbance and propagule pressure on establishment success. We experimentally introduced 46 ornamental alien and 45 native herbaceous plant species at different propagule pressures (i.e. numbers of seeds) in eight grassland sites with and eight grassland sites without soil tilling. Of these species, we determine the establishment success over the three years of the project, and assess how this relates to propagule pressure, soil disturbance and species traits. To determine the roles of species traits in establishment success, we assessed seed and germination characteristics, growth rates, induced and constitutive resistances, morphological responses to shading and competitive abilities for most of our study species in greenhouse experiments. Our results from the first two years show that seed mass and proportion of germination in the greenhouse are positively associated with germination in the field, whereas propagule pressure, soil disturbance, growth rate and the ability to produce induced and constitutive resistances against herbivores determine establishment success of seedlings.

These results indicate that propagule pressure, soil disturbance and species traits all affect establishment success, but that their relative importance changes over time.

8. Léonore Lovis

Identification of resistance of the cattle tick (*Boophilus microplus*) against acaricides

L. Lovis^{1,2}, J.-L. Perret², J. Bouvier², H. Sager² and B. Betschart¹

¹University of Neuchâtel, Institute of Biology, Laboratory of Parasitology, Switzerland

²Novartis Animal Health Research Center, St-Aubin (FR), Switzerland

The one-host tick *Boophilus microplus* is an important parasite of cattle and the key vector of bovine babesiosis (Texas fever), causing damage in many parts of the world, such as Australia, Mexico, Central and South America. In these countries, acaricides are widely used to control tick infestations, but the abundant use led to a selection of resistant subpopulations. Multidrug resistance of *Boophilus microplus* is spread worldwide. As an example, resistance against organophosphates, synthetic pyrethroids and amitraz, three main classes of acaricides, has developed in most of the South American countries. Resistance to macrocyclic lactones, a more recently used class, seems to be still rare, but present though (e.g. Brazil and Mexico). This PhD project was developed in this context. Its first objective was the comparison of the diagnostic performance of four *in vitro* tests to evaluate the resistance level of ticks to acaricides. Criteria were the stability of the test (data quality), the number of ticks, the quantity of compounds and the time required for testing, the user friendliness and the possibility to apply the test to large scale studies and on field strains. This comparison allowed the selection of one test, the larval tarsal test, for further evaluation of the resistance level of field isolates originating from various countries known to face resistance problems. A four-week in-depth study will be carried out in Colombia for tick collection in June 2010. Tick resistance in this country is described in the literature and reported by farmers, veterinarians and veterinarian authorities. We aim to see whether our results confirm this information.

9. Shanmugabalaji Venkatasalam

Plastoglobules : new destination for molecular farming

Plastoglobules (PGs) are lipid-containing structures present in all type of plant plastids. In chloroplasts they are primarily attached to thylakoid membranes (Kessler *et al.*, 1999). Plastoglobules isolated from chloroplasts are known to contain the prenyl quinones including plastoquinone and phyloquinone and α -tocopherol (Tevini *et al.*, 1985). The proteome of plastoglobules consist of twenty-three proteins (Vidi *et al.*, 2006; Ytterberg *et al.*, 2006). The identified proteins fall into three categories; plastoglobulins/PAP/fibrillins, plastid metabolic proteins and unclassified proteins. The plastoglobulin family in *Arabidopsis* consists of thirteen genes. Eight members of this family were identified in the plastoglobule proteome. There is significant interest in developing transgenic plants as expression factories for biopharmaceuticals, an area commonly referred to as molecular farming (Ma *et al.*, 2005). Plastoglobulin genes are highly conserved throughout the plant kingdom. It is therefore likely that homologous of AtPGLs could be successfully used as targeting vectors in many plant species. Transplastomic plants expressing PGL fusion proteins may potentially produce very high amounts of recombinant proteins. Transgenic chloroplast offer unique advantages in plant biotechnology, including high level foreign protein expression, absence of epigenetic effects

and gene containment due to lack of transgene transmission through pollen (Bock. 2007). In this respect, tobacco would have the advantages of not being a food crop and of being amenable to chloroplast transformation. Therefore we are interesting to make an optimum commercial system for vaccine production by using plastoglobulin.

10. Jean-Luc Perret

Industrial research, a productive ecosystem with complex interaction network and ecological niche switches

No abstract received

Poster Abstracts (in alphabetical order)

1. Daniel Bravo

Understanding the diversity and the metabolism of oxalotrophic bacteria from natural habitats

Daniel Bravo and Pilar Junier

Laboratory of Microbiology, Institute of Biology, University of Neuchâtel, CH-2000, Neuchâtel, Switzerland

Oxalic acid and calcium oxalate are widely distributed among plants, animals, fungi, and bacteria. Oxalic acid often accumulates as a metabolic product in plant cells, most commonly as the insoluble salt "calcium oxalate". Despite its relative insolubility and chemical stability, the accumulation of metal oxalates has rarely been observed in the geological record. This supposes a microbiologically mediated process as the main oxalate sink in natural environments. Oxalotrophic bacteria are able to use oxalate as a source of carbon and energy. These bacteria do not constitute a phylogenetic group but rather a functional group that consists of diverse taxa of microorganisms. Recently, oxalotrophic bacteria have been singled out as one of the main biological components of a novel and underestimated long-term carbon sequestration mechanism: the oxalate-carbonate pathway. In this pathway, oxalotrophic bacteria use the oxalate produced by plants and fungi, leading to the production of carbonate that can precipitate in the form of calcium carbonate in acidic tropical soils developed on carbonate-free parental material. In this study, new strains of oxalotrophic bacteria were identified and enriched from two tropical soils in which the oxalate-carbonate pathway has been detected. Enrichments in solid and liquid media were prepared using soils collected under the oxalogenic trees Verdolago (*Terminalia oblonga*; Bolivia) and Bahera (*Terminalia bellirica*; India), as well as from soils that were not under the influence of the trees (control soils). Evidence of oxalotrophy was obtained through the solubilization of Ca-oxalate as sole carbon source in mineral medium. More than a hundred new strains of oxalotrophic bacteria were isolated. The kinetics of oxalate consumption in the strains is currently studied using microcalorimetric methods. The strains will be identified using the 16S rRNA gene sequence. Additionally, the diversity of oxalotrophic bacteria *in situ* was studied by the amplification of the gene for one of the enzymes involved in the metabolism of oxalate. The gene *frc*, coding the formyl coenzyme A transferase, was used as a functional molecular marker to study the diversity of oxalotrophic bacteria in the same soil samples. PCR products were obtained in samples from both tree-influenced and control soils, indicating that oxalotrophic bacteria are ubiquitous in the soil. Currently, the diversity and abundance of oxalotrophic bacteria are being investigated by denaturing gradient gel electrophoresis (DGGE), sequencing, and quantitative PCR (qPCR) to establish whether oxalogenic trees have an influence on oxalotrophic bacterial communities in their associated soil. The presence of the *frc* gene will also be tested in all the new strains.

2. Thomas Chrobock

Fast and furious: ornamental alien plant species outperform natives in germination characteristics

Thomas Chrobock, Anne Kempel, Markus Fischer and Mark van Kleunen

Institute of Plant Sciences and Oeschger Centre, University of Bern, Altenbergrain 21, CH-3013 Bern

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 exposed 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.

3. Felice Di Lascio

Group living and cooperation in wild living rooks (*Corvus frugilegus*)

Cooperation and group living is widespread among animals and at first glance manhandles the traditional theory of natural selection proposed by Darwin 200 years ago. Animals are predicted to compete among each other and not to cooperate. Explaining cooperation and the maintenance of societies in nature has been one of the major tasks for behavioural ecologists in the last few decades and there are still a lot of unresolved issues. I am interested in cooperation in a broad sense with a

particular interest in how animals manage their relationships within a group. Exactly as fishes evolved gills to survive under water, social animals evolved specific strategies or capabilities in order to resolve the problems they face in their all-day life within their community. I am investigating some of the costs and benefits emerging from sociality as well as the different strategies that are employed to reduce the costs, notably those induced by conflicts, by studying colonies of wild living rooks (*Corvus frugilegus*) around Neuchâtel. This highly social corvid species lives in large colonies during the breeding period and forms flocks throughout the year. Hence, rooks are a particularly well suited species to study conflicts and cooperation in the wild. Furthermore, most recent studies that were interested in the sociality of this species were conducted in captivity and hence, evidence coming from the field is still needed. Finally, during my master thesis work I realised relatively soon that the individuals I observed differed from each other in their behaviour. For instance, some individuals were more reactive toward intruders than others or some males shared more food with their females than "average males", i.e., were more generous. Animal personalities have been defined as consistent behavioural differences between individuals and have been documented in a wide range of species. Astonishingly, the cooperative - uncooperative tendency of individuals, i.e., cooperative personality type, is still a relatively unexplored topic. Hence, I aim investigating whether rooks differ in their tendency to cooperate, whether these differences remain constant across different contexts throughout the year and what implication these differences have for individuals living in a group.

4. Slimane Dridi

Natural selection of learning rules in fluctuating environments

Evolutionary theory is often applied to explain the existence of innate behaviours of animals and other species. Natural selection generally favours innate behaviours that increase the mean fitness and decrease the variance in fitness of their carrier. However, it is well known that a wide range of animals have a learning ability. Then, one can ask the question: how does evolution account for learning behaviours and what kind of learning will be favoured by selection? In this work, we consider different kinds of learning (i.e. different learning rules) and use simulation techniques to test the effects of fluctuating environments on fitness. We use the model of Camerer & Ho (1999) in which learning rules can be differentiated according to three parameters: δ , the weight that is put on foregone payoffs; ϕ , the speed of learning; ρ , the level of forgetting. A goal of this research is to test the influence of these three parameters on the mean and variance of fitness and try to understand what are the evolutionary optimal values of these parameters. We predict that the frequency of environmental changes will affect the fitness of the different learning rules. For example, we expect that "sensitive" learning rules will achieve higher fitness in frequently changing environments. Preliminary results are presented concerning these hypotheses. In further research, we will investigate how the results of this study could be transposed to social behaviours.

5. Bertrand Fournier

Forensic science goes underground: the quest for new bioindicators

Bertrand Fournier^{1,3}, Ildiko Szelecz^{1,2}, Jens Amendt², Edward Mitchell^{1,3}

1University of Neuchâtel, Laboratory of Soil Biology, Neuchâtel, Switzerland

2Institute of Forensic Medicine, Goethe-University, Frankfurt am Main, Germany

3 Wetlands Research Group, WSL, CH-1015 Lausanne

Forensic science studies a variety of cases that are relevant to the legal system. One applicable tool for criminal investigations is the use of forensic entomology to estimate the PMI (=post mortem interval). But a decomposing cadaver also changes the environment belowground. In our study we investigate the effect of a decomposing cadaver on the underlying soil and whether these changes can be used as a possible tool in forensic science. Soil fauna does respond to changes in environmental conditions and therefore we investigate species composition and density of targeted groups of soil fauna underneath a decomposing cadaver. In parallel, we analyze physical, chemical and biological variables in the litter and soil samples in order to understand the environmental condition changes.

We collected samples starting in August 2009 from litter and soil underneath a decomposing pig, a fake pig (= bags filled with soil) and a control from three sites in a deciduous forest in Neuchâtel. The pig as showed in various studies is most acceptable as a model for the decomposition of a human corpse. The sampling will continue until complete soil resilience.

The main questions in our study are: 1) Can we use a taxonomic group for forensic investigations- are they an applicable tool? 2) How long does it take until the soil communities go back to normal? 3) What are the variables that have the strongest influence on the soil communities?

6. Erica Fumagalli

Cumulative cultural dynamics and demography: a coevolutionary approach

Culture is a major force in human evolution. Innovations such as agriculture, social organization, and other technologies have increased the vital rate of humans. Maladaptations, on the other hand, encompass customs and practices that may decrease it. Cultural traits therefore are likely to affect human population growth. Changes in size and composition of population, in turn, are itself crucial for the evolution and the accumulation of technology and maladaptations. But our knowledge of such demographical dynamics is still limited as most models so far rely on simple assumptions. Here, we develop a mathematical model in which technologies and by-product maladaptations are invented by individual learners, easily copied and used by social learners, and transmitted across generations. Because culture is a public good, costlier to produce than to imitate, the

interaction between individuals producing and copying culture can be regarded in term of a game theoretic trade-off. We study the effect of this trade-off on the coevolution between cultural dynamics and population size. In so doing, we let individuals interact in subdivided populations of finite size, which are subject to demographic and environmental stochasticity. We then analyze the effects of the emerging cultural dynamics on local and global population carrying capacities.

7. Fatma Gomaa

Biodiversity, Taxonomy, Phylogeny, and biogeographical distribution of testate amoebae

Fatma Gomaa, Edward Mitchell

Research in the past twenty years has shown that the largest part of the eukaryotic tree is constituted by unicellular organisms, most of which are commonly designated as protists. Yet, the phylogenetic and evolutionary relationships between these organisms are still not well understood. One of the major problems affecting the phylogenies in many branches is undersampling, which seriously biases the phylogenies at the branch scale, and furthers the whole picture of the tree. Here, we aim to 1) Place some unclassified testate amoeboid taxa in the eukaryotic tree. 2) Assemble molecular data based on gene analysis to contribute in the reconstruction of the Arcellinida tree. Our study of the Arcellinid diversity will lead us to shed light on some aspects of their evolution, i.e. 3) Evaluate the co-evolutionary relationships between testate amoebae and their endosymbionts.

8. Steffen Hagenbucher

Reduced foliage herbivory in *Bt* cotton benefits phloem-feeding insects

Steffen Hagenbucher¹, Dawn Marie Olson², John Ruberson³, Felix Wäckers⁴ and Jörg Romeis¹

¹ Agroscope Reckenholz-Tänikon Research Station ART, Reckenholzstr. 191, 8046 Zurich, Switzerland

² Crop Protection and Management Research Unit, USDA-ARS, Tifton, GA 31793, USA

³ Department of Entomology, University of Georgia, Tifton, GA 31794

⁴ LEC, Centre for Sustainable Agriculture, Lancaster University, Lancaster LA1 4YQ, UK

Genetically modified cotton plants that express Lepidoptera-active toxins from *Bacillus thuringiensis* (*Bt*) are grown on 15 million hectares worldwide. Numerous studies have established that these plants pose a negligible risk to non-target arthropods due to the narrow spectrum of activity of the expressed toxins. However, potential indirect effects of *Bt* cotton have received little attention. We have thus studied the natural inducible defence mechanisms of cotton, specifically the induction of plant terpenoids, and whether they are affected by the introduced insecticidal trait. We hypothesize that the reduced damage caused by caterpillars in *Bt* cotton would lead to a lower concentration of cotton terpenoids. This could leave the plant vulnerable to attack by other herbivores such as aphids, which do not induce a defence response by the plant. We tested this hypothesis by monitoring the population dynamics of cotton aphids (*Aphis gossypii* Glover) on Lepidoptera-damaged and undamaged *Bt*- and non-*Bt* cotton plants in the greenhouse and in a field experiment. As hypothesized, aphids performed better on *Bt* cotton that were less damaged by caterpillars compared to the non-transgenic control plants. In a next step of the project cotton terpenoids will be analysed by HPLC to test whether cotton terpenoids are responsible for the observed differences.

9. Angelos Katsanis

Intraguild predation between Harlequin ladybird *Harmonia axyridis* and European ladybirds

Angelos Katsanis, Laurence Golaz, Dirk Babendreier and Marc Kenis

CABI Europe-Switzerland, 1, Rue des Grillons, 2800 Delémont

Harmonia axyridis is a ladybird of Asian origin that is presently invading Europe. *H. axyridis* is suspected to affect native ladybird populations through intraguild predation and competition for food. As part of a larger risk assessment study, we are presently investigating the intraguild predation between *H. axyridis* and native ladybirds. Our aim is to screen as many native ladybirds as possible, but aphidophagous species are tested in priority because they share their diet with *H. axyridis* and are thus more likely to encounter the invasive species in the field. *Harmonia axyridis* and one of the native species are released in Petri dishes for 24 hours, in the following combinations: first instar larvae against eggs, first instars against first instars and last instars against last instars. Eggs of most indigenous species are more palatable for *H. axyridis* larvae than the reverse, except those of *Calvia quatuordecimguttata*. Competition tests between larvae showed that *H. axyridis* is an asymmetric predator of indigenous ladybirds, particularly in the last instar. A notable exception is *Anatis ocellata*, which often acted as predator of *H. axyridis*. In order to link the results obtained with the underlying mechanisms, we are analysing the chemical compounds of eggs that are not accepted or suitable for *H. axyridis* development.

10. Sébastien Kessler

The sensory ecology of the Afrotropical malaria mosquito, *Anopheles gambiae* Giles

Laboratory of animal physiology, Institute of Biology, University of Neuchâtel, Rue Emile-Argand 11, Case postale 158, 2000 Neuchâtel, Switzerland

The African mosquito *Anopheles gambiae* Giles remains one of the more efficient vectors of human malaria, especially of its more lethal form, caused by *Plasmodium falciparum*. The anthropophilic host preference of this species, as well its endophilic behaviour, guarantees a strong host-vector interaction favourable to a very high intensity of parasite transmission. Olfactory cues are largely responsible for the orientation of mosquitoes. In recent years, an important effort has been undertaken to identify human-specific kairomones that influence host seeking behaviour by female *An. gambiae*. However, despite this species becoming a model for studies on olfactory systems, very little is known about taste organs and contact chemoreceptors in this species, despite their importance in feeding site choice and biting response. The aim of my thesis is to gain insight into gustatory cues for *An. gambiae*, using behavioural, electrophysiological and molecular methods. In a first step, I will try to identify some gustatory stimuli and their associated taste receptor cells and we want localize these contact chemoreceptor cells using microscopy. Electrophysiological and molecular methods will be used to describe how these receptors function. Through this we will try to better understand the sensory ecology and physiology of one of the main vectors of malaria.

11. Sally Koegel

Sorghum bicolor and poplar; two model plants to study gene expression during mycorrhizal symbiosis

Koegel S, Courty PE, Boller T, Wiemken A

Botanical Institute, University of Basel, Hebelstrasse 1, CH-4056 Basel, Switzerland

In view of a sustainable agriculture for the 21st century, the use of conventional nitrogen fertilizer should be reduced in view of its costs and its negative impact on ground water. Plant symbioses are a key to reach this goal. While nitrogen-fixing bacteria are much studied in this respect, we focus on the importance of arbuscular mycorrhizal fungi, which may contribute to an efficient nitrogen uptake by the plants. In the arbuscular mycorrhizal symbiosis, the fungal partner delivers nitrogen and phosphorus to the plant in exchange of photosynthetically fixed carbon. Previous work has highlighted the possibility that inorganic nitrogen, in the form of ammonium and nitrate, may be retrieved efficiently by arbuscular mycorrhizal fungi, and transferred from the fungus to the plant through the "mycorrhizal interface" in the arbuscules. Recent studies have indicated that ammonium transporters of the plant, specifically expressed in the periarbuscular membrane surrounding the fungal arbuscule, may be a key for this process.

Here, our aim is to characterize all members of the ammonium transporter family in the cereal crop *Sorghum bicolor*, and to study the expression of the ammonium transporter genes upon inoculation with different arbuscular mycorrhizal fungi under different nitrogen conditions. *S. bicolor*, the genome of which has recently been sequenced, is one of the world's leading cereal crops, providing food, fibre and fuel across a range of environments and production systems. It has a particular ability to be productive even under strongly adverse conditions, tolerating much more severe drought than most other grain crops.

12. Anush Kosakyan

Barcoding of "Core Nebelas" inferred from COI sequences

Kosakyan A.¹, Heger T.J.^{1,2,3†}, Todorov M.⁴, Mitchell E.A.D.^{1,2,3}, and Lara E.¹

† T. J. Heger and A. Kosakyan have contributed equally to this work.

1. Laboratoire de biologie du sol, Université de Neuchâtel, Rue Emile-Argand 11, Case postale 158, 2009 Neuchâtel, Switzerland.

2. WSL, Swiss Federal Institute for Forest, Snow and Landscape Research, Ecosystem Boundaries Research Unit, Wetlands Research Group, Station 2, CH-1015 Lausanne, Switzerland.

3. Ecole Polytechnique Fédérale de Lausanne (EPFL), Laboratory of Ecological Systems, Station 2, CH-1015 Lausanne, Switzerland.

4. Institute of Zoology, Bulgarian Academy of Science, Sofia, Bulgaria.

The genus *Nebela* (Amoebozoa: Arcellinida) includes many common testate amoebae from soils and semi-aquatic habitats. Only few studies have examined the phylogeny of "core Nebelas" and only one was based on molecular methods (SSU rRNA) used, but with very partial coverage of the described morpho-species. Thus, the phylogenetic relationships among taxa and the definition of species are still largely dependent on morphological characters, which often causes confusion in phylogeny, taxonomy and the debate on biogeographical distribution of taxa. The aim of this research was to improve the phylogenetic frame and the taxonomy of "core Nebelas", in order to facilitate their potential use as bioindicators in paleo-ecology and environmental monitoring, and contribute to answering question on the global biodiversity and distribution patterns of these organisms. The relationship within "Core Nebelas" was studied using mitochondrial cytochrome oxidase I (mtCOI) sequences from most common species. The results show that genus *Nebela* is highly paraphyletic, and need to be split and redefined into monophyletic assemblages. In addition, it is interesting to notice that genus *Quadrullella* (one of the rare arcellinid genera capable of secreting its own plates) branches within the "core Nebelas".

13. Elvira de Lange

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

Elvira S. de Lange, Thomas Degen and Ted C.J. Turlings

FARCE lab, Institute of Biology, Neuchâtel University, Neuchâtel, Switzerland

Artificial selection of crop plants for increased yield and quality has had a cost for other potentially useful traits, including resistance to herbivores. Restoring defence traits in cultivated plants could be an effective way to combat pests. Besides direct defences, 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 lead to the loss of these indirect defence signals, as is the case for a maize root volatile that is emitted upon feeding by coleopteran larvae 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 *mexicana*, when induced with caterpillar regurgitant, are more attractive to the parasitoid wasp *Cotesia marginiventris* than cultivated maize, *Z. mays* ssp. *mays*. Another common parasitoid of caterpillars that occur on wild and cultivated maize, *Camponotus 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 insight into plant-mediated tritrophic interactions, but may also help in the development of novel crop-protection methods.

14. Christoph Lüthi

Impact of transgenic legumes expressing an alpha-amylase inhibitor on storage pests and their natural enemies

Christoph Lüthi, Fernando Álvarez-Alfageme, Jörg Romeis

Agroscope Reckenholz-Tänikon Research Station ART

Leguminous seeds are an important staple food and source of nutrition in many countries. Bruchid beetles (Coleoptera: Bruchidae) are responsible for the greatest post-harvest losses to stored legumes. A powerful strategy to control bruchid infestations is the combination of plant resistance factors and biological control provided by parasitoids. Potent resistance factors are α -amylase inhibitors (α AI) which inhibit the starch metabolism in sensitive insects. Genetic engineering allows to produce genetically modified (GM) legumes expressing α AI-1 from the common bean (*Phaseolus vulgaris*), which are subsequently protected from the attack by bruchids that are sensitive to this particular inhibitor. However, some bruchid species are not or insufficiently controlled by the GM trait. Thus, a combination of GM legumes with bruchid parasitoids might be a sustainable and effective control strategy. But parasitoids attacking resistant bruchids developing in GM seeds might be exposed to and harmed by the insecticidal trait, resulting in a reduced biological control function.

The main goal of our project is to study the compatibility of α AI-1 expressing chickpeas and cowpeas with common bruchid parasitoids. This includes the characterization of α -amylase activity in the parasitoids as well as tritrophic studies involving the GM seeds, different bruchid species and several parasitoids.

15. Walid Mahrez

Translating the language of histones – 1. Histone 3 Lysine 27 trimethylation

Walid Mahrez, Lars Hennig

Institute of Plant Sciences, Plant Biotechnology, ETH Zurich

Chromatin is a dynamic structure comprised of nucleosome subunits, each of which consists of DNA wrapped around a core of histone proteins. The histone tails, which protrude from nucleosomes, are subjected to a multitude of inherited, reversible, post translational modifications such as acetylation, methylation, phosphorylation, ubiquitylation, poly (ADP-ribosylation) and sumoylation, which facilitate the recruitment of regulatory proteins to distinct genomic regions and thus control gene activity.

Trimethylation of Lysine 27 on Histone 3 (H3K27me3) is an important dynamic modification correlated with stable gene repression that plays critical roles in regulating plant and animal development. These sites are methylated by an evolutionary conserved multimeric nuclear protein complex designed as Polycomb Repressive Complex 2 (PRC2) that has histone methyl transferase activity. H3K27me3 constitutes a recognition site for another group of protein complexes known as PRC1 in animals that confer stable and long-term gene silencing by influencing compaction and affecting the chromatin remodelling. So far, several protein members of such PRC1 complexes have been characterized from both invertebrates (*Drosophila*) and vertebrates (mammals); however, much less is known about PRC1-like functions in plants.

In this project I want to find out how H3K27me3 marks are translated into gene silencing in plants. The major approach is to identify H3K27me3-binding proteins. To achieve this goal, nuclear proteins were prepared from *Arabidopsis thaliana* and subjected to affinity chromatography, using synthetic modified or K27-trimethylated histone 3 peptides as bait. The eluted H3-associated proteins will be identified and analyzed by tandem mass spectrometry. I expect that this procedure will lead to the

identification of new candidates for subunits of plant PRC1 complexes. The identified proteins will be functionally characterized *in vivo* as well as *in vitro*, using a broad spectrum of state-of-the-art biochemical techniques in combination with molecular biology, genetics, and bioinformatics. The results will help to fully appreciate how Polycomb group proteins control development in plants and animals.

16. Cyril Montandon

Analysis of membrane protein complexes in the outer membrane of chloroplasts

Most of the chloroplast proteins are encoded in the nucleus and translated in the cytosol. Toc and Tic complexes (Translocon at the outer membrane of chloroplast and Translocon at the inner membrane of chloroplast, respectively) are the principal protein complexes known to import these proteins from cytosol into the chloroplast. Specificity of the import is assured through the recognition of an N-terminal transit peptide present in the chloroplast precursor proteins. This transit peptide is cleaved after importation. The core components of the Toc complex are two GTPase proteins (Toc159 and Toc33) and one channel protein (Toc75) (ref 1). We used Tandem Affinity Purification and Mass Spectrometry to identify interacting partners of Toc159 (ref 2). We used immunodetection, transgenic expression and bioinformatic prediction to confirm and characterise the most pertinent and promising interaction partners as exemplified in this poster for the LRR protein cPLRR1.

17. Ashok Munusamy Lakshamanan

Finding the new protein interactors of Toc159A

Ashok Munusamy Lakshamanan and Felix Kessler

Laboratory of Plant Physiology, University of Neuchâtel

A large number of chloroplast proteins encoded by nucleus are translocated into chloroplast post translationally through Toc-Tic pathway. The Toc complex comprises of three major components in the chloroplast outer membrane namely Toc159, Toc 34 the GTPase receptors and Toc75 the channel protein. Toc 159 apart from having G and M domains that are responsible for GTPase and membrane anchoring function respectively, it also has a more acidic A domain whose function is unclear. However, A domain is dispensable for the *in vivo* functions of Arabidopsis Toc159. From the works of others and our own group we know that A domain is hyperphosphorylated and also detected free from the membrane attached full length protein. It is our prime interest to study the proteins that interact with Toc159 especially A domain to address the putative functions of A domain in preprotein import into chloroplasts. As a first step in that direction, we performed TAP-tag pulldown coupled Mass spectrometry analysis and shortlisted potential candidates. My interest is to validate the interaction of A domain with a few hot candidates and follow up to find the functional relevance of the interaction. No abstract received

18. Alessandro Occhialini

Localization of AtRMR Receptors in plant cells

Alessandro Occhialini¹, Guillaume Gouzerh¹ and Jean-Marc Neuhaus¹

¹Department of Molecular Biology, Neuchâtel University UNINE

Vacuolar proteins reach the different types of vacuoles in plant cells via the secretory pathway by vesicular transport. It has been demonstrated that many vacuolar proteins are sorted to their final destination by cargo receptors. I will focus on RMR proteins (Receptor Membrane Ring-H2), a family of putative receptors, encoded by six genes in *Arabidopsis thaliana* (AtRMR), probably involved in protein transport to vacuoles. In fact these receptors were identified by their homology to the PA domain (Protease Associated Domain) present in the Vacuolar Sorting Receptors (VSR) which is well known to sort vacuolar proteins.

I study the localization of the different AtRMRs. I have generated constructs carrying different fluorescent protein reporters fused to AtRMRs to test by confocal microscopy. The localization was determined in *A. thaliana* transgenic plants and in *Nicotiana benthamiana* leaves transformed by agro-infiltration. The results obtained in *Nicotiana benthamiana* and *A. thaliana* transgenic plants indicate that AtRMR2 localizes in the membrane of ER. The co-localization with the viral protein p6 (Peremyslov *et al.*, 2004) supports this results.

The localization of AtRMR2 in our laboratory is completely different from the result of Park *et al.*, 2005. In fact they localized the receptors in the prevacuolar compartment and Golgi complex, compatible with the role of AtRMR2 in protein sorting to vacuole. If our localization is confirmed we could make new hypothesis about the role of this protein. Different results were obtained with AtRMR1 which perfectly co-localized with the Trans Golgi network marker SYP61 (Sanderfoot *et al.*, 2000) in *Nicotiana benthamiana*. This supports the role of AtRMR1 in protein transport to vacuole. To confirm the localization transgenic *A.thaliana* plants are being produced. In the last part of my work I also generated different deletion mutants in order to define the role of AtRMR domains in their localization.

19. Antoine Paccard

The genetics of adaptation in quantitative traits in *Arabidopsis lyrata*

In spite of the abundance of literature documenting the ecological shifts in natural population, the specific genes involved in evolutionary responses to changing environment have rarely been identified. There is a gap in our knowledge of the genetic mechanisms responsible for adaptation to environmental changes and this make it impossible to generate testable predictions about the extinction risk for populations forced to evolve in reaction to rapidly changing conditions.

My main project as a Phd student will be an evolutionary genetic experiment that will enable us to bridge the gap between adaptation data and theory questions. Numerous questions are still unanswered today: How many genes govern the relevant traits? What is the distribution of their effect size and what would be their distribution among the genome? Does adaptation to new environments usually involve the same genes and alleles? Does adaptation typically involve pre-existing genetic variation or new mutation? Is the alleles fixed early in the adaptive process greater than the effect of alleles fixed late in the adaptive process? Unfortunately we have no empirical tests of these predictions in nature. Understanding adaptation to this level is doable only for a few traits with a known genetic basis in model organisms like *A. thaliana* and determining which genetic changes are driven by natural selection will greatly aid our understanding and conserving the incredible biodiversity we see in nature.

I am presenting on this poster parts of the research plan I am hoping in following over this Phd. *A. lyrata* will be my study system. First, I will briefly present an experiment that I am currently doing on different populations of *A. lyrata* located in the great lakes area. We will be measuring flowering time and water use efficiency in order to see possible phenotypic correlations and microhabitat correlations. I will present a selection experiment that I will be doing on three important quantitative traits: Flowering time, water use efficiency and cold hardiness. I propose to enforce three selection intensities to investigate whether the strength of selection influences the genetics of adaptation. This experiment will be followed by a study on adaptation in natural population along a latitudinal gradient. I will develop links between habitat types, locally adapted traits and underlying genetics with a main emphasis on the traits described above

20. Christelle Robert

Being resistant in roots but susceptible in leaves

Christelle Robert¹, Matthias Erb¹, Bruce Hibbard³, Matt Higdon³, Joërg Degenhardt², Ted Turlings¹ & Claudia Zwahlen¹

¹ FARCE lab, Rue Emile Argand, 11, 2000 Neuchâtel, Switzerland

² Max-Planck Institute for Chemical Ecology, Hans-Knoll-Strasse 8, D-07745 Jena, Germany

³ USDA-ARS, 205 Curtis Hall, University of Missouri, Columbia, MO 65211, USA

Despite the numerous advances in pest management, the western corn rootworm (WCR), *Diabrotica virgifera virgifera*, is one of the most severe pests in North America. The WCR success can be partially explained by the loss of American maize varieties ability to emit (E)- β -caryophyllene, an attractive compound to WCR natural enemies. The transformation of non-emitting maize lines with a (E)- β -caryophyllene synthase gene from oregano resulted in a constitutive expression of the signal by the plants, and enhanced the effectiveness of biological control agents (Degenhardt et al., 2009).

Here, we report that restoring this belowground defence signal alters the plant susceptibility to leaf herbivores. Despite a similar proportion of infested plants, and similar number of larvae per plant between the emitting and non-emitting lines, the damage area per plant was higher in the emitting lines in field. Collecting the larvae revealed the presence of two main pest species: *Spodoptera frugiperda* and *Ostrinia nubilalis*. We are currently investigating the underlying mechanisms (e.g. feeding stimulants, reduced defence) of this increased susceptibility by conducting laboratory experiments. To date, our results show that *Spodoptera frugiperda* larvae perform better on (E)- β -caryophyllene emitting plants, and plant defence is being characterized. Elucidating the physiological processes that allow aboveground herbivores 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.

Degenhardt J; Hiltbold I; Köllner TG; Frey M; Gierl A; Gershenson J; Hibbard BE; Ellersieck MR; Turlings TCJ (2009): Restoring a maize root signal that attracts insect-killing nematodes to control a major pest. Proceedings of the National Academy of Sciences USA 106, 13213-13218

21. Jonathan Schramm

The hormones involved in AM symbioses?

During the arbuscular mycorrhizal (AM) symbiosis between plants and soil fungi, the morphology of the root system is affected from the global to the subcellular level in a genetically controlled way. It is assumed that specific genes control symbiotic development, possibly some acting at early time points, some at late time points and some during the entire process.

Gene expression during AM development was studied globally by microarray analysis. First, gene expression was followed in two independent time course experiments over the entire symbiotic cycle. Previous studies have shown that phytohormone levels are affected by AM symbiosis, and genetic evidence points to an implication of the hormones ABA, JA, and GA in the process. Here, we assess systematically the transcriptional response of petunia roots to all major hormones. Comparison of the

transcriptional patterns from the AM time course with the hormonal response will allow us to identify transcriptional overlaps that point to an involvement of hormones at specific stages of AM symbiosis.

Clustering and filtering of the expression data by using FiRe and STEM software led to the following major conclusions: numerous genes are strongly and stably activated during the entire AM symbiosis. A number of genes are induced mostly, but not exclusively, at early or late time points. Overlaps between hormone-related and mycorrhiza-related changes in gene expression patterns were searched, both for repression and activation. Genes with a specific pattern appeared to be activated by auxins, and, to a lesser extent, by salicylate and jasmonate. Since genes which overlapped between AM and Me-JA or SA also overlapped with auxins, auxin-like compounds could be enough to explain this transcriptional pattern.

22. Islam Sobhy

Do plant strengtheners increase the attractiveness of maize to parasitic wasps?

Sobhy, I. S.¹, Sarhan, A. A.², El-Husseini, M. M.³, Mandour, N. S.² and Turlings, T. C.J.¹

¹FARCE lab, Institute of Biology, Neuchâtel University, Neuchâtel, Switzerland

²Department of Plant Protection, Faculty of Agriculture Suez Canal University, Ismailia, Egypt

³Department of Economic Entomology, Faculty of Agriculture, Cairo University, El-Giza, Egypt

Host location and selection process, cues associated with the host such as volatile compounds emitted by plants as a consequence of herbivore activities play a role in attracting parasitoids to patches infested with hosts. Therefore, plants under attack can benefit from attracting parasitoids and this herbivore-induced volatile emission is considered to be an indirect induced plant defence. In maize, a number of a biotic and biotic factor can modulate the quality and quantity of the herbivore-induced volatile blend, which in certain cases may have consequences for parasitoid attraction.

Recent studies found that BTH, which is known to induce the plant's defence against pathogens, also enhances the plant's indirect defense, *i.e.* its attractiveness to parasitoids. Furthermore, Laminarin induce the formation of antifungal compounds in alfalfa cotyledons. Nevertheless, the mechanism of BTH in the plant is already well known, while the mechanism of polysaccharides in plant is not fully understood. In our studies we performed series of 6-arm olfactometer experiments using the tri-trophic model consists of *Zea mays*, *Spodoptera littoralis*, and 3 species of endoparasitoids to test the effect of both BTH and Laminarin on the attraction of maize plants to the studied wasps. Furthermore, the volatile emission of maize plants was measured. Four different treatments were tested; *Spodoptera littoralis* damaged plants, artificial damaged plants, undamaged plants and filter paper.

The results indicate that both Laminarin and BTH have a significant effect on the attraction of maize plants infested with *S. littoralis* and artificial damaged plants to parasitoids. Meanwhile, the effect of those materials is regardless in the undamaged plants and the filter paper treatments. Therefore, Both BTH and Laminarin are enhancing the attractiveness of maize plants to the parasitic wasps.

References

(1) Journal of Chemical Ecology 29: 145-162.

(2) Physiological Entomology 29: 45-55.

(3) Biological Control 46:178-186.

23. Sebastian Soyk

Beta-amylases as regulators of gene expression

Sebastian Soyk, Heike Reinhold and Samuel Zeeman

Institute of Plant Sciences, Plant Biochemistry, ETH Zurich

Plant growth and development is underpinned by carbohydrate metabolism. Sugars serve as energy source and substrates for the biosynthesis of major cellular components. The balance between carbon utilisation and storage is important for plant survival and requires a continuous monitoring and adjusting of nutrient availability. Therefore, sugars not only act as nutrients but also as signalling molecules. High levels of sugars repress photosynthesis and induce carbohydrate storage, whereas low levels trigger catabolic processes and a retardation of growth. However, due to the dual role of carbohydrates as an energy source and signalling molecules, it is a challenge to unravel their impact on plant growth, development and stress responses.

Recently, our group identified two β -amylases (*BAMs*) in *Arabidopsis* as potential sugar signalling components. Usually *BAMs* are enzymes which degrade starch to maltose in the chloroplast at night. In contrast, *BAM7* and *BAM8* were shown to localise to the cell nucleus. Both isoforms contain beside their glycosyl hydrolase domain a conserved DNA-binding domain of the BZR1 type, first described in the transcriptional regulators *BES1* (*bri1-EMS-suppressor 1*) and *BZR1* (*BRASSINAZOLE RESISTANT 1*), which are involved in brassinosteroid signalling. Phenotypic analysis of *BAM8* over-expressing plants (*BAM8-OX*) in combination with transcriptional profiling supports the idea that there is interplay between *BAM7/BAM8*-mediated regulation of gene expression and brassinosteroid signalling pathways. Additional findings demonstrate the ability of *BAM8-OX* plants to develop in the presence of high glucose levels, which inhibit the development of the wild type. The observed glucose insensitivity points towards a disturbance of the cellular sugar signalling network, suggesting that *BAM8* plays a role in adjusting carbon utilisation during plant development.

24. Dev Sriram Sriranganadane

***Aspergillus* protein degradation pathways with different secreted protease sets at neutral and acidic pH.**

During growth in a protein medium at neutral pH, *Aspergillus fumigatus* and *Aspergillus oryzae* were shown to secrete neutral and alkaline endoproteases, an X-prolyl peptidase (DppIV) and leucine aminopeptidases (Laps) which are non-specific monoaminopeptidases. Laps cannot remove any amino acids from a peptide N-terminal X-Pro sequence. However, large peptides generated from protein digestion by endoproteolysis can be further digested into amino acids and X-pro dipeptides by the synergistic action of Laps and DppIV.

We have shown that *A. fumigatus* secretes a distinct set of proteases at acidic pH which includes an aspartic endoprotease of the pepsin family (Pep1), tripeptidyl-peptidases of the sedolisin family (SedB and SedD) and a novel prolylpeptidase, AfuS28. Using neuropeptide Y 1-36 and 3-36, we show that Seds degrade peptides from their N-terminus into tripeptides, however Pro in P1 and P'1 position acts as a stop residue. Seds and AfuS28 synergistically digest large peptides with proline residues into amino acids, di- and tripeptides. In a complementary manner, X-X-Pro and X-X-X-Pro sequences can be removed by AfuS28 thus allowing Seds further sequential proteolysis. In conclusion, both alkaline and acidic sets of proteases contain exoprotease activity capable of cleaving after proline residues not bypassed by other exoproteases.

25. Yan Sun

Assessing Ecosystem Impact of and Recovery from Invasive Plants

Yan Sun¹, Urs Schaffner², Heinz Müller-Schärer¹

¹University of Fribourg

²CABI Europe-Switzerland

My PhD project aims to assess the ecosystem impact of and recovery from invasive plants using both biogeographic and community-based approaches. In the biogeographic approach, we will compare ecosystem impact of the same plant species in its native and its introduced range, while in the community-based approach we will compare the impact of invasive and of native dominant species in the same habitat. We will conduct field experiments in habitats that are naturally invaded by exotic plant species, and will also create experimental field plots varying in plant species richness that will be artificially invaded by exotic and native dominant species. The underlying hypotheses are that a) the ecosystem impact of an invasive plant differs fundamentally between its native and its introduced range, and that b) the ecosystem impact of an invasive species differs fundamentally from that of a dominant native species. Furthermore, we predict that c) adding an invasive alien plant species to plant communities in the introduced range results in the shift of ecosystem patterns (e.g. relationship between plant species richness and productivity), while adding the same plant species to plant communities in the native range does not. Field studies will be complemented by pot studies to disentangle the role of the genetics of the invasive species from differences in resident above- or belowground communities as drivers of the expected ecosystem impacts. Provided that either the biogeographic or the community-based approach will reveal different ecosystem impact of invasive and native plant species, we will assess whether variation in eco-physiological within the invasive species or between the invader and the native competitors can at least partially explain the observed results.

In our experiments we will use *C. stoebe* with its three *C. stoebe* geo-cytotypes (diploid European, tetraploid European and tetraploid North American geocytotype) as a model species, but also include a variety of other plant species that have either become invasive in Europe or are native to Europe but have become invasive elsewhere.

26. Marie Vance

Adaptation to Microhabitat in *Arabidopsis lyrata*

No abstract received

27. Tina Wunderlin

Studying diversity of spore-forming microorganisms in natural communities

Tina Wunderlin & Pilar Junier

Laboratory of Microbiology, Institute of Biology, University of Neuchâtel, CH-2000, Switzerland

The study of bacterial endospores has been generally restricted to the domains of medical research and food technology (well-known examples of this are *Bacillus anthracis* and *Clostridium botulinum*). By contrast, the diversity and function of spore-forming microorganisms in the environment is not yet well understood. New species of spore-forming bacteria (i.e. *Carboxydotherrmus hydrogeniformans* Z-2901) and new metabolic functions connected to bacterial spore-formers (e.g. metal reduction) have been reported recently. This suggests that both the metabolic and ecological diversity of spore-forming bacteria is far from being comprehensively assessed. One of the main difficulties when studying spore-forming microorganisms is the inability to specifically target this group within a complex microbial community. Therefore, the aim of this study is to develop a method to effectively separate microbial spores from a complex mix (i.e. including other cells or environmental matrix). So far, a combination of physical and chemical treatments is needed in order to achieve the best results in separation experiments with

known cultivable spore-forming bacteria (*Bacillus subtilis*, *B. megaterium* and *B. alvei*). In addition, the potential to develop specific molecular markers to study the diversity of spore-forming bacteria *in situ* without cultivation is also investigated. A total of 57 genome sequences of spore-forming bacteria were retrieved from genome databases (CMR and IMG), from which 27 genomes are compared to identify a core of genes involved in sporulation. So far, six genes common to all genomes analyzed were identified. Phylogenies based on the common genes for sporulation show few differences with phylogenies based on the 16S rRNA gene. These genes need to be analyzed for the identification of susceptible candidate genes for developing molecular markers to study the diversity of spore-forming microorganisms *in situ*.

28. Shu-Yi Yang

Rice phosphate transporters OsPT11 and OsPT13 are essential for arbuscular mycorrhizal symbiosis

Shu-Yi Yang¹, Caroline Gutjahr¹, Akio Miyao², Hirohiko Hirochika² and Uta Paszkowski¹

¹ Université de Lausanne, Department de Biologie Moléculaire végétale, CH-1015, Switzerland.

² Division of Genome and Biodiversity Research, National Institute of Agrobiological Sciences (NIAS), Tsukuba, Ibaraki 305-8602, Japan.

Many plants obtain phosphate from the soil via the symbiosis with arbuscular mycorrhizal (AM) fungi. In rice we found that two phosphate transporters genes, *OsPT11* and *OsPT13*, are specifically expressed in roots colonized by AM fungi (1, 2). While *OsPT11* belongs to a group of orthologous AM-specific phosphate transporters reported from a number of plant hosts of AM fungi, no homolog for *OsPT13* has been reported from dicotyledonous plants. *OsPT11* is strongly expressed in roots colonized by phylogenetically distant *Gigaspora rosea* and *Glomus intraradices*. In contrast, induction of *OsPT13* is weaker in both symbioses but specificity of expression is comparable to *OsPT11*.

We aim at understanding how these two transporters contribute to symbiotic phosphate uptake of rice plants colonized by different AM fungi and what their relevance is for the formation of the AM symbiosis. *OsPT11* and *OsPT13* can complement the yeast phosphate uptake mutant (PAM2) phenotype, confirming that they encode phosphate translocators. Insertional mutant alleles, perturbing gene expression have been identified for both genes from mutants collection Fungal development of *Glomus intraradices* was significantly reduced in both mutants with *ospt11* displaying a stronger phenotype compared to the *ospt13*. Interestingly, arbuscule morphology remained wild type. Inoculation of both mutants with *Gigaspora rosea* also resulted in a significant reduction of total root length colonization although the effect was less than in the *Glomus intraradices* symbiosis pronounced, indicating that the interaction with *Glomus intraradices* is more dependent on an intact symbiotic phosphate uptake machinery. In summary, these results suggest that both phosphate transporters are necessary for wild type colonization by the respective fungus, but not for the development of arbuscules.

(1) Uta Paszkowski, Scott Kroken, Christophe Roux & Steven P. Briggs (2002) Rice phosphate transporters include an evolutionarily divergent gene specifically activated in arbuscular mycorrhizal symbiosis. *PNAS*, **99**: 13324

(2) Sonia Guimil, Hur-Song Chang, Tong Zhu, Ane Sesma, Anne Osbourn, Christophe Roux, Vassilios Ioannidis, Edward J. Oakeley, Mylene Docquier, Patrick Descombes, Steven P. Briggs & Uta Paszkowski (2005) Comparative transcriptomics of rice reveals an ancient pattern of response to microbial colonization. *PNAS*, **102**: 8066

Participants list (in alphabetical order)

First name	Last name	E-mail	Talk N°	Poster N°
Sanaa	Ayachi	sanaa.ayachi@unine.ch		
Dirk	Balmer	dirk.Balmer@unine.ch		
Benoît	Boachon	benoit.boachon@unine.ch		
Lorelise	Branciard	lorelise.branciard@unifr.ch		
Daniel	Bravo	daniel.bravo@unine.ch		1
Charles	Chappuis	charles.chappuis@unine.ch		
Saran	Cheenacharoen	saran.cheenacharoen@wsl.ch		
Thomas	Chrobock	thomas.chrobock@ips.unibe.ch		2
Felice	Di Lascio	felice.dilascio@unine.ch		3
Slimane	Dridi	slimane.dridi@unine.ch		4
Flavia	Ercolin	flavia.ercolin@unifr.ch		
Kevin	Farnier	kevin.farnier@unine.ch	1	
Woodbridge A.	Foster	foster.13@osu.edu	6	
Bertrand	Fournier	bertrand.fournier@unine.ch		5
Jérôme	Frei	jerome.frei@unine.ch		
Erica	Fumagalli	erica.fumagalli@unine.ch		6
Fatma	Gomaa	fatma.gomaa@unine.ch		7
Alexandre	Gurba	alexandre.gurba@unine.ch		
Steffen	Hagenbucher	steffen.hagenbucher@art.admin.ch		8
Min	Hahn	min.hahn@unifr.ch		
Dik	Heg	dik.heg@iee.unibe.ch	3	
Katrin	Hermann	hermann@ips.unibe.ch		
Sylvia	Humbert	sylvia.humbert@unine.ch	5	
Caroline	Joris	caroline.joris@unine.ch		
Angelos	Katsanis	a.katsanis@cabi.org		9
Anne	Kempel	kempel@ips.unibe.ch	7	
Sarah	Kenyon	sarah.kenyon@unine.ch		
Sébastien	Kessler	sebastien.kessler@unine.ch		10
Sally	Koegel	sally.koegel@stud.unibas.ch		11
Yuppayao	Kophimai	yuppayao.kophimai@wsl.ch		
Anush	Kosakyan	anush.kosakyan@unine.ch		12
Elvira	de Lange	elvira.delange@unine.ch		13
Leonore	Lovis	leonore.lovis@unine.ch	8	
Christoph	Lüthi	christoph.luethi@art.admin.ch		14
Walid	Mahrez	mahrezw@ethz.ch		15
Meryll	Martin	meryll.martin@unine.ch		
Georg	von Mérey	georg.vonmery@unine.ch		
Barbara	Molnar	barbara.molnar@unine.ch		
Cyril	Montandon	cyril.montandon@unine.ch		16
Ashok	Munusamy Lakshamanan	ashok.munusamy@unine.ch		17
Tom	van Noort	tom.vannoort@unine.ch		
Alessandro	Occhialini	alessandro.occhialini@unine.ch		18
Antoine	Paccard	antoine.paccard@unine.ch		19

First name	Last name	E-mail	Talk N°	Poster N°
Jean-Luc	Perret	jean-luc.perret@novartis.com	10	
Chantal	Planchamp	chantal.planchamp@unine.ch		
Therese	Pluess	therese.pluess@unifr.ch	2	
Christelle	Robert	christelle.robert@unine.ch		20
Jonathan	Schramm	jonathan.schramm@unifr.ch		21
Islam	Sobhy	islam.sobhy@unine.ch		22
Sebastian	Soyk	soyks@ethz.ch		23
Dev	Sriranganadane	devsriram.Sriranganadane@unine.ch		24
Egidio	Stigliano	egidio.stigliano@unine.ch		
Yan	Sun	y.sun@cabi.org		25
Marie	Vance	marie.vance@unine.ch		26
Shanmugabalaji	Venkatasalam	venkatasalam.shanmugabalaji@unine.ch	9	
Alexis	Walter	xavier.walter@unine.ch		
Tina	Wunderlin	tina.wunderlin@unine.ch		27
Shu-Yi	Yang	Shu-Yi.Yang@unil.ch		
Isabelle	Zaugg	isabelle.zaugg@unifr.ch		
Renate	Zindel	renate.zindel@art.admin.ch	4	