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MUNICH GRADUATE SCHOOL FOR  
EVOLUTION, ECOLOGY AND SYSTEMATICS

**EES** LMU

# WELCOME TO THE 8<sup>th</sup> EES CONFERENCE



**Program & Abstracts**

**October 2<sup>nd</sup>, 2014 Biocenter, LMU in B.01.027**

## About the EES conference 2014

The EES Conference 2014 offers the second-year master students and last-year PhD students a space to present their research to the EES community. This is the opportunity of a “scientific” welcome to the new generation of EES Master students, coming from different parts of the world. The presentations inspire the new EES generation to formulate questions that will lead their own ways in evolutionary research. We congratulate the graduating Master students class of 2014 and wish them all the best in their future careers. Welcome to the 8<sup>th</sup> EES Conference! Pictures from an exciting year in EES (2014).



Pictures: EES Events 2014, graduation ceremony 2014, best poster, best master talk, best PhD talk and best lecturer.

Pictures from an exciting year in EES (2013).



Pictures: EES Events 2013, graduation ceremony 2013, EES conference, Open house day, EES excursion.

**PROGRAM, EES Conference 2.10.2014, Biocenter, LMU**



- 9:00**     **Opening words**  
Professor Dr. John Parsch
- 9:10**     **EES PhD talks**  
9:10     Amanda Glaser-Schmitt  
*CG9509*: identifying the links between adaptive *cis*- regulatory divergence and function - An evolutionary and functional analysis of gene regulatory evolution
- 9:30     Katharina Bönzel  
The evolutionary history of the wild tomato species *Solanum chilense*: north-south colonization associated with local adaptation to new environments
- 9:50     Camila Villavicencio  
Social and environmental modulation of hormones and behavior in the black redstart
- 10:10**    **Coffee break**
- 10:30     Sidonie Bellot  
Natural history, taxonomy, biogeography and genome evolution of the worldwide, but species poor endoparasite family *Apodanthaceae* (*Cucurbitales*) - with a focus on internal and horizontal gene transfer
- 10:50     Jacob Rusek  
Diagnostic single nucleotide polymorphism (SNP)-based markers for taxon assignment of the *Daphnia longispina* complex
- 11:10     Malika Ihle  
Fitness benefits of mate choice for compatibility in a monogamous species
- 11:30**    **Poster presentations**  
Why look at the posters? 3rd semester EES students
- 11:45**    **Lunch (Foyer near room C.00.013)**
- 12:30 - 14:00**     **Poster session (C.00.013)**
- 13:15 - 14:15**     **EES Faculty meeting (B.01.015)**
- 14:30**    **EES Master Talks**  
14:30     Lorena M. Romero Prada  
Salt-tolerance evolution in natural populations of the wild tomato species *Solanum chilense*
- 14:45     Shankari Subramaniam  
Metapopulation dynamics in two specialised tansy aphid species-A simulation study
- 15:00     Frederic Dieter Benedikt Schedel  
Mitogenome phylogeny of lake Tanganyika cichlids (Teleostei: *Cichlidae*)
- 15:15     Hannah Fried-Petersen  
A new fish in town: Effects of the invasive *N. melanostomus* on native fish and macroinvertebrate communities in the Danube River
- 15:30     Diogo Barros  
The effects of urbanization on behaviour and reproductive success in Great tits (*Parus major*)
- 15:45     Jeffrey Zielich  
Functional analysis of *cis*-regulatory elements in the *TotA-TotC* intergenic region of *Drosophila melanogaster*
- 16:00**    **Coffee break**
- 16:00**    **Prize committee meeting (room B.01.015)**
- 16:30**    **Awards and graduation ceremony**

## PhD Talks

### Sidonie Bellot

Department of Biology, Systematic Botany and Mycology, Ludwig-Maximilians University, Munich, Germany

#### **Natural history, taxonomy, biogeography and genome evolution of the worldwide, but species-poor endoparasite family Apodanthaceae (Cucurbitales) - with a focus on internal and horizontal gene transfer**

Relatively few flowering plants are parasites on other flowering plants, and overall this strategy evolved only 13 times. Parasitic plants obtain some or all their resources from the host through direct cellular connections (plasmodesmata), and their vegetative habits and ability to photosynthesize are accordingly modified. These changes are most dramatic in endoparasites, which spend their entire life inside the host plant. There are four families of endoparasites, of which I studied the only worldwide one, the Apodanthaceae. They consist of strands of cells living inside Fabaceae or Salicaceae stems from which they emerge once a year to produce tiny sessile flowers. Apodanthaceae have no green tissues.

To better understand the evolution of this enigmatic family, I first revised their taxonomy and systematics, which had not been done since the early 1970s. I observed or dissected flowers from ca. 785 collections (obtained on loan from all relevant herbaria) and carried out field observations in Australia, Iran, and Zimbabwe. The two species I studied, *Pilostyles aethiopica* and *P. haussknechtii*, have strictly unisexual flowers pollinated by flies of the genera *Chrysomya*, *Stomorhina* (Calliphoridae) and *Timia* (Ulidiidae). Both species appear to be dioecious because any one host had either male or female flowers parasite flowers, but rarely both.

I also generated a molecular phylogeny of the family that includes all 10 species from the two genera that I recognize, using nuclear (18S) and mitochondrial (*matR*) genes. The topology confirmed my morphology-based groups, with at least 5 species in the Americas, 1 in Africa, 1 in Iran and 3 in Australia. I then used the phylogeny to compare different ways of modelling heterogeneity in substitution rates. For small data sets, such as mine, Random Local Clocks model, implemented in BEAST since 2010, are a valuable alternative to the default UnCorrelated LogNormal relaxed clock model. Once calibrated with outgroup fossils or host ages, however, the two models gave drastically different divergence times for the parasites, yet Bayes factors were unable to consistently distinguish between them.

Because of their permanent cellular linkage to the host, endoparasites are prone to integrate host DNA into their genomes, and of course they also undergo degradation of the plastome. I used shotgun Illumina sequencing reads from the genomic DNA of the Australian *P. hamiltonii* and of the Zimbabwean *P. aethiopica*, to study their mitochondrial and plastid genomes. The results suggest that both parasite species have lost their plastid genomes similar to the only other endoparasite studied in this respect, *Rafflesia lagascae*, and that both have integrated lots of plastome and host DNA into their mitochondrial genomes.

### Katharina Böndel

Evolutionary Biology, Biozentrum, Planegg-Martinsried, Ludwig-Maximilians University, Munich, Germany

#### **The evolutionary history of the wild tomato species *Solanum chilense*: north-south colonization associated with local adaptation to new environments**

Demography and adaptation are important factors that determine the evolution of plant species. Many plant species are substructured into populations or demes connected by migration (metapopulations). The spatial distribution of populations and migration patterns depend on the means of dispersal. Since plants are sessile organisms, they also have to cope with both biotic and abiotic stresses. Therefore adaptations to local environmental conditions are essential to ensure survival and duration of the species.

Wild tomatoes are native to a broad range of different habitats with a multitude of abiotic conditions in South America. They constitute therefore an ideal system to study demography and natural selection. I investigated the evolution of the wild tomato species *Solanum chilense*, which in comparison to other wild tomato species occurs in the driest and coldest habitats. Pooled-sequencing and analyses of 30 genes from 23 populations revealed 1) a decrease of genetic variation from north to south indicating a colonization from north to south, 2) a substructure of at least four groups indicating a north-south colonization through at least three bottlenecks, and 3) signatures of local adaptation predominantly in populations from the marginal ranges of the species

distribution. The later includes signatures of positive selection in coastal populations and signatures of positive and balancing selection in mountain populations.

In summary, my results suggest that demography plays an important role in the evolutionary history of *S. chilense* and that local adaptation for key abiotic stresses occurs more frequently in the marginal ranges of the species distribution.

### **Amanda Glaser-Schmitt**

Evolutionary and Functional Genomics, Biozentrum, Ludwig-Maximilians University, Munich, Germany

#### **CG9509: identifying the links between adaptive *cis*- regulatory divergence and function An evolutionary and functional analysis of gene regulatory evolution**

Gene expression variation is extensive and is believed to contribute substantially too many of the observed phenotypic differences between species and populations. The regulatory changes behind this variation provide a rich source of raw material for evolution. This talk focuses on regulatory changes in the *D. melanogaster* gene *CG9509*, which shows a 2-3-fold increase in expression in a derived, European population in comparison to an ancestral, sub-Saharan African population. The expression increase is due to variation in an upstream *cis*-regulatory region, called the *CG9509* enhancer, which has undergone a selective sweep in the European population. This talk is divided into three main parts, each focusing on one main finding. First, I will present evidence that the positive selection on the *CG9509* enhancer extends to additional cosmopolitan populations and that the selective sweep likely occurred in the source population of Asia and Europe, after *D. melanogaster*'s expansion out of sub-Saharan Africa but before the two populations separated. Second, I will discuss the sites within the *CG9509* enhancer that we identified as contributing to the observed *CG9509* expression difference both in adults and larvae as well as their likely origins. In the third part of the talk, I will discuss *CG9509*'s function, which is currently unknown, as well as our work identifying both a phenotype and how an increase in *CG9509* expression could be adaptive.

### **Malika Ihle**

Max Planck Institute for Ornithology, Department Behavioural Ecology & Evolutionary Genetics, Ludwig-Maximilians University, Munich, Germany

#### **Fitness benefits of mate choice for compatibility in a monogamous species**

For many decades research on mate choice has focused on preferences for quality indicators, yet in some species mating preferences are largely idiosyncratic (with little consensus about attractiveness), suggesting that such preferences might target genetic or behavioral compatibility.

Very few studies have attempted to quantify the fitness consequences of allowing versus preventing such idiosyncratic mate choice. In our captive populations of zebra finches, when freshly laid eggs are individually cross-fostered for incubation and rearing, embryo mortality (before hatching) primarily depends on the identity of the genetic parents, while offspring mortality during the chickrearing period depends on foster-parent identity. Therefore, when mate choice is prevented, we expect to see an increase in embryo mortality if mate choice targets genetic compatibility (for embryo viability), and an increase in chick mortality if mate choice is aiming at behavioral compatibility (for better chick rearing). In communal breeding aviaries, we monitored the fitness and behavior of recently wild-derived zebra finches in experimental pairings resulting from either free mate choice or forced pairings, using a design where variation in overall partner quality is not a confounding factor. Contrary to the compatible genes hypothesis, pairs from both treatments showed equal rates of embryo mortality. Yet, in line with the behavioral compatibility hypothesis, chosen pairs were better at raising chicks and overall achieved a 37% higher fitness. Further exploratory analyses reveal several interesting differences in behavior and fitness components between such 'love' and 'arranged marriages'.

**Jakub Rusek**

Evolutionary Biology, Biozentrum, Ludwig-Maximilians University, Munich, Germany

**Diagnostic single nucleotide polymorphism (SNP)-based markers for taxon assignment of the *Daphnia longispina* complex**

To trace population/phylogenetic dynamics in hybrid species complexes, tools for fine-scale genetic analyses are necessary, along with long-term comparative studies of natural populations. Diagnostic single nucleotide polymorphism (SNP) marker allow for taxonomic assignments in recently diverged complexes with ongoing hybridization. In the present study, we focused on the freshwater crustacean *Daphnia longispina* hybrid complex. We developed species-specific SNPs taking advantage of transcriptome data from a key species of this species complex, the annotated genome of a related *Daphnia* species and well-defined reference genotypes from parental species. Altogether eleven nuclear loci with several species-specific SNP sites were identified in sequence alignments of three species. A PCR-RFLP assay was developed for screening populations by SNP-genotyping. Taxon assignment by RFLP-patterns was nearly perfectly concordant with microsatellite genotyping of European field samples. Finally, we were able to amplify short regions of two SNP loci in formaldehyde-preserved samples dating back to the year 1960 and to confirm the presence of informative SNPs by cloning. These species-specific SNP markers provide valuable tools to access and study the long-term impact of various environmental factors on hybridization and biodiversity changes in this species complex. SNP-based genotyping, via RFLP patterns or high-throughput analyses will allow for targeting evolutionary dynamics at different time scales.

**Camila Villavicencio**

Max Planck Institute for Ornithology, Department Behavioural Ecology & Evolutionary Genetics, Ludwig-Maximilians University, Munich, Germany

**Social and environmental modulation of hormones and behavior in the black redstart**

Most organisms live in seasonal environments and partition their adult life cycle into different life history stages. Endocrine secretions are important modulators of life history stages in most vertebrates. The steroid hormone testosterone affects several traits of animals including physiology, morphology and behavior. Seasonal elevation of testosterone often correlates with aggressive and mating behaviors and may interfere with parental care. In addition, in socially monogamous species, male-male interactions may trigger increases in testosterone. This implies that testosterone influences aggressive behavior, but aggressive behavior can also feedback on testosterone levels. Testosterone has been related with territorial and mating behavior in a wide variety of taxa. However these relationships are not always straightforward. For example, the black redstart (*Phoenicurus ochruros*), a socially monogamous bird species, is territorial not only during the breeding season, but year-round. Further, black redstarts do not increase testosterone during male-male challenges. Thus, the objective of my study was to investigate the role of testosterone and its relationship with different behaviors and life-history stages, as well as looking for environmental effects on testosterone modulation in males of this species. I correlated testosterone with aggressive behavior during different life-history stages and contexts. In addition I correlated testosterone with parental care and extra-pair behavior. The results show that - although testosterone levels were higher at the beginning of the breeding season - aggressive behavior was stable among stages. Regardless of context, testosterone did not increase during male-male challenges. Further, testosterone did not correlate with parental care, but paternity loss was related to testosterone in male black redstarts. In combination with prior work my data suggest that testosterone plays only a minor role in the control of territorial behavior and does not interfere with parental care, but most likely is related to mating behavior in this species. In summary, my study adds to the growing evidence that current theory regarding hormone-behavior relationship needs to be refined and that there is still much to learn about how hormones and behavior interact. Therefore, I propose that the control of territorial and parental care behaviors in species that are territorial throughout their annual life cycle can be decoupled from testosterone.

## Master Talks

### Diogo Barros

Max Planck Institute for Ornithology, Department Behavioural Ecology & Evolutionary Genetics, Ludwig-Maximilians University, Munich, Germany

#### **The effects of urbanization on behaviour and reproductive success in Great tits (*Parus major*)**

As a result of an increasingly demanding human life style, urban areas inevitably tend to expand leading to a significantly higher degree of anthropogenic pressure on wild communities. These pressures might change the ecological dynamics in wild fauna jeopardizing ecosystem sustainability. Despite the growing interest in urban ecology, little is known about selection pressures induced by urbanization. This project aimed at assessing the influence of specific environmental parameters – such as light, noise and temperature – that are characteristic for urban environments on individual behavior and fitness of Great tits (*Parus major*). Using a recently established great tit nest box population I repeatedly measured behavioral traits such as aggressiveness and flight initiation distance and recorded reproductive success along several urban-to-rural gradients. I tested for the repeatability of the observed behaviors, assessed behavioral syndromes (also referred to as personality) and calculated the change of behaviors across the urbanization gradients. I also tested whether reproductive success, i.e. the number of chicks that fledged, is a function of the level of urbanization. Temperature and relative humidity were found to be the most significant urban component to influence birds' behaviors, with temperature contributing towards more aggressive and bolder individuals and humidity having an inverted relationship. Aggression was found to not be correlated with boldness, which corroborates with previous findings for urban birds. Temperature was also the most influential variable in reproductive success. Contrary to our expectations, fitness was found to slightly increase with temperature. Moreover, temperature seems to increase clutch size but reduce survivability. This project provides insights on how urbanization shapes individuals to be more aggressive and bolder, but less docile. It also suggests that urban birds are fitter but have higher nestling mortality rates.

### Declan O'Flaherty

Evolutionary and Functional Genomics, Biozentrum, Ludwig-Maximilians University, Munich, Germany, and university of Montpellier, France

#### **The epidemiological consequences of dispersal and synchrony on *Paramecium caudatum* and its parasite *Holospira undulate***

Parasitism has been called “the most popular lifestyle on earth” and, as such, its effects permeate almost every conceivable ecological paradigm (Price 1980). Since recorded history, disease outbreaks have swept through communities, cities, countries and even entire continents, often with extreme consequences for human and animal populations (Russel 2006; Wolfe *et al.* 2012). Yet, despite their importance, we lack a fundamental understanding of such outbreaks. As computing power and statistical methodologies have developed, a wealth of theoretical models of host-parasite systems have emerged, hinting at the importance of spatial structure, temporal variation and stochasticity on disease outbreaks. Yet, empirical data testing these theories remains scarce. In this paper, we investigate the epidemiological consequences of the basic ecological principles of synchrony and migration in an established study population under controlled experimental conditions. Using the *Paramecium caudatum* - *Holospira undulata* host-parasite system, we generated simple, two-population meta-populations experiencing a range of migration. Consistent with prevailing theory, we found that increasing levels of connectedness between environmentally uncorrelated populations produces epidemics of increasing severity and persistence (Grassly & Fraser 2006). By providing empirical, reproducible data on how key ecological concepts such as synchrony and migration effect epidemiological dynamics, studies such as ours both test current theoretical wisdoms and suggest potential avenues for future research.

**Hannah Fried-Petersen**

Evolutionary Biology, Biozentrum, Planegg-Martinsried, Ludwig-Maximilians University, Munich, Germany

**A new fish in town: Effects of the invasive *N. melanostomus* on native fish and macroinvertebrate communities in the Danube River**

Biological invasions have and will continue to shape the structure and function of ecosystems around the world. The majority of studies in invasion biology focus on terrestrial ecosystems and especially plants. However, there is evidence that freshwater ecosystems are experiencing larger biodiversity declines from invasive species. The Ponto-Caspian region (Black and Caspian Sea regions) has been a source of some of the most widespread invaders worldwide. The Danube River empties into the Black Sea and has thus been subjected to invasions from these notorious species. Particularly notable is the invasive round goby fish, *Neogobius melanostomus* because of its numerical dominance over native and other invasive fish species. My collaborators have been monitoring the “invasion front” of the round goby as it moves up the Danube River. This study uses this monitoring data to address three questions about the effects of the round goby on native species: 1) How native fish communities change, 2) How the condition and abundance of native fish changes at the species level and how this is related to their proximity to the round goby in the food web, and 3) How benthic macroinvertebrate communities change. Some important results from these investigations are that various diversity indices of the fish community are shown to have lower values in sections of the Danube where the round goby has been present for a longer time. There is also an effect of round goby abundance and invasion status on native species condition and abundance at the species level and in some cases this is related to the trophic niche of the native species. It also seems that it is important to consider the “time since invasion” to understand the effects on abundance and condition. Studies on the effects of invasive species tend to focus on more general parameters, such as abundance, of the affected natives and the ability to also investigate the effect on condition of the natives is one novel approach of this study. Results of these analyses further confirm the need to develop methods to contain the spread of the round goby and bring its numbers down in sections of the Danube where it has already established.

**Lorena M. Romero Prada**

Evolutionary Biology, Biozentrum, Planegg-Martinsried, Ludwig-Maximilians University, Munich, Germany

**Salt-tolerance evolution in natural populations of the wild tomato species *Solanum chilense***

The wild tomato species *Solanum chilense* is able to live successfully across a wide range of habitats facing different types of environmental conditions (drought, cold, soil salinity). In this study, I investigated local adaptation of *S. chilense* to different soil salinities. I assessed the variation in response to salt stress for eight different populations of *S. chilense* from diverse habitats using a standard plant physiology method (chlorophyll fluorescence emission). Analysis of photosynthesis yield in plants exposed to salt stress showed that all eight populations possess high salt tolerance indicating that the species can be considered as salt tolerant. However, I also observed within and between population variations in responses to salt stress.

Gene expression analysis of eight candidate genes for salt stress response (*jerf1*, *jerf3*, *dhn1*, *tas14*, *dreb1*, *Ice1*, *areb1*, and *er5*) identified *tas14* as a reliable marker for assessing the variation of salt stress responses in *S. chilense*. The physiological and gene expression results of this study showed that plants from the coastal population LA2750 showed a uniform high tolerance to high salinity conditions and a low variation of *tas14* expression while the high altitude population LA2931 exhibited a variable response in the salt stress experiment and a higher variation in *tas14* expression.

Key words: *Solanum chilense*, wild tomato, salt tolerance, population variation, candidate genes, photosynthesis yield, *tas14*, dehydrin, gene expression variation.

**Frederic Dieter Benedikt Schedel**

Bavarian State Collection of Zoology (ZSM), Systematische Zoologie, Biozentrum, Planegg-Martinsried, Ludwig-Maximilians University, Munich, Germany

### **Mitogenome Phylogeny of Lake Tanganyika cichlids (Teleostei: *Cichlidae*)**

Of the African Great Lakes, Lake Tanganyika (LT) undisputedly harbors the most diverse cichlid assemblage with approximately 250 species, distributed over twelve endemic and four non-endemic cichlid tribes. Although many studies have tried to clarify the phylogenetic relationship of these tribes, many uncertainties regarding the phylogenetic placement of the different LT-cichlid clades remain to this day. These ambiguities can be attributed to insufficient sequence data, incomplete taxon sampling and discordant phylogenetic signals in multilocus datasets. Here a highly resolved phylogeny encompassing almost all major lineages of the East African radiation is presented, based on ten mitochondrial protein coding genes (concatenated alignment 7917 bp) and 84 taxa. Moreover the impact of increased sequence data on size-range of confidence intervals of node age estimations has been explored. The massive increase of mitochondrial sequence data helped only in some cases to reduce the confidence intervals of node age estimations. However it improved bootstrap values notably, allowing a refined understanding of the evolutionary history of Lake Tanganyika cichlid tribes and associated lineages. The monophyly of all major clades of the East African cichlid radiation (EAR) as recognized in previous studies were confirmed in this mtDNA-study. Moreover two additional lineages were recognized here for the first time: "*Orthochromis*" sp. "Lufubu" representing the sister group to a clade consisting of the *Pseudocrenilabrus*-like cichlids, Tropheini plus *Haplochromis vanheusdeni*, modern Haplochromini and Malawi Haplochromini; *Haplochromis vanheusdeni* representing the sister group to the LT endemic Tropheini underlying the importance of including riverine lineages when studying the evolutionary history of LT cichlids. Additionally, new findings about the relationship of endemic LT tribes with much stronger support are presented here. The Lamprologini revealed not to be the sister group of the Eretmondini as was the case in previous mtDNA-studies, but form the (weakly supported) sister group to all remaining members of the EAR (except for Bathybatini and Boulengerochromini). For the first time, a highly supported (BS: 100) monophyletic clade of three ancient Lake Tanganyika mouthbrooder tribes encompassing the Perissodini, Cyprichromini and Benthochromini (PCB-clade) was recovered based on mt-DNA data. Further the previously postulated relationship of Haplochromini and Malagarasi-*Orthochromis* could be confirmed for the first time with acceptable support (BS: 76). By improving the knowledge about the relationship of Lake Tanganyika associated cichlids, this study provides an opportunity for future studies to gain fine-grained inferences about the relative timing of speciation in Lake Tanganyika, and about the absolute timing, once improved calibration points become available and mtDNA data will be complemented with high density nuclear DNA data.

### **Shankari Subramaniam**

Evolutionary Biology, Biozentrum, Planegg-Martinsried, Ludwig-Maximilians University, Munich, Germany

### **Metapopulation dynamics in two specialised tansy aphid species-A simulation study**

Metapopulation dynamics are studied to understand the evolution of species on patchy landscapes with limited gene flow. The genetic structure of such populations helps to identify the underlying population mechanisms which are at play, such as extinction, colonisation, and migration. Several studies focus on the theoretical aspects of such systems, while others attempt to infer the dynamics by using molecular genetic markers. The main question addressed in this study is whether parameterization of a metapopulation model is possible with the use of genetic data. To this end, I develop a simulation model to describe the colonisation and extinction dynamics of two species of specialised tansy aphids: *Macrosiphoniella tanacetaria* and *Metopeurum fuscoviridae*, which exhibit metapopulation structure. I compute statistics that describe the genetic structure of these populations from microsatellite loci which have been characterized for these species and compare the values for simulated data to statistics obtained for populations observed in the field (by Loxdale et al., 2011). I then use Approximate Bayesian Computation methods to estimate the probabilities of migration and extinction which can produce such a genetic structure. In order to test the validity of these estimates, I carry out posterior simulations and once again compare the simulated statistics to the observed to test the ability of the model in resulting in the observed statistics. The study suggests that the metapopulation model can indeed reflect population substructure. Estimates for the rate of migration and extinction indicate that migration might be lower than expected, and that more complicated dynamics may need to be considered to better explain the

observed genetic structure (such as predation and competition). I then discuss the potential of the model to be applied to future studies on metapopulations and metacommunities.

### **Loukas Theodosiou**

Evolutionary Biology, Biozentrum, Planegg-Martinsried, Ludwig-Maximilians University, Munich, Germany, university of Montpellier, France

#### **Origin and maintenance of asexuality in *Artemia***

Contagious parthenogenesis (or contagious asexuality) is a process where parthenogenetic lineages sometimes produce functional males (rare males), which can mate with coexisting females of a close related sexual species and produce new parthenogenetic lineages. So far, an important experimental limitation to understand the genetic causes of this process was the difficulty to conduct crosses between rare males and their close related sexual species. *Artemia* is a promising model species to overcome this obstacle. In our lab we have successfully conducted crosses between rare males and females of their closest related sexual species which is *Artemia* spK. These crosses have given us a unique opportunity to map the asexual genome of *Artemia* and reveal its distinct genomic background compared with sexual counterparts. However, before this is possible it is essential to have the genetic map of *Artemia* spK. In this project we constructed the two sex-specific linkage maps of *Artemia* spK by using 589 highly informative SNP markers. We identified 21 male and 21 female linkage groups ( $2n=42$ ) covering 486 cM and 423 cM respectively. Considering the haploid genome size of *Artemia* spK we found a recombination rate of 0,23 cM / Mbp in females and 0,2 cM / Mbp in males which is low compare to *Artemia franciscana* and other Crustaceans. Low recombination rate in *Artemia* spK is intriguing and open avenues for exciting research in many disparate scientific fields. Finally, our linkage map will be an invaluable tool for genomic comparisons with the future map of diploid parthenogenetic lineages of *Artemia* and will cast light on the traits causing contagious asexuality.

### **Cynthia Y Wang**

Bavarian State Collection of Zoology (ZSM), Systematische Zoologie, Biozentrum, Planegg-Martinsried, Ludwig-Maximilians University, Munich, Germany

#### **Dentitional diversity and evolution in Pseudoxyrhophiine snakes (serpents: *Iamprophiidae*) using 3D imaging**

Madagascar and the nearby Indian Ocean islands are home to a large radiation of lamprophiid snakes of the subfamily Pseudoxyrhophiinae. This speciose subfamily is restricted to these islands with the exception of five species, which are found on mainland Africa and the Yemeni island of Socotra. Many pseudoxyrhophiine genera are morphologically distinct and ecologically diverse but few species have been studied in detail because of the rarity of specimens in collections and in the wild. In order to elucidate a potential adaptive radiation and describe its morphological diversity, I investigated the dentition of this subfamily, which has been implicated in cases of dietary specialization. Using three-dimensional reconstructions based on micro-computed tomography scans of 70 species, I compared phylogenetic clades within the subfamily that displayed divergent dentition and diet. My results suggest that certain dentitional adaptations may be correlated with diet and that this may explain differences in morphology between different taxa. The results also help to clarify the relationship between morphology, functional anatomy, and ecology in the convergent evolution towards particular adaptations in snakes.

### **Jeffrey Zielich**

Evolutionary and Functional Genomics, Biozentrum, Ludwig-Maximilians University, Munich, Germany

#### **Functional analysis of *cis*-regulatory elements in the *TotA-TotC* intergenic region of *Drosophila melanogaster***

Because it has recently colonized many worldwide habitats in association with human globalization, *Drosophila melanogaster* represents a promising model system for addressing evolutionary genetic questions. Preliminary

