

Ludwig Maximilians University of Munich



14th Annual DZG Evolution PhD Meeting 2009



Munich Botanical Gardens

March 5th – 8th 2009

General Information

Meeting Venue

Botanical Garden Munich-Nymphenburg
Menzinger Str. 65
80638 München

Oral and Poster Presentations

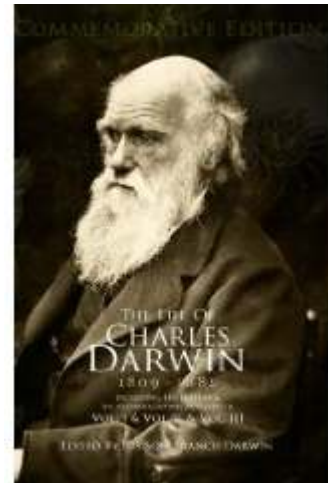
Invited speakers: 60 minutes (45 min plus 15 min for discussion)

Student talks: 15 minutes (12 min plus 3 min for discussion)

Lectures will be held in the Grand Lecture Hall, the location of which will be indicated by signs. Poster sessions will take place upstairs on the first floor around the corner from the entrance staircase. There are two poster sessions, one on Friday from 13:15h-14:15h and on Saturday from 15:15h-16:15h.

Best Talk Award

The best student talk will be awarded with a book prize (200th Birthday edition of *The Life of Charles Darwin*). In order to determine the winner we will do a poll of the entire group. You will find attached in this booklet a form with a list of all the talks, please check off your favourite after the last talk on Sunday. We will then collect all the ballots and announce the winner.



Name Badges

After the meeting we kindly ask you to return your name badges to the boxes provided at the lecture hall exit. If you need any help or

have questions, please feel free to ask any of the organizers or volunteers at the meeting.

Gastronomy: Coffee Breaks and Dinners

There will be coffee, tea, water, juice and snacks provided at all breaks throughout the meeting. There will be a dinner organized on each of Thursday, Friday and Saturday night (see details on locations below). Thursday and Friday are optional and on Saturday is the social event, the cost of which is covered by your registration fee. Dinner also includes one drink, such as beer, wine, cola, juice, etc.

How to get there

By car

Coming by car from the city centre take the Menzinger Straße and follow the road signs towards the motorway (Autobahn) to Stuttgart (A8).

However, once in Munich, we strongly recommend using public transportation due to heavy traffic and limited parking space.

Public Transport

Directions:

The easiest way to get to the Botanical Garden from the city center is by taking a tram (line 17, direction Amalienburgstrasse) from Sendlinger Tor or Hauptbahnhof.

Please see below for maps of trains and trams.

Recommended MVV Tickets:

We suggest: The 3-Day Inner District Ticket = 3 Tage Tageskarte:

Description: If you wish to use the MVV offers for the inner district for several days, either alone or with a group, the 3-day ticket is definitely the right choice for you. The single version is valid for one adult and the partner version is valid for up to five adults. The single ticket for 3-days inner district costs 12.30 EUR,

the partner ticket costs 21.00 EUR. The tickets have to be validated before traveling and are valid until 6 am of the fourth day.

For more information and maps online, see the MVV website at: www.mvv-muenchen.de/en/home/passengeraeinformation/index.html

Organizers and Contact Information

Sonja Grath



Stefan Laurent



Jennifer Lohr



Iris Fischer



Rebecca Meredith



Lisha Naduvilezhath



Anja Hörger



Ricardo Wilches



Rob Morrison



E-mail:

Sonja: grath@biologie.uni-muenchen.de

Stefan: laurent@zi.biologie.uni-muenchen.de

Jennifer: jennifer.lohr@campus.lmu.de

Phone Contact:

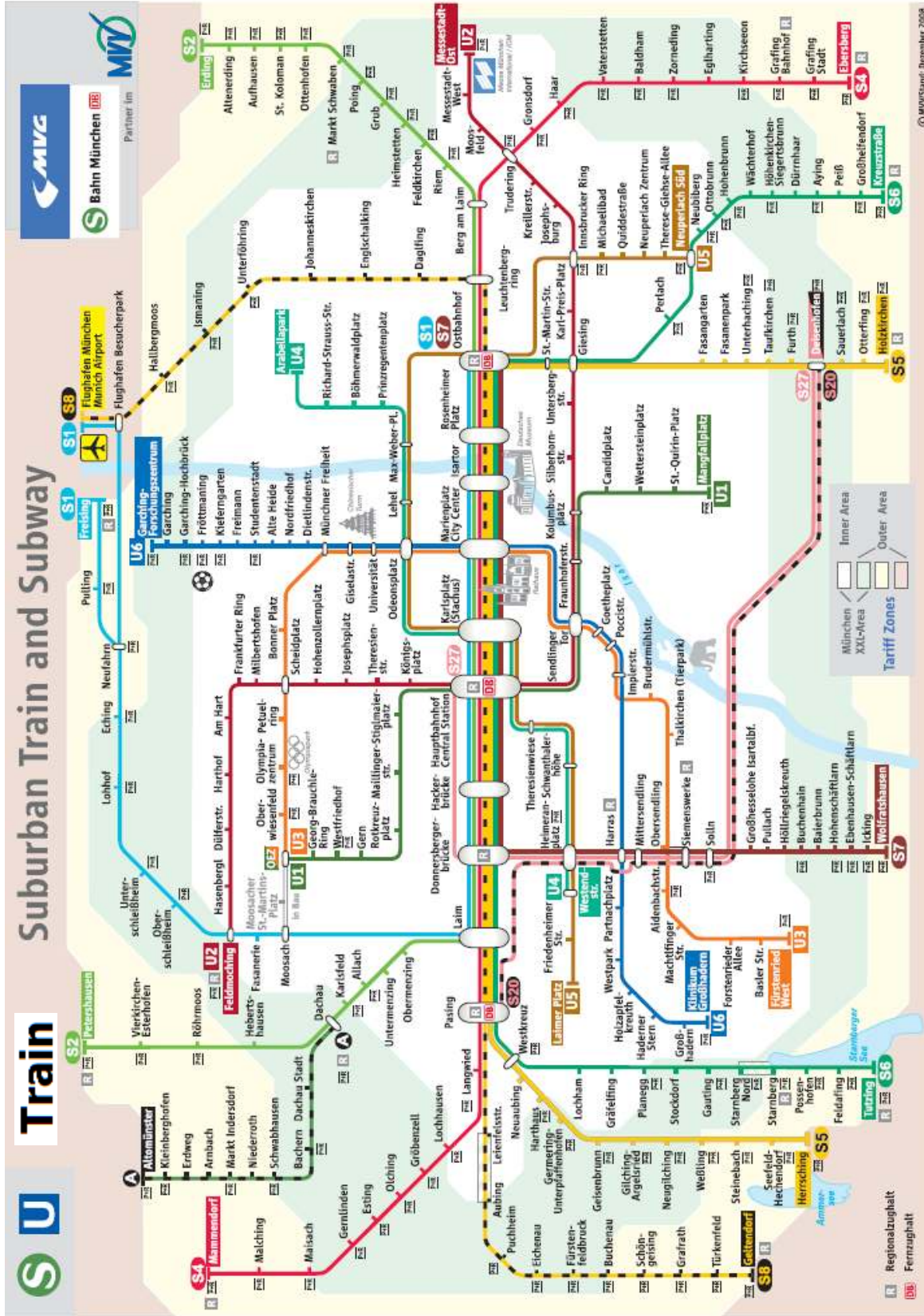
Hotline: +49 (0) 178 / 132-9934

Stefan: +49 (0) 178 / 506-5923

The hotline phone will be available from Thursday through Sunday. Volunteers and Organizers will be wearing labelled badges, so they are easy to spot. Please feel free to ask anyone for assistance at anytime.

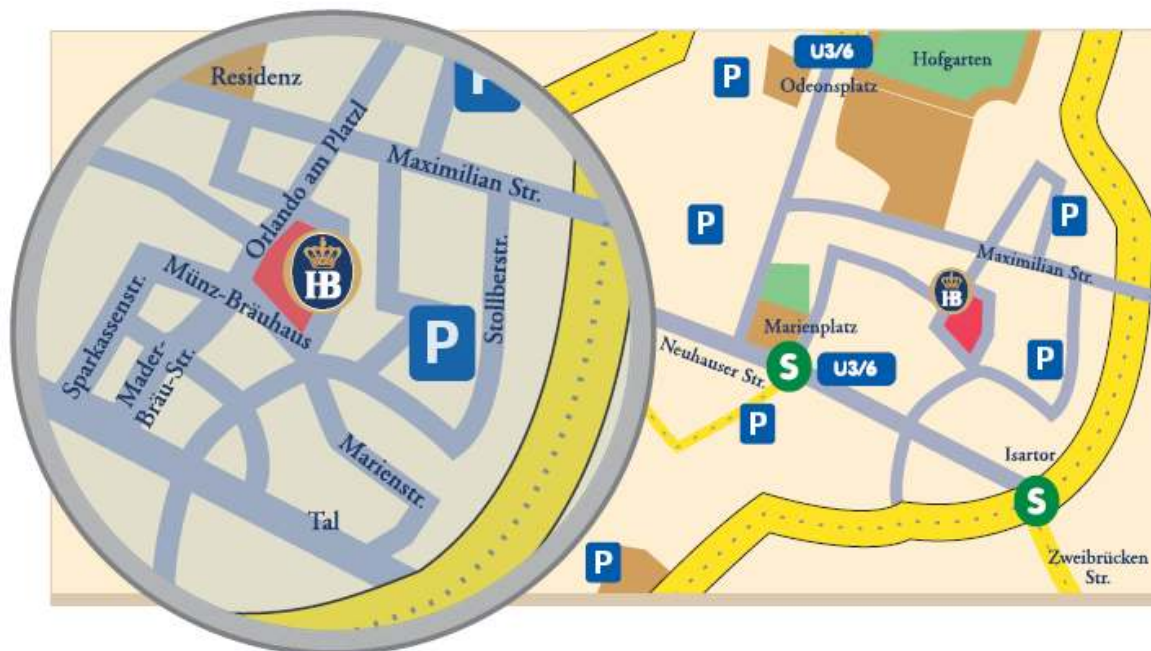
Sponsorship

This meeting is supported by the DZG as well as the LMU Munich graduate program of ecology, evolution and systematics (EES). For more information about the EES program please contact Elisabeth Brunner (brunner@biologie.uni-muenchen.de) or Pleuni Pennings (pennings@lmu.de).

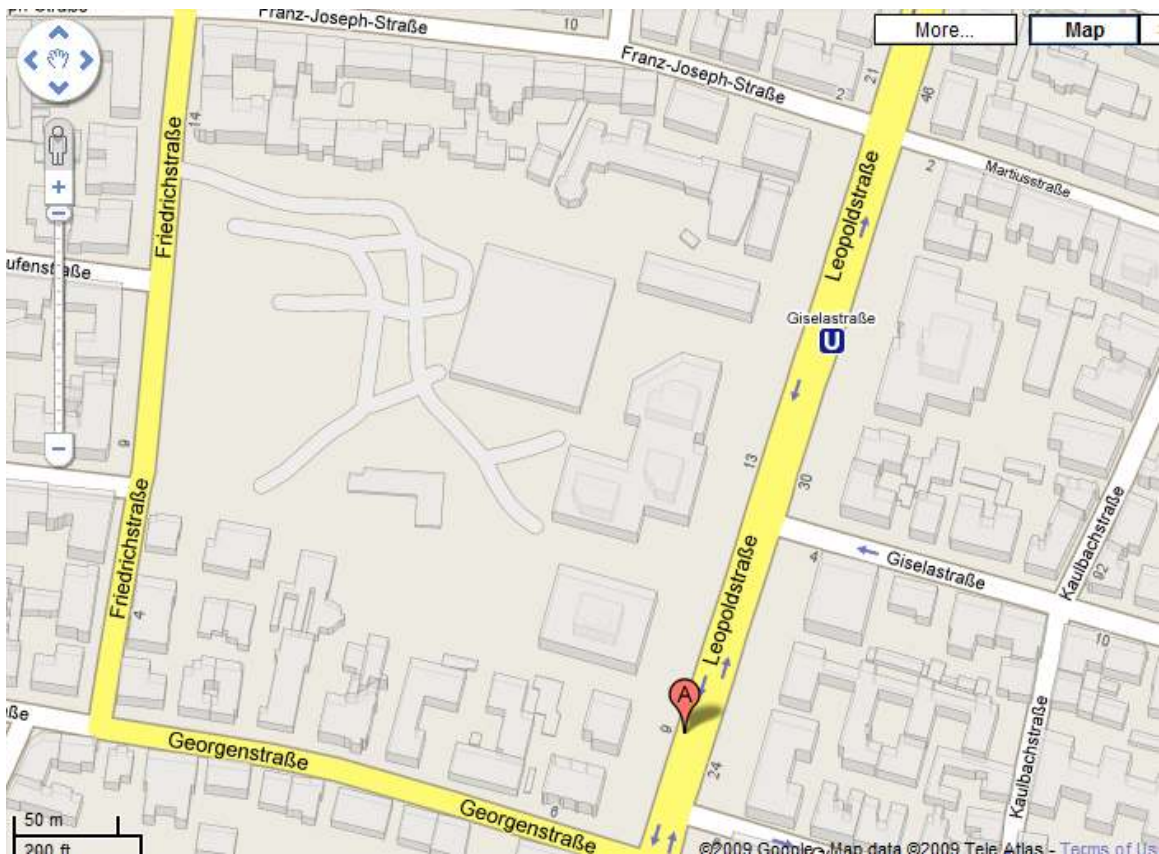


Locations of Planned Dinners:

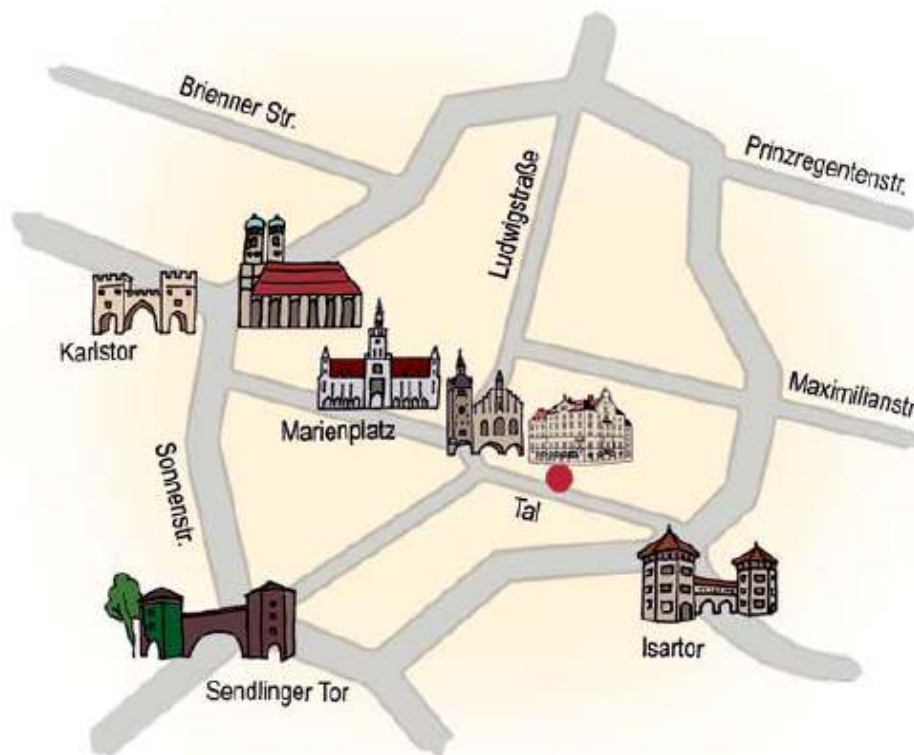
(1) Thursday Night: **19:00 at Hofbräuhaus**, Platzl 9, Central Munich, Altstadt, Near Marienplatz, Subway-Stop: Marienplatz(U3/6) and S-bahn. www.Hofbraeuhaus.de/en/index_en.html



(2) Friday Night: **20:00 Café Munich**, at Leopoldstrasse 9,
Schwabing 80802 = Subway-Stop Gieselastrasse (U3/6).
www.cafemunich.de



(3) Saturday Night: **Social: 19:00 at Weisses Bräuhaus, Tal 7**,
80331 Munich = Subway-Stop Mariensplatz. www.weissesbrauhaus.de



Invited Speakers

The Evolution of Noncoding DNA in *Drosophila*

Penelope R. Haddrill / University of Edinburgh



Making Sense of Mammals: Why Evolution Matters

Olaf Bininda-Emonds / Carl von Ossietzky University of Oldenburg



The Evolution of Chemical Communication in Insects

Dr. Thomas Schmitt / Albert-Ludwigs-Universität Freiburg



General Overview of Time Schedule

Thursday

17h – 19h

Registration and Poster Hanging

19h

Welcome Dinner: Hofbräuhaus
(at own cost)

Friday

9h-9:30h

Late Registration

9:30h-10h

Welcome and Overview of
Schedule

10h-11h

Plenary Talk: Bininda-Emonds

11:15h-12:15h

4 Student Talks

12:15h-13h

Lunch (complementary)

13h-14h

4 Student Talks

14h-14:45h

Poster Session

14:45h-15:45h

4 Student Talks

16h-17h

4 Student Talks

17h

Tour of Botanical Gardens

20h

Dinner at Café Munich (at own
cost)

Saturday

10h-11h

Plenary Talk: Penelope Haddrill

11:15h-12:15h

4 Student Talks

12:15h-13h

Lunch (complementary)

13:00h-14h

4 Student Talks

14:15h-15h

3 Student Talks

15h-15:45h

Poster Session

15:45h-16:30h

3 Student Talks

19h

Social Event: Weisses Bräuhaus
(covered by conference fee)

Sunday

10h -11h		Plenary Talk: Thomas Schmitt
11:15h-12:15h		4 Student Talks
12:15h		Goodbyes

Program of Talks and Events

Thursday March 5th

17h-19h		Registration and Poster Hanging
19h		Welcome Dinner: Hofbräuhaus

Friday March 6th

9h-9:30h		Late Registration
9:30h-10h	Haszprunar	Welcome and Overview of Schedule
10h-11h	Bininda-Emonds	Plenary Talk: Making Sense of Mammals: Why Evolution Matters
11h-11:15h		Coffee Break
11:15h-11:30h	Eitel	The Placozoa – A Unique Model System to Study Basal Metazoan Evolution

11:30h-11:45h	Datzmann	Origin of Morphological Adaptations to a Frugivore Life Style in Bats
11:45h-12h	Rösler	Shaking at Current Opinions on Evolution of Sense Organs in Insects”
12h-12:15h	Rigers	Molecular Evolution of Metallothioneins in Antarctic Teleost Fish (<i>Notothenioidei</i>)
12:15h-13h		Lunch
13h-13:15h	Hutter	X-chromosome vs. Autosomes: Nucleotide and Expression Diversity in <i>Drosophila</i>
13:15h-13:30h	Halligan	High Rate of Adaptive Protein Evolution in Wild Mice
13:30h-13:45h	Rashidi	Evolution of Asymmetric Damage Segregation
13:45h-14:30h		Poster Session
14:30h-14:45h	Gowin	Sex Specificity of Cuticular Hydrocarbons in Bumblebees (Hymenoptera, Apidae)

14:45h-15h	Brandt	Female Response to Male Sex-Pheromone Blends in the Species Complex of the Genus <i>Nasonia</i> (Hymenoptera: Pteromalidae)
15h-15:15h	Leonhardt	Cuticular Terpenoids in Old World Stingless Bees – Role of Trees?
15:15h-15:30h		Coffee Break
15:30h-15:45h	Huber	Communication of The Ant <i>Lasius Platythorax</i>
15:45h-16h	Menzel	Tropical Parabiogenic Ants: Mutualistic Partnership or Parasitic Exploitation?
16h-16:15h	Wurdack	Surprisingly Social – Eusociality in Digger Wasps
16:15h-16:45h	Pohl	Risk Evaluation and Decision Making in Slavemaking Ants
16:45h-17h		Break, End of Day
17h-18h		Tour of Botanical Gardens (Optional) by Rita Verma, Delsy Trujillo and Pablo Duchon
20h		Dinner at Café Munich

Saturday March 7th

10h-11h	Haddrill	Plenary Talk: The Evolution of Noncoding DNA in <i>Drosophila</i>
11h-11:15h		Coffee Break
11:15h-11:30h	Tellier	Coalescence Methods to Estimate Ecological Parameters of Seed Bank and Metapopulation Structure.
11:30h-11:45h	Hörger	Evolution of Pathogen Resistance in the Wild Tomato
11:45h-12h	Westram	Testing for Local Adaptation in a Freshwater Host-Parasite System
12h-12:15h	Kopp	Adaptation of a Quantitative Trait to a Moving Optimum
12:15h-13h		Lunch
13h-13:15h	Franz	Digestion and Methane Production in Herbivores: Is Digestion a Limiting Factor for Body Size
13:15h-13:30h	Werner	Gigantism and Reproduction – One Factor Why Some Dinosaurs Could Reach Such Extreme Body Sizes in Comparison to Terrestrial Mammals?

13:30h-13:45h	von Oheimb	History of Tibetan Plateau Lakes: A Reconstruction Based on the Phylogeography of the Gastropod Genus <i>Radix</i>
13:45h-14h	Kornobis	Groundwater Amphipods Survived Ice Age Underneath Glaciers in Iceland
14h-14:15h		Coffee Break
14:15h-14:30h	Nahavandi	Phylogeography and Rates of Molecular and Morphological Changes in the Ponto-Caspian Amphipod <i>Pontogammarus maeoticus</i> (Sowinsky 1894)
14:30h-14:45h	Germerodt	Breeding Suppression in Small Mammals: a Predator-Induced Coexistence of Strategies?
14:45h-15h	Kingma	Faithful Males do not Bring Flowers: Radical Loss of an Extreme Extra-Pair Mating System
15h-15:45h		Poster Session
15:45h-16h	Clemente	Bayesian Approach to Estimate a Change in θ in a Population

16h-16:15h Krämer Implication of Climate Change on the Susceptibility of the European Lobster (*Homarus Gammarus*): Relationship of the Biofilm and the Survival of Lobster Populations

16:15h-16:30h Deppermann Population Structure of the American Lobster (*Homarus Americanus*)

16:30h End of Day

19h Social Event at Weisses Bräuhaus

Sunday March 8th

10h-11h Schmitt Plenary Talk: The Evolution of Chemical Communication in Insects

11h-11:15h Coffee Break

11:15h-11:30h Heidemann Molecular Gut Content Analyses of Nematode Prey in Soil Microarthropods

11:30h-11:45h Rosenberger High Genetic Divergences in Cytochrome Oxidase One (COI) in the Soil Living Oribatid Mite *Steganacarus magnus* Indicates a Pre-Glacial Colonization of Europe

11:45h-12h	Franzke	When Eating will be Stress – Effects of Extreme Environmental Stresses on Fitness and Morphology in A Field Grasshopper
12h-12:15h	Pennings	Documentary “An Evolutionary Arms Race”
12:30h		End of Day, Goodbyes

Posters: Authors and Titles

Apfelbeck	Territorial Behaviour and Testosterone in Black Redstarts (<i>Phoenicurus Ochruros</i>)
Bank	The Maintenance of Two Incompatible Alleles in a Subdivided Population
Heiler	<i>Dreissena rostriformis bugensis</i> in Germany: Successful Invaders Lacking Genetic Variance
Hinz	Genetical Background and Cellular Mechanisms of Kin Recognition In Zebrafish (<i>Danio Rerio</i>)
Klöpfel	Hybridisation and the Collapse of Behavioural Isolation Barriers
Kobbenbring	Olfactory Imprinting and Kin Recognition in Zebrafish (<i>Danio Rerio</i>)
Morrison & Wilches	Bad or Good Taxonomy: Does it Kill, Can it Save, or is it Just Irrelevant?
Rabus	Growing Large and Bulky in the Presence of the Enemy: An Inducible Morphological Defence in <i>Daphnia Magna</i> against the Predatory Tadpole Shrimp <i>Triops Cancriformis</i>

- Rettelbach Competitive Speciation: Effects of Genetic Architecture and Spatiality
- Sradnick Spatial Analysis of a Grasshopper Hybrid Zone
- von der Chevallerie Patterns of Proliferation In *Trichoplax Adhaerens* (Placozoa)

Plenary Speakers Abstracts

The Evolution of Noncoding DNA in *Drosophila*

Penelope R. Haddrill / University of Edinburgh

Protein-coding DNA comprises only a small fraction of most eukaryotic genomes; the majority of these genomes is comprised of noncoding DNA. Furthermore, the number of genes varies surprisingly little between eukaryotes, whereas the amount of noncoding DNA varies dramatically. It is known that noncoding DNA contains functional elements that control, for example, the level and specificity of gene expression and the regulation of replication. Given these observations, it has been hypothesised that organismal complexity might be more related to the amount and the functionality of noncoding DNA than that of coding DNA. I will discuss various projects examining patterns of evolution in noncoding DNA in an attempt to shed light on the selective and non-selective forces acting on noncoding DNA, using several members of the *Drosophila melanogaster* subgroup as model species. Specifically, I will examine the distribution of functional elements in noncoding DNA and look for the signatures of both negative and positive selection in these regions. I will also discuss evidence for the action of non-neutral process operating on the base composition of noncoding DNA. Finally, I will examine the effect of variation in recombination rate on the evolution of noncoding sequences; since the efficacy of selection is expected to vary with recombination rate, this may therefore shed light on the strength of selection operating on noncoding DNA and go some way towards predicting the function of noncoding elements under selection.

Making Sense of Mammals: Why Evolution Matters

Olaf Bininda-Emonds / Carl von Ossietzky University of Oldenburg

In this talk, I show how employing an evolutionary perspective has led to numerous new insights and even a few surprises concerning mammalian biology and ecology. In particular, I focus on the role played in this regard by so-called supertrees generated from the combination of existing phylogenetic information. Because of the larger size and more comprehensive nature, supertrees have enabled us to test a wider range of hypotheses than before and with greater statistical power. I conclude with a look at the mammalian supertree, a phylogenetic estimate for nearly all living mammals species, and the surprises that this evolutionary tree has already provided us.

The Evolution of Chemical Communication in Insects

Dr. Thomas Schmitt / Albert-Ludwigs-Universität Freiburg

Insects heavily rely on their olfactory senses within species to find mating partners, accept kin or maintain integrity in their social group (pheromones). Therefore, they use highly specific chemicals or compositions of chemicals which provide certain information on the identity and/or quality of a potential mate or kin. Little is known how sexual and natural selection leads to the use of these specific chemical signals by the sender. Between species, insects predominantly use chemicals to find and/or identify their resources (kairomones). It is not well understood how receiver's perception is influenced by change of prey or specialization. My research group uses a variety of model organisms - mainly Hymenoptera and Coleoptera - to study how selection shapes the signal on the sender's side and the specificity of the perception on the receiver's side.

Student Talks Abstracts

Molecular Evolution of Metallothioneins in Antarctic Teleost Fish (Notothenioidei)

Bakiu Rigers, Santovito Gianfranco, Irato Paola and Piccinni Ester
/ University of Padua

Metallothioneins (mts) are low-molecular-weight and sulfur-rich molecules, widely distributed in nature. They play a homeostatic role in the control and detoxification of heavy metals. Previous research indicates that mts have also the capacity to scavenge reactive oxygen species metabolites (ros). Whilst studying the evolution of metallothioneins in teleost, we have investigated mt evolution in a group of teleost fish, namely the notothenioidei. Using molecular biology techniques to characterise the coding region and untranslated regions (5' utr and 3' utr) of metallothionein isoforms, we have examined many species of notothenioids: seven species of the nototheniidae family (*Trematomus hansonii*, *T. newnesi*, *T. eulepidotus*, *T. pennelli*, *T. lepidorhinus*, *Pleuragramma antarcticum* *E. gobbionotothen gibberifrons*), one species from the artedidraconidae family (*histiodraco velifer*) and the last species from the bathydraconidae family (*cygnodraco mawsoni*). The relationships among the different isoforms were inferred by using maximum likelihood (ml) and bayesian methods. Other teleost fish mt sequences (present in genbank) were considered in the phylogenetic analyses. these results indicate that two paralogous mt genes (mt-1 and mt-2) are present in notothenioids. We found several discrepancies between mt gene genealogy and species phylogeny by the comparison of notothenioid mts tree topology and the phylogeny of the considered species. Using paml, we accepted the hypothesis that these genes have been subject to selection pressure different from each other and from the ancestor gene. Additional

research projects, using different methodologies, are in progress with the aim of achieving a more complete picture of mt evolution within this group of organisms.

Female Response to Male Sex-Pheromone Blends in the Species Complex of the Genus *Nasonia* (Hymenoptera: Pteromalidae)

Karin Brandt, Jan Buellesbach, Christopher Greim and Thomas Schmitt / University of Freiburg

Males of the parasitic jewel wasp *Nasonia* (Hymenoptera: Pteromalidae) produce a long-range sex pheromone to attract females. In the cosmopolitan species *N. vitripennis* males synthesize a mixture of (4*R*, 5*R*)- and (4*R*, 5*S*)-5-hydroxy-4-decanolide with a minor compound of 4-methyl quinazoline. In contrast, the sex pheromone of *N. giraulti* and *N. longicornis*, which occur in sympatry with *N. vitripennis* in eastern and western North America, respectively, consists of (4*R*, 5*S*)-5-hydroxy-4-decanolide and 4-methyl quinazoline. (4*R*, 5*R*)-5-hydroxy-4-decanolide occurs if at all than only in traces. Within zones of sympatry, there might be a high probability of interspecific copulations as both species occur microsympatrically, e.g. they even parasitize the same fly host pupae. However, all three *Nasonia* species are infected with *Wolbachia* which cause a cytoplasmatic incompatibility and act as postzygotic hybridisation barrier. This postzygotic hybridisation barrier might drive the evolution of female mate discrimination. In this study we focus on the behavioural response of *Nasonia* females to conspecific and heterospecific male sex pheromones. Therefore, we compare the response of *N. vitripennis* females which live in microsympatry with *N. giraulti* with females from allopatric strains. In order to avoid interspecific mating, females from microsympatric populations are expected to show an increased discrimination against heterospecific male pheromones.

Bayesian Approach to Estimate a Change in θ in a Population Clemente Florian / University of Vienna

The pattern of single nucleotide polymorphisms (SNPs) contains potential information about the demographic history of a population. For instance, population size changes affect the underlying genealogical tree structure which is responsible for a certain pattern in SNP data. This pattern can be observed and permits the estimation of demographic and genetic parameters of a population. One typical parameter of interest is $\theta = 4N_e\mu$, where N_e is the effective population size and μ the neutral mutation rate per generation. If the population undergoes a size change this leads to a change in θ . In this work, we introduce a tool in a Bayesian framework that can detect a population size change at a certain time in the past using SNP data from multiple loci based on the standard model of coalescence theory (R. R. Hudson, 1991). The probabilities of the observed SNP data are calculated depending on a given demographic scenario. Applying the Metropolis algorithm (Metropolis and Ulam 1949, Metropolis et al. 1953), different demographic histories are proposed in an iterative procedure. After sufficiently many iterations, the posterior distribution of the demographic history is approximated which describes the population size change that led to the observed pattern in the SNP data.

Origin of Morphological Adaptations to a Frugivore Life Style in Bats

Thomas Datzmann / University of Erlangen-Nürnberg

Bats of the family Phyllostomidae show a unique diversity in nutrition including taxa that are highly specialised on insects, blood, small vertebrates or birds, fruits or nectar. Such feeding specialisations are usually accompanied by morphological, physiological and behavioural adaptations. Several attempts were made to resolve the phylogenetic relationships within this family in

order to reconstruct the evolutionary shifts and adaptations accompanied by nutritional specialisations. Nevertheless, the evolution of nectarivory remained equivocal. In this study we revealed strong support for diphyly of nectarivorous phyllostomids. Phylogenetic reconstructions, based on a concatenated nuclear- and mitochondrial data set, revealed strong support for the exclusion of the genera *Lonchophylla* and *Lionycteris* from the *Glossophaginae* and an own subfamily - *Lonchophyllinae*. This is remarkable, because their morphological adaptations to diet closely resemble each other. Rostrums are elongated, front teeth are moved, reduced, even lost, the tongues are elongated and they are able to hover in front of blooms. Further, our phylogenetic reconstructions reveal that all mainly frugivorous phyllostomid subfamilies comprising of Rhinophyllinae, Stenodermatinae and Carollinae plus the insectivorous Glyphonycterinae build a monophyletic clade. This suggests a unique origin of morphological adaptations to a frugivore life style within these bats. These relationships also suggest that the Glyphonycterinae evolved insectivory secondarily. In the middle of the Oligocene (32-25~Mya) phyllostomid bats began to exploit new niches. The shift to a vegetarian diet could have triggered the diversification of these bats in many distinct species in the following Miocene (23-5~Mya).

Population Structure of the American Lobster (*Homarus Americanus*)

Jana Deppermann and Gabriele Gerlach / Carl von Ossietzky
University of Oldenburg

The American Lobster, *Homarus americanus*, is distributed along the American East Coast up to the coast of Labrador, Canada. Lobsters mostly inhabit costal waters and are concentrated in rocky areas where shelter is available. Offshore stocks occur along the continental shelf in the vicinity of submarine canyons out to depths of 700m To date, little is known about the impact of both, the

mobile larval stage and the migration behaviour of adults, on connectivity and genetic homogeneity of lobster populations . As the American Lobster is an economically important species it is of crucial importance to provide information about stock structure and population connectivity to ensure a sustainable management. Since the southern populations of the lobster are heavily shell diseased it is important to understand whether migration could spread this disease. To analyze genetic exchange among lobster populations from different locations from the east coast of the US we used newly developed EST (expressed sequence tags) linked microsatellites. EST linked markers are thought to be under selection and might show differences in local adaptation. In some of these markers we found significant genetic differences between populations suggesting limited connectivity and differential selection. The F_{ST} values were up to 10 times higher than in neutral microsatellite markers. Our results show that populations are more structured than previously assumed indicating that larval dispersal might not lead to genetic homogeneous populations.

The Placozoa – A Unique Model System to Study Basal Metazoan Evolution

Michael S. Eitel and Bernd Schierwater / University of Veterinary Medicine Hannover

Placozoans are small disc shaped marine animals. The phylum Placozoa was erected in 1971 by K.G. Grell although the first and only approved species, *Trichoplax adhaerens*, was already described in 1883 by F.E. Schulze. These animals attracted little attention for nearly a century until scientists studied ultrastructural features in the 1970s. Morphological traits like the existence of only four cell types and the lack of any axial organisation always pointed to a very basal position within the Metazoa. With the beginning of the molecular genetics era this view could be supported also from a molecular systematics perspective. The nuclear genome of *Trichoplax adhaerens* and several other

molecular studies gave further hints for a basal phylum Placozoa, which has been debated highly controversially. Within the Placozoa little is known about the phylum composition. Three studies in the last years were able to show genetically clearly separated clades, indicating the existence of several highly distinct species lineages or even higher taxonomic units. With an increasing amount of genetic data and additional morphological analyses one might be able to understand the phylogenetic structure of the Placozoa. Here we report on a comprehensive ‘total evidence’ analyses placing the Placozoa at the very base of diploblastic animals and resolving basal metazoan relationships. We additionally present data on the hitherto unknown placozoan systematics using a combination of morphological characters and mitochondrial and nuclear marker genes.

Digestion and Methane Production in Herbivores: Is Digestion a Limiting Factor for Body Size?

Ragna Franz / University of Zurich

Some characteristics inherent to feeding and digestion in herbivores may set nutritional limits to an increase in body size – and these aspects are essential for our understanding of the digestive physiology, both of extant and extinct herbivorous species. For example, selectivity and therefore diet quality is said to decline considerably with body size, while metabolic losses occurring during fermentative digestion become more pronounced (like e.g. methane losses). In our present study, these effects will be evaluated in a quantitative way, to allow for an extrapolation to body sizes of Sauropods. By using controlled trials the methane production of giant tortoises of different body sizes, a ruminant species (sheep) and three mammalian hindgut fermenting species (Guinea pigs, rabbits and Shetland ponies) was measured in metabolism chambers. The allometry of methane losses was quantified, in relation to food and energy intake and energy metabolism. These results will help to understand the adaptations

we would have to infer for extreme gigantism in terms of digestive physiology, even of the largest herbivores ever, the Sauropods.

When Eating Will be Stress – Effects of Extreme Environmental Stresses on Fitness and Morphology in a Field Grasshopper

Alexandra Franz / University of Bielefeld

Environmental stress can affect nutrients in plants. When insects interact with those plants by eating them, their fitness and morphology can be changed. Out of it my question results, how grasshoppers perform under stressed environments. To answer this question I created a common garden experiment in a greenhouse with three plant stress groups: drought, control, heavy rain. Plants were moistened with three different water additions and grasshoppers were eaten on these plants from hatching until sexual maturity. After last moult and reproduction time of females I contained some fitness and morphological parameters which showed differences between the simulated extreme weather event treatments. Also I recorded courtship songs from males to look how the three regimes affect signaling in males and constrain the sexual selection and mating systems in grasshoppers. Therewith I will start to approach the long-term goal of my project to understand how ecological factors and environmental perturbation may shape mating systems and alter sexual selection and to understand the relative contributions of signaling modalities to the sexual selection process.

Breeding Suppression in Small Mammals: a Predator-Induced Coexistence of Strategies?

Sebastian Germerodt and S. Halle / Friedrich Schiller University of Jena

Breeding Suppression in small mammals, especially voles, is interpreted as an antipredatory behavior. Olfactorial cues of their highly specialized ground predators, *Mustella spec.*, are a possible stimulus to indicate an increased predation risk and initialize this behavior. The mechanism is still unknown. A reduced foraging behavior and decreased energy uptake can obviate pregnancy, but breeding suppression means also lower energy-demands. Non-breeding, obviously, counteracts the principle of fitness-maximization, so this behavior should be a trade-off between actual survival and reproductive value. This system can be interpreted as a coexistence of two distinct behavioral standards, mediated by predator dynamics. A possible explanation is that these strategies differ in their activity-patterns, while a predator visits the patch. The subpopulation of non-breeding females achieve a lower mean predation-risk while it is increased for the breeding ones. Therefore females suppressing breeding shift predation-risk and 'hide' behind the activity of the breeding ones. We try to establish an individual-based model, which compares the outcomes of the two strategies and their self-adjusting frequencies in a metapopulation. Beside the effects of patch- and population sizes of the subpopulations, we investigate the isolation of patches and exchange between them via dispersal of prey on the strategy frequencies.

Sex Specificity Of Cuticular Hydrocarbons In Bumblebees (Hymenoptera, Apidae)

Johannes Gowin, Cordula Neumann and Thomas Schmitt / University of Freiburg

Cuticular hydrocarbons are ubiquitous in insects and function e.g. as desiccation barrier and recognition cues. In a previous study, we could show that cuticular hydrocarbon (CHC) profiles tend to be species specific in bumblebees. Moreover, sex specific differences within the species *Bombus terrestris* have been tentatively disclosed. The qualitative and/or quantitative differences in CHC profiles concerning sex specificity are not yet uncovered. Also the evolutionary history of potential qualitative sex specific differences in the CHC profiles will be investigated by comparison of the CHC profiles with a molecular phylogenetic tree. Therefore, analyses of CHCs of eight species of the genus *Bombus* (Hymenoptera, Apidae) from different clades (*Tharacobombus*, *Bombus*, *Melanobombus*, *Kallobombus*) using gas chromatography coupled with mass spectrometry (GC-MS) were conducted. The results are also discussed towards their significance for mate recognition.

High Rate of Adaptive Protein Evolution in Wild Mice

Daniel L. Halligan, Fiona Oliver, Adam Eyre-Walker, Bettina Harr and Peter D. Keightley

We have inferred the distribution of selective effects of mutations at nonsynonymous sites using polymorphism data for 60 genes collected from 15 wild-caught *Mus mus castaneus* individuals. Our results support the conclusion that *M. m. castaneus* populations are highly polymorphic and therefore imply a very large effective population size. Consistent with this, we infer that selection is highly effective in wild mice, such that > 90% of mutations at nonsynonymous sites are effectively selected against. This value is more similar to that observed in *Drosophila* populations than in humans, where >30% of amino-acid mutations

have been inferred to be effectively neutral. Furthermore, by comparing observed divergence at nonsynonymous sites between *M. m. castaneus* and its close relatives, *M. famulus* and the rat, to that expected, we infer that more than 60% of amino acid substitutions have been driven by positive selection. This also supports the conclusion that the strength of selection acting on wild mice is more similar to that observed in *Drosophila* than in humans.

Molecular Gut Content Analyses of Nematode Prey in Soil Microarthropods

Kerstin Heidemann / University of Goettingen

Predator-prey interactions in below-ground food webs are not very well investigated. Stable isotope analyses and feeding experiments indicate that several soil microarthropod species are not typical decomposer species, e.g. oribatid mites. Those taxa may rather be predators, consuming e.g. Nematoda. The aim of the present study was to investigate if nematodes serve as prey for soil microarthropods. This study aimed at understanding the importance of nematodes for soil food webs, especially to mites. Therefore, in a no-choice laboratory feeding experiment two nematode species (*Phasmarhabditis hermaphrodita* and *Steinernema feltiae*) were offered to nine species of soil mites. In a second field experiment it was investigated if the findings of the laboratory study can be extrapolated to natural field conditions. Hence the two nematode species were dispersed in a beech forest and the number of successful recoveries of the nematode DNA in the gut of potential predators was measured by PCR. *Gamasina* and some oribatid mite species consumed nematodes in the no-choice laboratory experiment whereas other oribatid mite species did not feed on nematodes. *P. hermaphrodita* was generally preferred over *S. feltiae* indicating that *S. feltiae* has a protection mechanism against predation. The field experiment confirmed that soil microarthropod species that have not been assumed to be

predators feed on nematodes. Overall, these findings indicate that predation of nematodes by soil microarthropods is an underestimated parameter of soil food webs and that nematodes are consumed by a wide range of soil microarthropods that have previously been assumed to be typical decomposers.

Evolution of Pathogen Resistance Pathways in Wild Tomato

Anja Hörger, Laura Rose and Wolfgang Stephan / Ludwig-Maximilians University of Munich

Plants face several challenges over their life times by parasitic organisms. The genetic components of signaling pathways involved in plant immunity are now well characterized at the molecular level. Different forms of selective constraints are expected to occur depending on the role and position of genes within a defense response pathway. Since most studies have focused thus far on resistance genes, the most upstream components of disease resistance pathways, little is known about the evolution of downstream components. We used population genetic methods to study and compare the evolution of one upstream and three downstream genes involved in the same defense response pathway in populations of a wild tomato species (*Solanum peruvianum*) from South America. Different evolutionary patterns were observed in these genes. While the upstream gene, which is involved in pathogen recognition, appears to be subject to balancing selection, we found evidence for strong purifying selection acting on two of the downstream genes. At the third downstream gene, we found evidence for purifying selection in some domains and balancing selection in others. We are currently developing functional assays to determine the consequences that variation in these downstream loci imparts upon host defense.

Communication in The Ant *Lasius Platythorax*

S. Huber and V. Witte / Ludwig-Maximilians University of Munich

Several reasons were brought up as to why invasive ants are extraordinarily successful, including small body size, opportunistic nesting, unicoloniality, and parasite release. Our hypothesis considers an additional possibility for the success of these ants, a competitive advantage due to sophisticated communication abilities. To test this, we compared the communication system of a native formicine ant with those of two invasive formicine ant species that had been investigated earlier. Our results support the hypothesis of a more flexible communication system in the invasive species *Paratrechina longicornis* and *Anoplolepis gracilipes*. These two ants similarly have uncoupled the signals for attraction and for orientation in separate pheromone sources, the Dufour gland and the hindgut respectively. Contrarily, in the native ant *Lasius platythorax*, these two signals are combined in one pheromone source, the hindgut. These results suggest that *L. platythorax* cannot react as fast and efficiently to newly discovered food resources. We hypothesize that invasive ants may outcompete native ant species because they are able to forage more efficiently.

X-chromosome vs. Autosomes: Nucleotide and Expression Diversity in *Drosophila*

Hutter, Stephan

Comparing levels of DNA polymorphism between the X-chromosome and the autosomes in *Drosophila melanogaster* leads to surprising observations. Under the standard neutral model the ratio of X-linked to autosomal diversity should be approximately 0.75. Yet, we find that in ancestral African populations this ratio is significantly higher, while in derived non-African populations it is significantly lower. Multiple hypotheses have been proposed to explain this pattern, including demographic history, unequal sex-

ratios, levels of recombination and natural selection. We made use of large scale genome scan data to model demographic history and unequal sex ratios in two *Drosophila melanogaster* populations. While polymorphism patterns in African flies are well explained by our model, non-African flies show unusually low levels of nucleotide polymorphism on the X-chromosome. This suggests the additional action of natural selection in this population. Polymorphism on the gene expression level also shows interesting features. Overall levels of expression diversity are similar between populations, despite the African population having a significantly larger effective population size. This independence of population size can be explained by stabilizing selection governing levels of gene expression. However, expression diversity is consistently lower for X-chromosomes than for autosomes in both ancestral and derived populations. This pattern seems to arise due to the paucity of highly variable male-specific genes on the X-chromosome.

Faithful Males Do Not Bring Flowers: Radical Loss of an Extreme Extra-Pair Mating System

Sjouke A. Kingma, Michelle L. Hall, Gernot Segelbacher and Anne Peters / Max Planck Institute for Ornithology

Mating outside the pair-bond is surprisingly common in socially monogamous birds, but rates of extra-pair paternity (EPP) vary widely between species. Although differences in life-history and contemporary ecological factors may explain some interspecific variation, evolutionary forces driving EP mating remain largely obscure. Also, since there is a large phylogenetic component to frequency of EPP, evolutionary inertia may contribute substantially to contemporary EP mating patterns. However, the relative importance of plasticity and constraints on incidence of EP mating remains largely unknown. We demonstrate extremely low levels of EPP in the purple-crowned fairy-wren, a member of the genus with the highest known levels of EPP in birds. In addition, we show absence of all extreme behavioral and morphological adaptations

associated with EP mating that characterize other fairy-wrens. Phylogenetic parsimony implies that this entire suite of characteristics is lost in concert. Nonetheless, many life-history and breeding parameters that are hypothesized to drive interspecific variation in EPP are not different in the purple-crowned fairy-wren compared to its promiscuous congeners. Such radical loss of an extreme EP mating system with its full complement of adaptations from a lineage of biologically very similar species indicates that evolutionary inertia does not necessarily constrain interspecific differences in EPP. Moreover, if inter-specific variation in EPP is regularly determined by apparently minor interspecific differences, this may be one reason why the evolution of EPP is still poorly understood.

Adaptation of a Quantitative Trait to a Moving Optimum

Michael Kopp and Joachim Hermisson / University of Vienna

A long-standing question in evolutionary biology has been whether adaptation occurs primarily through small or large mutational steps. For adaptation after a sudden environmental change, it has now become clear that evolution to a new optimum involves larger and fewer steps than previously thought. However, little is known about adaptation in a gradually changing environment. We will present a simple population genetics model that can help to address this issue. Under the assumption that the optimal value of a quantitative trait increases at a constant rate, we calculate the expected time to fixation of individual mutant alleles with different phenotypic effects, the order in which mutations of different effects become fixed during short bouts of adaptation, and the distribution of the phenotypic effects of mutations fixed over longer time scales. A common finding in all three scenarios is that mutations are most likely to contribute to adaptation if they have intermediate size. This result can be explained by a trade-off between the initial and final selection coefficients – small mutations are only weakly selected for, whereas large mutations

initially over-shoot the optimum and become beneficial only at a later time. The exact value of the preferred mutational effect size decreases with the mutation rate and the selection strength and increases with the rate of environmental change. Depending on these parameters and on the distribution of new mutations, we can distinguish between cases in which the pattern of adaptive substitutions is determined primarily by either genetic or environmental factors.

Groundwater Amphipods Survived Ice Age Underneath Glaciers in Iceland

Etienne Kornobis and Snæbjörn Pálsson / University of Iceland

Two new endemic species of subterranean freshwater amphipods, *Crangonyx islandicus* and *Crymostygius thingvallensis* were recently discovered in Iceland and described as potential Ice Age sub glacial survivors. *C. islandicus* belongs to family of known subterranean amphipods which has representatives both in North America and Eurasian continent and is widespread in the active volcanic zone of Iceland. Conversely, *C. thingvallensis* defines a new family within amphipods and is rare. We conduct genetic analysis at different levels in order to test the sub-glacial refugia hypothesis, as well as assessing the taxonomic status of those species. Considering *C. islandicus* populations, sequences from the two mtDNA genes (CO1 and 16S RNA) revealed a high haplotype diversity among populations. The correlation between genetic and geographic distances observed between sampling sites implies that these populations diverged within Iceland. Moreover the largest genetic divergence, observed between populations from the North and the South, corresponds to a split around 1 million years ago. Since Iceland was covered by glaciers 10 000 years ago, this confirms earlier conclusion, that this species has survived the glacial periods in subglacial groundwater underneath the lava fields. This two species belonging to the Crangonyctoidae super family, the phylogenetic relationships within this group will be

clarified using nuclear 18S and 28S RNA gene sequences. As the Crangonyctoidae group has representatives in both North America and the Eurasian continent, it may be possible to infer the origins of these two species from the phylogeny and to go further by suggesting colonization scenarios.

Implication of Climate Change on the Susceptibility of the European Lobster (*Homarus Gammarus*): Relationship of the Biofilm and the Survival of Lobster Populations

Philipp Krämer and Gabriele Gerlach / Carl von Ossietzky
University of Oldenburg

The European lobster (*Homarus gammarus*) is part of the German Red List of endangered species. The catch rates around Helgoland collapsed from 80.000 individuals landed per annum before the Second World War to 200 specimens after the last bombardment in 1952. Despite all efforts by intensive breeding and protection programs a recovery of the lobster stock could not be observed. The aim of the proposed project is to analyse different factors underlying this lacking recovery. Changing environmental conditions, particularly, the raising water temperature (2°C above normal) may affect the natural biofilm as well as the susceptibility of juvenile lobsters and thereby decrease the resistance against pathogenic diseases. In my study I will analyse the bacterial load of juvenile lobster in relationship to their growth and survival under varying environmental regimes. I will conduct experiments under natural and controlled conditions in the laboratory to assess the effects of climate change on natural lobster populations. This is the first time climate change induced alterations in the biofilm will be observed regarding their effects on hatchery reared lobster. The project will provide a tool to investigate actual problems by determining the effects of future environmental conditions on the durability and continuity of marine species. The situation will be compared to the situation of the closely related American lobster, *H. americanus* which suffers from a significant increase of a

bacterial disease of the outer shell. Comparably symptoms had been observed for several crustacean species in the European area, including the European lobster.

Cuticular Terpenoids in Old World Stingless Bees – Role of Trees?

Sara Leonhardt, Nico Blüthgen and Thomas Schmitt / University of Würzburg

Stingless bees (Apidae: Meliponinae) have a pantropical distribution and are regarded as important pollinators in tropical ecosystems. Like other eusocial insects, stingless bees have a complex chemical communication system and make use of various chemical compounds for different purposes (e.g. trail following and sex pheromones). So far, the cuticular chemistry of stingless bees has received only little attention and most studies on this subject have been performed in neotropical meliponines. We have investigated the cuticular chemistry of seven stingless bee species from Borneo and have further started to analyze the cuticular chemistry of Australian meliponines. In both bees from Borneo and bees from Australia we found cuticular terpenes which contrasts with findings in New World meliponines. The general composition of the bees' cuticular terpene profiles chemically resembles resin of tree taxa frequently used by the bees for resin collection. Bees from Borneo mainly express sesqui- and triterpenes in their cuticular profiles which are also the main components of dipterocarp resins whereas our analyses revealed different terpenes in the cuticular profiles of several Australian bee species. The latter terpenes were also found in resin from an Australian eucalypt tree. Thus, cuticular terpenoids may be a specific feature of Old World meliponines, but differences in the cuticular terpenoid composition between bees from Borneo and bees from Australia suggests that local tree resin chemistry influences the chemical composition of stingless bee profiles with regard to terpenoids.

Tropical Parabiotic Ants: Mutualistic Partnership or Parasitic Exploitation?

Florian Menzel and Nico Blüthgen / University of Würzburg

Among ants, aggression between different colonies or species is ubiquitous. However, there are exceptions to this rule. Species of the genera *Crematogaster* and *Camponotus* often tolerate each other; associations between species of these genera include the joint exploitation of food resources, trail sharing, and even common nests (parabioses).

In the tropical rainforest of Borneo, parabiotic associations between *Crematogaster modiglianii* and *Camponotus rufifemur* are common. It is still unknown whether these associations are mutualisms, i.e. whether both partners gain a net advantage, or whether one partner exploits the other (commensalism or parasitism). I therefore studied the ecological advantages derived from the associations as well as the chemical and behavioral mechanisms underlying the high interspecific tolerance. My results indicate that parabiotic species of both genera possess highly unusual cuticular profiles. Ants use their cuticular hydrocarbons as recognition cues, i.e. to discriminate between nestmate and non-nestmate. The unusual cuticular substances in parabiotic ants hence may be the cause for the unusually high but exclusive interspecific tolerance between the two parabiotic partners. Moreover, both species seem to profit from the association through mutual benefits during food resource exploitation and nest defence.

Phylogeography and Rates of Molecular and Morphological Changes in the Ponto-Caspian Amphipod *Pontogammarus maeoticus* (Sowinsky 1894)

Nahid Nahavandi, V. Ketmaier and R. Tiedemann / University of Potsdam

The Ponto-Caspian region includes the Black, Azov and Caspian Seas and had undergone a number of dramatic geological changes throughout its history. From 5.8 to 5 million years before present the Black Sea and Caspian Sea depressions became separated and the fauna in each basin evolved independently. Among the crustaceans found in the area, amphipods constitute a major group. *Pontogammarus maeoticus* is the most abundant and widely distributed amphipod along the Iranian coast of the Caspian Sea. Its distribution is not limited to the Caspian Sea, but includes also the Black and Azov Seas, thus embracing the entire Ponto-Caspian area. The species can therefore be considered an optimal guiding organism to test the competing hypotheses available in the literature on the evolution of the Ponto-Caspian fauna. The aims of this study were: to derive an exhaustive phylogeographic hypothesis for *P. maeoticus* across its entire distribution range with the aid of both molecular and morphological data and to determine whether the phylogeographic architecture of the species reflects the geological evolution of the Ponto-Caspian area. Thirteen locations along the southern shorelines of the Caspian Sea and two sites along the western shorelines of the Black Sea were sampled for the study. A total of 103 individuals were screened for sequence polymorphism at two mitochondrial loci (COI and ND5, 622 and 657 bp, respectively). The molecular screening was coupled with a morphometric analysis of twenty-three selected characters. Analyses on separate data partitions identified 51 haplotypes for COI and 30 haplotypes for ND5; the two genes together defined a total of 61 haplotypes. Both morphology and molecules were concordant in identifying a major phylogeographic break between the two sampled basins. This is in remarkable agreement with what

already known for a variety of taxonomically unrelated groups from the same area and highlights the geological evolution of the basins as a major force in determining patterns of biodiversity.

An Evolutionary Arms Race

Pleuni Pennings, Brant Backlund, Robert Sigl, Marion Hartl, Christoph von Beeren, Sofia Lizon, Peter Hayden, Chris Tegg

Did you know that spiders can read ant trails? These spiders and snails in the Malaysian rainforest depend on army ants for housing and food, but the army ants move frequently to new nest sites. This results in tens of thousands of ants marching together to find a new place to live. But if one looks carefully at the marching ants, one can see some surprising things! Volker Witte (LMU Munich) works on army ants in the rainforest near Kuala Lumpur. Volker divides his time between the rainforest (to observe the ants) and the laboratory in Munich (to do modern chemical analysis of smells and trails). He wants to understand how the snails and the spiders have adapted to the ants and what counter-adaptations have evolved in the ants.

Risk Evaluation and Decision Making in Slavemaking Ants

Sebastian Pohl and Susanne Foitzik / Ludwig-Maximilians University of Munich

Collective decision making is important for social insects that live in large and complex societies. But often only a few individuals acquire information relevant for the whole colony. In the host parasite system of the obligate slavemaking ant *Protomognathus americanus* and its *Temnothorax* host species, slavemaker scouts leave their colony to look for host nests. They have to decide whether to attack a host nest or not, taking into account the raiding risk, represented by the defending host workers, as well as the benefit they may gain in terms of raided host pupae. We investigated the occurrence of slave raids, host nest assessment and

the final decision making by the slavemaking ant colony by conducting a series of behavioural experiments in the laboratory. In choice trials we confronted slavemaker colonies with two host nests differing in one demographic factor, i.e. the number of pupae or workers, to analyse which attributes of host colonies are considered by the scouts in their decision process. We found that *P. americanus* colonies show increased raiding activities when the slave: slavemaker ratio inside the slavemaker colony is low, indicating non optimal provisioning being a trigger to start host localisation patterns. *Protomognathus americanus* colonies preferentially attacked large host colonies, whereas they showed no preference for host colonies with more pupae. However, high amounts of host brood combined with low host worker numbers influenced their decision, showing that decision making processes in *P. americanus* do not rely solely on simple yes or no rules, but comprise more complex evaluation results.

Evolution of Asymmetric Damage Segregation

Armin Rashidi, Tom Kirkwood and Daryl Shanley / Newcastle University

Evolutionary origins of ageing are linked to asymmetric segregation of damage at mitosis. Damaged structures that escape degradation tend to form insoluble aggregates and, if the cell survives to divide, will be inherited by the daughter cells. The effects of stochastic fluctuations that arise in small systems with low numbers of aggregates have not been studied before. Furthermore, the contribution of resource allocation trade-offs to evolution of asymmetry is not known. We developed a stochastic model consisting of 1000 unicellular organisms in an environment with limited resources. The mode of damage segregation is subject to random mutations. Cellular events are extrinsic death (due to cell-cell competition for resources), proliferation, damage accumulation, intrinsic death (due to accumulated damage), and mutation in the gene controlling segregation asymmetry. The

segregation coefficient, σ , ranged between 0.5 (each unit of damage has equal chances of ending up in each of the two daughter cells) and 1.0 (all damage segregating into one of the cells) and was averaged over the population. The population was monitored until σ reached a plateau, representing the outcome of evolution. In contrast to previous models, we observed that the entire continuum between symmetry and complete asymmetry were possible outcomes of evolution depending on model parameters. Damage severity, high rates of damage accumulation, and slow proliferation rates are factors that increase the selection force for asymmetry. The results fit the data on three organisms (*S. cerevisiae*, *S. pombe*, and *Candida albicans*) that use different segregation strategies. Given the trade-off between reproductive and maintenance investments, and their same-direction effects on selection pressure, the model highlights the prominent role of environmental stress on evolution of asymmetry.

High Genetic Divergences in Cytochrome Oxidase One (COI) in the Soil Living Oribatid Mite *Steganacarus magnus* Indicates a Pre-glacial Colonization of Europe.

Martin Rosenberger / Technical University of Darmstadt

The last glacial maximum (LGM, ~10-12 kya) had significant impact on the biodiversity of the Northern Hemisphere which has been demonstrated by numerous phylogeographic studies of above-ground and aquatic systems. Strangely, soil-living species have never been investigated, probably because the above-ground patterns have been assumed to be universal. In contrast to above-ground systems, which primarily rest on primary producers, the soil food webs are based on detritus; biotic and abiotic factors are also more stable in soil. The universality of above-ground recolonization patterns is therefore questionable. The oribatid mite *Steganacarus magnus* (Acari, Acariformes, Oribatida) is a Holarctic, soil-living, detritivorous microarthropod. Adults are remarkably cold resistant but larval and nymphal stages depend on

plant material. *Steganacarus magnus* therefore is an ideal model organism to investigate the impact of the LGM on soil-organisms. We collected 128 individuals from 16 countries (31 locations) across Europe and analysed the variation in a 675 bp fragment of cytochrome c oxidase (COI). We identified 91 haplotypes with maximum average p-distances between populations of 28.3 %; maximum within population distances were 16.6 %. High genetic divergences suggest a pre-LGM differentiation of *Steganacarus magnus* and are the highest found for any invertebrate and suggest that its colonisation dates back to the pre-glacial period of Europe. Notably, *Steganacarus magnus* represents a monomorphic species that can be easily recognised. The conserved morphology contrasts with the high genetic variability and suggests high selection constraints on morphology of soil-animals.

Shaking at Current Opinions on Evolution of Sense Organs in Insects

Anja Rösler / Justus Liebig University of Gießen

Auditory receptor organs evolved many times at different positions of the insect body. Within the taxon ensifera, the gryllids and tettigoniids have developed ears at the tibia of the foreleg. But the origin and homology of these auditory systems is discussed for more than a century (Strauß and Lakes-Harlan, 2009). Data from molecular phylogeny suggest a synapomorphic origin of gryllid and tettigoniid tibial ears (Jost and Shaw, 2006), whereas phylogenies based mainly on morphology suggest a convergent origin (Desutter-Grandcolas, 2003). The latter hypothesis is based on neuroanatomical differences between gryllids and tettigoniids. It is further reinforced by recent findings, that many non-hearing tettigoniid taxa have a sense organ homologous to the auditory receptor cells (the crista acustica homolog, CAH; Strauß and Lakes-Harlan, 2009) which might function as a specialized vibration receiver. By contrast, the first phylogeny hypothesis requires a multiple reduction of ears in many different taxa.

Examples of such a reduction can be found within the tettigoniids (Lakes-Harlan et al., 1991), whereby neuronal elements seemed to be more stable against evolutionary transition than accessory structures. Here we investigated the sense organs of a non-hearing gryllid (*Phaeophilacris bredoides*). The results have implications on the hypothesis of reduction of neuronal elements and their function, especially in respect to the theory of convergent evolution of hearing in ensifera. *P. bredoides* has only a few receptor cells in the tibial sense organ. Thus, it seems that strong reduction can also occur in the nervous system. Consequently, the occurrence of a CAH is no indication for hearing reduction in the tettigoniid lineage.

Coalescence Methods to Estimate Ecological Parameters of Seed Bank and Metapopulation Structure.

Aurélien Tellier, Stefan Laurent and Wolfgang Stephan / Ludwig Maximilians University Munich

Wild tomato species, which originated in western South America and the Galapagos Islands, are found in a wide range of habitats, and have thus to cope with various abiotic (e.g. temperature fluctuations, drought) and biotic stresses (e.g. attack by pathogens and herbivores). In order to study molecular signature of adaptation, we develop here first a demographic model taking into account the life history traits of such species, namely seed bank, spatial structure of populations and range expansion. Our aim is to explain the discrepancies between the high effective population size inferred from genetic data and the very small census population sizes observed in nature. Metapopulation structure with restricted migration among demes and seed banks are two well known mechanisms increasing effective population size. Here we estimate parameters of seed banks (germination rate and maximum life expectancy of seeds) and of metapopulation (migration rates) using an Approximate Bayesian Computation framework. We also investigate how bias in the unknown total number of demes in the

metapopulation affects these estimates. Finally, we show how different sampling schemes, population sampling, species wide sample or a mixture of the two, affect the statistical power of inference of the various model parameters.

History of Tibetan Plateau Lakes: A Reconstruction Based on the Phylogeography of The Gastropod Genus *Radix*

Parm Viktor von Oheimb / Justus Liebig University of Gießen

The massive Tibetan Plateau located in central Asia is a key region for controlling climate and environment at regional and global scales. During the Pleistocene epoch (1.8-0.01 Mya), large scale glaciation processes took place in the area. These glaciations influenced the ocean circulations as well as the global climate. Today, about 1,600 lakes with an area greater than 1 km² are distributed over the Tibetan Plateau. The evolutionary and limnological history of these lakes is on the one hand closely related to geodynamics and on the other hand to glaciation and climate. Only from very few lakes, however, rough age estimates are available. The aquatic gastropod genus *Radix* (Hygrophila, Lymnaeidae) is used as a model organism to investigate the history of the Tibetan Plateau lakes. *Radix spp.* are widely distributed on the plateau, and belong to the first invaders of a newly developed lake (e.g. after retreat of a glacier). Specimens of *Radix* from several lake systems were collected on a first expedition to the eastern Tibetan Plateau in autumn 2008. These samples are recently investigated using mitochondrial genes (COI, LSU rDNA) in order to test hypotheses of lake age and formation using phylogenetic and phylogeographic methods as well as molecular clock analyses. Preliminary results show a remarkably high genetic diversity of *Radix* on the plateau either pointing to multiple invasions from different sources or to intra-plateau evolution. The dataset will be extended in future with additional populations from the western plateau and surrounding regions as well as with additional markers in order to obtain a more precise

phylogeographical picture of the Tibetan *Radix*. Furthermore fossil *Radix* will be investigated in an associated project. This approach will allow outlining lake histories that shall be used to generate a more detailed picture of the history of the Tibetan Plateau.

Giantism and Reproduction – is the Reproduction Strategy of Dinosaurs One Factor Why Some Dinosaurs Could Reach Such Extreme Body Sizes in Comparison to Terrestrial Mammals?

Jan Werner and Eva Maria Griebeler / Johannes Gutenberg University of Mainz

Reproductive parameters often correlate with body size. Kurtén (1953) already pointed out that body size limits of any taxon are not only related to mechanical or physiological constraints, but are also related to the scaling of its reproductive parameters. Janis and Carrano (JC, 1992) stated that terrestrial non-passerine birds show no significant decline in number of offspring per clutch and total annual number of offspring with increasing body mass in contrast to terrestrial mammals. Using terrestrial non-passerine birds as “dinosaur analogs” JC concluded that this difference in reproductive strategies, may have resulted in a different ability of dinosaurs and mammals to evolve and sustain large-bodied species over evolutionary time. Large dinosaurs had a higher potential reproductive output than similar sized mammals and therefore a decreased risk of extinction under environmental disturbances. We tested the hypothesis of JC i) for a larger dataset of terrestrial herbivorous birds (N = 116) and mammals (N = 376) than analysed by JC, ii) we additionally controlled for phylogenetic effects and iii) we fitted sauropod (herbivorous dinosaurs, largest known terrestrial animals) clutch sizes in our avian and mammalian datasets. Our results strongly supported the hypothesis of JC. Birds have a higher potential reproductive output than similar sized mammals, independent of the analysis method used, and we found

that sauropod clutch sizes did not fit to litter sizes of mammals but fit well to those of birds.

Testing for Local Adaptation in a Freshwater Host-Parasite System

Anja Westram Caroline Baumgartner, Irene Keller and Jukka Jokela / Eawag, the Swiss Federal Institute of Aquatic Science and Technology

Local adaptation of animal populations to characteristics of their environment is a common phenomenon. These characteristics can include abiotic factors like temperature, but also biotic factors like parasitism or predation. Host-parasite interactions are especially prone to local adaptation, as they involve coevolutionary arms races and therefore favour quick adaptation. We investigated local adaptation in the interaction between the freshwater amphipod *Gammarus fossarum* and its acanthocephalan parasites. Cages were used to expose *G. fossarum* from various source populations to parasites in two Swiss streams with different parasite prevalence in a reciprocal transplant experiment. We found no evidence of local adaptation between *G. fossarum* and their Acanthocephalan parasites - that is, there was no consistent pattern in the host's ability to deal with local versus non-local parasites. However, we found that animals from a high infection site were generally less susceptible to the parasite, irrespective of its origin. In addition, we detected local adaptation to other aspects of the habitat: Animals survived significantly better in their local stream than at a foreign site. Our results suggest that adaptive differences between the populations do exist in our system (and are not prevented e.g. by gene flow), with respect to some unknown habitat factors. Adaptation to parasites does not manifest itself as local adaptation, but as a generally reduced susceptibility to parasites in *G. fossarum* from a highly parasitized population.

Surprisingly Social - Eusociality in Digger Wasps?

Mareike Wurdack, Carlo Polidori and Thomas Schmitt / University of Freiburg

Eusociality is defined by reproductive division of labor, overlapping generations and cooperative care of young. Lower levels of sociality may lack one of those qualities. The most prominent examples for eusociality occur in Hymenoptera. While ants are obligatory eusocial, bees and wasps consist of both social and solitary species. Digger wasps (Crabronidae & Sphecidae), on the other hand, normally show a solitary lifestyle. *Cerceris*, the largest crabronid genus with more than 900 species which occur on all continents, comprises a few exceptional species that show communal nesting. One example of a social species is *Cerceris rubida*. The nests of this mediterranean species are inhabited by up to 8 females. Such cohabitation was assumed to be the result of random nest choice combined with low intraspecific aggression. An alternative hypothesis is that *C. rubida* is eusocial. In an eusocial species, nestmate recognition and queen signalling are important factors. The cuticular hydrocarbon profiles of *C. rubida* females show nest specific patterns with great differences between nests. This allows guards at the nest entrance do not only fend off parasitoid intruders but also distinguish between nestmates and non-nestmates. Nest foundresses differ from the following generations in size and cuticular hydrocarbon profile. These foundresses appear to share a chemical quality that could function as a potential queen signal. Analysis of relatedness and fertility within nests will reveal more about the degree of sociality in this species.

Poster Presentation Abstracts

Territorial Behaviour and Testosterone in Black Redstarts (*Phoenicurus Ochrurus*)

Beate Apfelbeck and Wolfgang Goymann / Max Planck Institute
for Ornithology

Songbirds breeding in the temperate zones have to deal with a seasonally changing environment. To cope with these predictable changes, their behaviour and physiology also differs between seasons. The steroid hormone testosterone, for example, shows a seasonal pattern in most male songbirds: blood levels are low during winter and high during the breeding season. Testosterone levels during breeding are often higher than necessary for sperm production or sexual behaviour. The challenge hypothesis predicts that this is due to competition between males for territories and mates. However, testosterone does not rise in all species in response to an intruder into their territory. I tested the hypothesis that differences in the hormonal response to an intruder are due to differences in breeding season length. Songbird species with a short breeding season should not elevate testosterone levels during territory defence as elevated testosterone levels can affect paternal care. To control for phylogeny, I tested populations of the same species, namely the black redstart, breeding at different altitudes. However, both populations showed no increase in testosterone levels in response to a male intruding into their territory despite being below the physiological maximum as injections of Gonadotropin releasing hormone (GnRH) verified. Baseline as well as GnRH-induced testosterone levels of males differed with age and aggressiveness. This study shows that breeding season length might not be a universal explanation for distinct hormonal responses to social interactions between species.

The maintenance of two incompatible alleles in a subdivided population

Claudia Bank / University of Veterinary Medicine Vienna

One possible step on the way to parapatric speciation is the evolution of incompatible alleles. If these incompatibilities are maintained in the population for a long time, they could contribute to the evolution of postzygotic isolation between subpopulations. This phenomenon has been studied extensively in allopatry as well as for continuous population ranges, but little is known about the conditions under which this scenario holds for a parapatric regime consisting of two subpopulations. Here, we study a deterministic migration-selection model with two demes and two alleles at one locus. We attempted to identify the amount of gene flow between the niches, that enables a polymorphism to be maintained, if there is selection against the heterozygotes in each deme (incompatibility) and a selective benefit of one allele in one respective deme (local adaptation). In the case where underdominance and local adaptation act symmetrically in both demes, we found an analytical solution for the maximal migration rate, whereas asymmetrical cases could only be solved numerically. Our results reveal a surprisingly strong effect of symmetry of the selection parameters on the strength of a stable polymorphism.

***Dreissena Rostriformis Bugensis* in Germany: Successful Invaders Lacking Genetic Variance**

Katharina C. M. Heiler, Christian Albrecht and Thomas Wilke / Justus Liebig University Giessen

Genetic characters of invasive species are regarded as fundamental to species invasion success. While invasion theory predicts that introduced populations exhibit a reduced genetic variation due to bottlenecks (founder effect), it remained a paradox how these populations are able to persist, adapt to their new environment and

dramatically increase population sizes that can threaten other species and even ecosystems. In the last years evidence is accumulating that this so-called “genetic-diversity-paradox” may be explained by the way of multiple introductions that lead to overcome genetic constrictions. And indeed, many studies revealed high genetic variation in established populations of invasive species. However, relatively little research has been done on the genetics of species that recently became invasive. This may be due to the fact that invasive populations are often recognized after a population has already established. The freshwater bivalve *Dreissena rostriformis bugensis* (quagga mussel) offers an ideal opportunity to study the population genetics in an early stage of invasion. Originally distributed in a small area nearby the Black Sea, the quagga mussel turned up 2006 in Western Europe and 2007 in Germany. Genetic analyses of the mitochondrial COI-gene in recently established populations (presumably founder populations) revealed surprisingly low genetic variance within and between populations. Despite this lack of genetic variance in COI, more populations were found indicating an ongoing spread of the quagga mussel. Future research will be based on these data to recognize genetic changes and invasion success in invasive populations of the quagga mussel over time.

Genetical Background and Cellular Mechanisms of Kin Recognition In Zebrafish (*Danio Rerio*)

Cornelia Hinz and Gabriele Gerlach

The ability to discriminate between genetically related and unrelated conspecifics is an important process for the operation of kin selection. Kin recognition can explain the evolution of social behavior as altruism and allows individuals to avoid inbreeding. Several mechanisms for the discrimination of kin and non-kin have been proposed.

In zebrafish (*Danio rerio*) kin recognition is based on phenotype matching and allows individuals to recognize even unfamiliar kin

by olfactory cues. Juveniles learn an olfactory template of their relatives by imprinting on day six post fertilization. Little is known about the nature of kin-odor and the cellular mechanisms to detect these chemosignals. Genes of the major histocompatibility complex (MHC) play a critical role in immune response. But it could be shown that these genes also influence social interactions, such as mate choice but also kin recognition. Products of the MHC genes, the MHC- molecules, present peptide ligands to the immune system and thus are essential for the discrimination of self and non-self. The same peptides are already accepted as olfactory cues that influence mate choice decisions and pregnancy block. The aim of this study is to examine the role of the MHC genes in kin recognition and MHC-peptides as the possible source of kin-odor in zebrafish. Predominantly we study the connection between MHC-genotype and social behavior in different contexts. Therefore, we developed a method for genotyping zebrafish MHC-alleles and investigate responses of zebrafish larvae to artificially synthesized MHC-Peptides.

Hybridisation and the Collapse of Behavioural Isolation Barriers

Anja Klöpfel, Alexander Hübner, Sylvia Fähsing, Jan Sradnick and Norbert Elsner / Georg August University of Göttingen

Courtship and calling songs are the most important prezygotic isolation borders in gomphocerine Grasshopper species. But from time to time these barriers don't effect, resulting into hybrids with less fitness compared to their parents. Why are those well established borders overridden and do they influence the parental populations? One example of breaking down the borders is the behavioural and morphological clearly distinguished grasshopper species *Stenbothrus rubicundus* and *S. clavatus*. On the Tomaros Mountain, in north-western Greece, one can find pure populations of each species, but also males with intermediate song characters. The hybrid songs can contain novel elements, which are even more

complex than the parental one, thus offering a new target for sexual selection. In playback experiments the courtship songs are displayed. The *S. rubicundus* are not able to distinguish between *S. clavatus* and their own courtship song. Hybrids can not distinguish at all, they answer to both, parental and hybrid songs. The possible reason for this incorrect choice of the *S. rubicundus* females might be the similarity of songs produced by completely different organs.

Olfactory Imprinting and Kin Recognition in Zebrafish (*Danio Rerio*)

Simon Kobbenbring and Gabriele Gerlach / Carl von Ossietzky University of Oldenburg

Kin recognition is the ability to recognize related individuals and forms the basis to all social behaviour. The present study investigates imprinting of the zebrafish (*Danio rerio*) on relevant cues. We aim to determine which stimulus type triggers imprinting in zebrafish: visual, olfactory and/or physical contact. During a certain period the larvae were exposed to different cues of a related full-sibling group (kin) or an unrelated full-sibling group (non-kin). This period of exposure to cues includes the sensitive phase for imprinting (6 days post-fertilization) in zebrafish. The olfactory preferences of juvenile zebrafish were tested in an odour choice flume. We obtained evidence that zebrafish larvae need a combination of visual and olfactory cues of related fish to imprint on the odour of kin. Zebrafish larvae exposed during five consecutive days to olfactory and visual cues of kin but without physical contact subsequently preferred kin odour. Furthermore, zebrafish larvae exposed to olfactory and visual cues of unrelated conspecifics did not imprint on the scent of the foster family. However, zebrafish larvae used to kin-water but in visual contact with unrelated conspecifics did not prefer the odour of kin. We suggest that zebrafish larvae need a combination of visual and olfactory cues of related fish to imprint on their siblings. Thus, in juvenile zebrafish there is a predisposition for visual and olfactory

cues of kin. In nature, this may be important to avoid miss-imprinting, which otherwise could lead to inbreeding.

Growing Large and Bulky in the Presence of the Enemy: An Inducible Morphological Defence in *Daphnia Magna* against the Predatory Tadpole Shrimp *Triops Cancriformis*

Max Rabus and Christian Laforsch / Ludwig Maximilians University of Munich

The cladoceran *Daphnia magna* is known to alter its life history and behaviour in the presence of predators, e.g. fish. However, little is known about inducible morphological defences in this species so far. Here, we report that *D. magna* expresses morphological defences in response to an ancient invertebrate predator, the tadpole shrimp *Triops cancriformis*. *D. magna*, which were kept in direct contact with the predator, had a significantly larger body, a greater carapace width and a longer tail spine at age of first reproduction compared to the non-predator exposed conspecifics. Those changes in morphology make the induced morphs less susceptible to the gape limited-predator *T. cancriformis*. Predation trials show that those morphological changes act as effective protection against *T. cancriformis*. In a long term experiment, where we recorded the morphological parameters throughout the whole lifespan of the daphniids, we could observe that induced *D. magna* are better defended at nearly any time of their life. Moreover, we could show that the expression of the single parameters changes over time, which suggests that the protective function of those parameters also changes during the lifetime of *D. magna*.

Competitive speciation: Effects of genetic architecture and spatiality

Agnes Rettelbach

The question of speciation is one of the most fundamental and interesting questions in biology. It is also one of the main topics of evolution research as the underlying mechanisms are still not fully understood. As empirical treatment of the problem is difficult, theoretical approaches are very important. Speciation in sympatry or parapatry through resource competition has become a strongly debated topic in the last years since empirical and theoretical results strengthened the evidence. Competitive speciation can occur if negative frequency-dependence leads to disruptive selection and, in sexual populations, to evolution of assortative mating. We consider the effects of genetic architecture and spatiality on the evolution of assortative mating in a simple model of competitive speciation. We find, that with more complex genetics more evolutionary opportunities arise. This can have a positive effect on the possibility of speciation. Furthermore, we find that spatial structure even without local adaptation can facilitate speciation.

Spatial Analysis of a Grasshopper Hybrid Zone

Jan Sradnick, Anja Klöpfel, Alexander Hübner, Sylvia Fähsing and Norbert Elsner / Georg August University of Göttingen

To get an overview of the degree of hybridization within a population of hybrid grasshoppers it is indispensable to classify the parental species. In the case of the two gomphocerine grasshopper species *Stenobothrus clavatus* and *St. rubicundus* it is very easy. They differ in the morphology of antennae, the wings, in number and position of the pegs on the hindleg and many other characters. A gradual shift of the wing structure was observed, leading away from the hybrid zone on the Tomaros Mountain. Individuals, closer to the hybrid zone, show more similarities to the respective other

species than the rest of the observed individuals. This effect is more apparent in the species of the *St. clavatus*. Only a small number of pure individuals could be found in the southern hybrid zone. The data of wing morphometry indicate that most of the individuals from the Tomaros do not correspond in shape and pattern to the pure individuals of the respective species. The *St. rubicundus* individuals on the Tomaros Mountain have slightly changed antennae morphology in contrast to the parental population. Intermediate forms were found in the wing morphology as well as in the antennae morphology. In conclusions one can say, that despite the occurring selection some morphological characters migrate from one species into the other.

Patterns of Proliferation In *Trichoplax Adhaerens* (Placozoa)

Karolin von der Chevallerie, B. Schierwater and E. Moreno /
University of Veterinary Medicine Hannover

The enigmatic marine invertebrate, *Trichoplax adhaerens*, is thought to be most closely related to the hypothetical ancestor of all metazoan animals. Its basal position within the metazoan tree of life and its simple organization makes Placozoa a suitable and important model organism for investigations on basic cellular mechanisms like cell cycling. Up to now, cell proliferation in *Trichoplax* has been monitored by microscopy only. We here present the first experimental data on the detection of cell proliferation in the placozoan *Trichoplax adhaerens* by means of BrdU incorporation. Additionally, apoptosis was monitored via the TUNEL staining method. The results of this study suggest that cell proliferation in Placozoa is highly abundant and spatially restricted, depending on the developmental stage of the animal. Under normal culturing conditions apoptosis is scarce and distributed irregularly. In an attempt to amplify amount of cells undergoing apoptosis, animals were irradiated via X-rays. There was no measurable effect caused by irradiation, and the organisms were able to survive a treatment up to 500Gray. Individuals

entering the degenerative (dying) phase show visibly more cells undergoing apoptosis.

Bad or Good Taxonomy: Does it Kill, Can it Save, or is it Just Irrelevant?

William Morrison III, Jennifer Lohr, Pablo Duchen, Ricardo Wilches, Delsy Trujillo, M Mair, and S. Renner. / Ludwig Maximilians University of Munich

Identification is the basis for conservation and usually involves scientific names. However, scientific naming (taxonomy) has built-in instabilities that result in name changes, raising the issue of whether taxonomic change has consistent impacts on conservation efforts. We pragmatically distinguish “good” and “bad” taxonomy, with “good” taxonomy representing the most recently published taxonomy, and “bad” taxonomy being the previous taxonomic treatment, replaced by new data. Our review finds four outcomes of taxonomic change, namely good taxonomy protects, taxonomy is irrelevant, good taxonomy kills (or bad taxonomy protects), and bad taxonomy kills. There is no evidence of a consistent effect in taxonomic change on conservation, although splitting taxa may tend to increase protection and taxonomic change may have least effect on the conservation of charismatic organisms.

List of Participants

Last name	Institution	email
Apfelbeck, Beate	MPI for Ornithology	apfelbeck@orn.mpg.de
Bakiu, Rigers	University of Padua	rigers.bakiu@unipd.it
Bank, Claudia	Uni of VetMed Vienna	claudia.bank@univie.ac.at
Brandt, Katrin	University of Freiburg	Karin_brandt@gmx.de
Catalán, Ana	LMU Munich	ana.catalan@gmail.com
Clemente, Florian	University of Vienna	Florian.clemente@vu-wien.ac.at
Datzmann, Thomas	Uni of Erlangen- Nürnberg	thomas.datzmann@museum.hu-berlin.de
De Sousa, Marco Aurelio	Uni-Hohenheim	ovemvet@hotmail.com
Deppermann, Jana	University of Oldenburg	Jana.deppermann@uni-oldenburg.de
Duchen, Pablo	LMU Munich	pduchen@gmail.com
Eitel, Michael	Veterinary Uni of Hannover	michael.eitel@ecolevol.de
Fabian, Alexander	LMU Munich	elmadrileno@aol.com
Fähsing, Sylvia	University of Göttingen	Sylvia_Faehsing@gmx.de
Franz, Ragna	University of Zurich	ragnafranz@gmx.de
Franzke, Alexandra	University of Bielefeld	alifranzke@gmail.com
Geiger, Matthias	ZSM & LMU Munich	matthias.f.geiger@stud.uni-muenchen.de
Germerodt, Sebastian	FSU Jena	Sebastian.Germerodt@uni-jena.de
Gowin, Johannes	University of Freiburg	johannesgowin@googlemail.com

Heidemann, Kerstrin	University of Göttingen	zarp@gmx.net
Heiler, Katharina	Justus Liebig University	katharinaheiler@gmx.de
Hinz, Cornelia	University of Oldenburg	Cornelia.hinz@uni-oldenburg.de
Hollandt, Florian	University of Potsdam	Florian.hollandt@googlemail.com
Hörger, Anja	LMU Munich	hoerger@zi.biologie.uni- muenchen.de
Huber, Stefan	LMU Munich	Stefanhuber5@gmx.net
Hübner, Alexander	University of Göttingen	Huebner-Alexander@web.de
Lohr, Jennifer	LMU Munich	jennifer.lohr@campus.lmu.de
Kingma, Sjouke	MPI for Ornithology	kingma@orn.mpg.de
Klöpfel, Anja	University of Göttingen	akloepf@gwdg.de
Kobbenbring, Simon	University of Oldenburg	simonkobbenbring@yahoo.de
Kopp, Michael	University of Vienna	Michael.kopp@univie.ac.at
Kornobis, Etienne	University of Iceland	etk1@hi.is
Krämer, Philipp	University of Oldenburg	philipp.kraemer@uni- oldenburg.de
Kühbandner, Stephan	LMU Munich	Marsupials@web.de
Leingärtner, Annette	University of Bayreuth	annette.leingaertner@freenet.de
Leonhardt, Sara	University of Würzburg	Sara.leonhardt@biozentrum.uni- wuerzburg.de
Linnenbrink, Miriam	LMU Munich	linnenbrink@bio.lmu.de
Madduppa, Hawis	University of Bremen	madduppa@yahoo.com
Mendes, Ana	LMU Munich	mendes@biologie.uni-muechen.de
Menzel, Florian	University of Würzburg	menzel@biozentrum.uni- wuerzburg.de
Modlmeier, Andreas	LMU Munich	modlmeierandreas@gmx.de

Müller, Lena	LMU Munich	lmueller@bio.lmu.de
Nahavandi, Nahid	University of Potsdam	nahavand@uni-potsdam.de
Nöbel, Sabine	University of Siegen	noebel@biologie.uni-siegen.de
Pamminger, Tobias	LMU Munich	tobias_pamminger@yahoo.de
Piskol, Robert	LMU Munich	piskol@bio.lmu.de
Pool, Sebastian	LMU Munich	pohl@bio.lmu.de
Rabus, Max	LMU Munich	max_rabus@web.de
Rashidi, Armin	Newcastle University	armin.rashidi@ncl.ac.uk
Meredith, Rebecca	LMU Munich	rebeccamere@yahoo.com
Rettelbach, Agnes	University of Vienna	agnes.rettelbach@univie.ac.at
Rosenberger, Martin	Technical Uni Darmstadt	martin.rosenberger1@freenet.de
Rösler, Anja	Justus-Liebig- University	Abernmauke@gmx.net
Sradnick, Jan	University of Göttingen	jsradni@gwdg.de
Delsy, Trujillio	LMU Munich	delsytrujillo@gmail.com
von der Chevallerie, Karolin	Veterinary Uni of Hannover	karolin.chevallerie@ecolevol.de
von Oheimb, Parm Viktor	Justus Liebig University	parm.von.oheimb@gmx.de
Werner, Jan	University of Mainz	wernerja@uni-mainz.de
Westram, Anja	EAWAG	anja.westram@eawag.ch
Wilches, Ricardo	LMU Munich	ricardowilches@cable.net.co
Morrison, William	LMU Munich	william.robert.morrison@gmail.com
Wurdack, Mareike	University of Freiburg	mareike.wurdack@biologie.uni- freiburg.de

