

## **Dolors Amorós Moya**

*Affiliation:*

Institute for Evolution and Biodiversity, University of Münster

*Scientific field of research:*

Molecular evolution

*Study system:*

*E. coli*

*Title:*

Rapid evolution in regulatory elements compensates for codon usage bias cost

*Abstract:*

There is a redundancy of codons in the genetic code and the relative frequency of the synonymous codons varies among species and among genes. Non-optimal codon usage decreases gene translation efficiency, potentially leading to a fitness cost. This codon bias is particularly important in determining the success of horizontal gene transfers. We have mimicked a horizontal gene transfer event into a foreign genome in order to study the fitness cost associated to codon usage bias, and to the adaptation and eventually fixation process of newly transferred genes. A protocol was set up to test the evolution of three versions of an antibiotic resistance gene under antibiotic selective pressure. Each of these gene versions encodes for the same protein but they differ in their sequence codon usage adaptation with regard to the codon usage of the recipient organism (*Escherichia coli*). After 358 generations of our experimental evolution study, we have observed that bacteria carrying genes with a suboptimal codon usage are ten to twenty times more sensitive to antibiotic than those carrying the corresponding optimal version. This fitness cost can be overcome through evolution under selection, by fixation of both *in cis* changes in the gene promoter and *in trans* changes in the host bacterial genome. However, no mutations in the coding sequence of the gene have been found after 358 generations under selection. Some of the mutations are shared among bacterial lines and constitute experimental evidence for convergent molecular adaptive evolution. The initial high fitness cost of non-optimal codon usage has been seen therefore as a minor obstacle to gene fixation upon horizontal transfer. The rapid evolution of regulatory mechanisms has revealed to be of a great importance in the adaptation to new environmental and genetic situations.

## **Sophie Armitage**

*Affiliation:*

Institute for Evolution and Biodiversity, University of Münster

*Scientific field of research:*

Insect immunity

*Study system:*

*Drosophila melanogaster*

*Title:*

Specific immune priming and the evolution of *Dscam* across the arthropods

Sophie Armitage, Rebecca Freiburg, Ignacio González Bravo & Joachim Kurtz

*Abstract:*

Innate immunity is evolutionarily ancient; it is the first line of defence for vertebrates and invertebrates against parasites. To understand how the insect innate immune system combats parasites it is necessary to have an insight into both immunological mechanisms, and into how the evolutionary pressures of abundant and rapidly evolving parasites have shaped immune defence. Key to this understanding is knowledge about how the immune system recognises parasite antigen diversity: Down's syndrome cell adhesion molecule (*Dscam*) has been proposed to be a good candidate for recognition of specific antigens by insects and may also be involved in immune priming (phenomenologically similar to immune memory in vertebrates). I will first present preliminary experimental data on the phenomenon of specific immune priming in wild-type *Drosophila melanogaster*. In future a similar experimental design will be applied to *Dscam*-mutant flies to hopefully allow us to test whether *Dscam* plays a role in specific immune priming. Second, I will present an analysis of the evolution of the *Dscam* gene family across the arthropods. Some *Dscam* exons have undergone massive expansions resulting in mutually exclusive alternative splicing that in *D. melanogaster* can potentially result in thousands of different isoforms, and can putatively provide diversity for parasite recognition; we therefore also examined the evolution of the alternatively spliced exons across arthropod species.

## **Ratih Aryasari**

*Affiliation:*

GeoBio-Center, LMU Munich

*Scientific field of research:*

Systematics and population genetics

*Study system:*

Sponges

*Title:*

Population genetic structure of several sponge (*Porifera*) species in Indonesian Archipelago

*Abstract:*

Sponges (PORIFERA) are unique multicellular animals in the marine ecosystem, which have great values for the ecosystem itself and also for human kind because of their economic potential. Indonesia is one of several countries that have the highest sponge diversity. The oceanography of the Indonesian Archipelago is dominated by the Indonesian throughflow (ITF) current, which could influence marine larval dispersal, including sponges. Details on population connectivity may potentially provide important information for management efforts. Genetic structure will be examined, using ribosomal ITS1, ITS2, and a fragment of the 28S gene sequences on a small scale among populations in the Spermonde Archipelago, South Sulawesi, and on a large scale throughout the Indonesian Archipelago (North Sulawesi, East Kalimantan, Thousand Islands, Bali and Ternate).

**Uwe Balthasar**

*Affiliation:*

University of Glasgow, Scotland

*Scientific field of research:*

Palaeontology

*Study system:*

Brachiopods

*Title:*

Phosphate versus carbonate – Insights into the origins of the brachiopod shell

*Abstract:*

Brachiopods are among the first phyla to appear in the fossil record and due to their mineralised shells have an excellent fossil record. Their shells are either mineralised with calcium phosphate (organophosphatic) or calcium carbonate (calcite) and, assuming brachiopods are monophyletic, calcitic shells had to evolve from organophosphatic shells or vice versa. Recent discoveries of organophosphatic stem group brachiopods suggest that the bivalved brachiopod body plan evolved through the successive reduction of a multi-element organophosphatic tube. Microstructural studies of these stem group brachiopods and the oldest known organophosphatic crown group brachiopods supports the view that an organophosphatic composition represents the ancestral shell type for brachiopods. Furthermore, the results suggest a trend towards successively reduced degrees of apatite mineralization in the course of the stem-crown group transition. This trend in reduced deposition of calcium phosphate is interpreted to reflect a switch from a vagrant to a sessile life style in the basal stem group which made it increasingly more difficult to maintain an expensive phosphate budget as food intake (i.e. the phosphorous source) was now largely dependent on seasonality or currents. This pressure to find 'cheaper' phosphorous solutions probably contributed to the emergence and success of calcitic shells in brachiopods.

## **Lutz Becks**

*Affiliation:*

University of Toronto / University of Cologne

*Scientific field of research:*

Evolution of sex, population dynamics

*Study system:*

Aquatic systems, rotifers

*Title:*

Dispersal between heterogeneous environments favors sex

*Abstract:*

Explaining the dominance of sexual reproduction over asexual reproduction in nature is one of the biggest challenges in evolutionary biology. Several theories have been developed in the past defining among others ecological conditions that favor sexual reproduction. We present here the results of our empirical test of one of those predictions using cyclic parthenogenetic rotifers. Monogonont rotifers can switch between sexual and asexual reproduction, and the switch between the two is a variable genetic trait and changes in the propensity for sexual reproduction within a population can be used to estimate selection for the rate of sex. Our experiment confirms the prediction that sex is advantageous when dispersal between divergent selecting environments leads to genetic associations that may not be favored by selection. Under these conditions, sex is advantageous because it breaks down these genetic associations. We show that dispersal between homogeneous environments selects against the rate of sex (a decrease in trait to response to invest into sex) while dispersal between two heterogeneous environments lead to an increase in the rate of sex in the rotifer populations.

**Andrés Felipe Carvajal & Mónica Arias**

*Affiliation:*

EES Program, LMU Munich

*Scientific field of research:*

Host-parasite interactions

*Study system:*

*Daphnia galeata*

*Title:*

Do fish affect *Daphnia galeata*?

*Abstract:*

Parasite-host interactions are very important because they can shape the structure of an ecosystem due to the host fitness reduction and the effect this could imply on the food chain. Planktivorous fish are predators of zooplankton and the fish density fluctuations could have a major effect in the prey they feed on. In order to assess this issue, the interaction between fish density and a waterflea's (Cladocera: *Daphnia galeata*) reproduction, density and parasites, was evaluated. Using samples collected from an 8 year period of the Rimov Reservoir in Czech Republic, data on fecundity, clutch size and parasite prevalence of *D. galeata* was obtained and compared with the fish density. The prevalence of three common parasites (CAUL: *Caulerya mesnili*, a protozoan gut parasite; BROOD & HEAD: oomyces in the brood pouch and in the head, and MICR: intracellular microsporidia) was assessed. Theoretically, fish would tend to feed more on *Daphnia* with parasites that color their body (MICR & BROOD) and a decline in fish density would allow major prevalence of such parasites. Fecundity and clutch size of *D. galeata* were not correlated with the fish density over the study period. The parasite CAUL was the one with highest prevalence overall and the other parasites were found in much less prevalence; hence, my hypothesis could not be tested. Nevertheless, the results presented constitute a tool for understanding the dynamics *in situ* of parasite-host interactions and their effect on the food chain of an aquatic ecosystem.

## Ana Catalán

### *Affiliation:*

Max Planck Institute for Neurobiology / EES Program, LMU Munich

### *Scientific field of research:*

Evolutionary genomics

### *Study system:*

*Drosophila melanogaster*

### *Title:*

Evolution of CO<sub>2</sub> behavioural response in *Drosophila*

### *Abstract:*

CO<sub>2</sub> can elicit different behavioral responses in insects. In mosquito CO<sub>2</sub> is a cue to find a host whereas in *Drosophila melanogaster* it triggers an avoidance response. In *Drosophila*, the chemosensory neurons that respond to CO<sub>2</sub> are located in the antenna and co-express two chemosensory receptors Gr21a and Gr63a. In CO<sub>2</sub> behavioral response experiments I found that *D. melanogaster* and *D. ananassae* show a threefold stronger CO<sub>2</sub> avoidance in comparison to *D. simulans*, *D. sechellia* and *D. erecta*. To characterize the CO<sub>2</sub> response in the melanogaster group 11 species are going to be tested further in additional behavioral paradigms with additional odors. I will analyze putative differences in the olfactory system of *Drosophila* species by using species F1 hybrids and genetic marker proteins to fluorescently label CO<sub>2</sub> neurons in the periphery and neurons in the central brain. Analysis of these hybrids will allow addressing if there is a difference in the number of CO<sub>2</sub> neurons and in the innervation of the brain between those species. With quantitative PCR the expression level of Gr21a and Gr63a of the 11 species will be measured. A McDonald-Kreitman and Ka/Ks test will be done in order to detect natural selection in the CO<sub>2</sub> receptors. The correlation between the behavioral assays and the sequence and expression data is going to help us understand the evolution of the CO<sub>2</sub> response in *Drosophila* and other insects such as mosquito.

## **Nayden Chakarov**

### *Affiliation:*

Department of Animal Behavior, University of Bielefeld

### *Scientific field of research:*

Intraguild predation, parasite-host interactions

### *Study system:*

Common buzzards (*Buteo buteo*) preyed by goshawks (*Accipiter gentilis*). Both preyed by eagle owls (*Bubo bubo*)

### *Title:*

Can top predators react adequately to predation stress?

### *Abstract:*

Intraguild predation is the complex interaction between member species of a guild, that both compete for resources and kill each other. Non-lethal effects by intraguild predation are costly behavioural responses to avoid predators. Among others intraguild prey can adapt by restricting its habitat use to predator free zones i.e. distance-sensitive avoidance or by totally avoiding habitats favoured by the intraguild predator. In my study population life histories of common buzzards *Buteo buteo* have been explored over the past 20 years, while dynamically coexisting with goshawks *Accipiter gentilis*, prominent competitors for breeding grounds and predators of buzzards. In the last 7 years a new apex predator, the eagle owl *Bubo bubo* has re/entered the community and is expected to further shift the life history adaptations of both buzzards and goshawks. I will present results showing different impacts of this apex predator on the population and the individual response levels of its intraguild prey.

## **Juliana Chacón**

### *Affiliation:*

Systematic Botany and Mycology & EES Program, LMU Munich

### *Scientific field of research:*

Molecular phylogenetics and biogeography

### *Study system:*

Family Alstroemeriaceae (Liliales)

### *Title:*

Evolutionary patterns of the family Alstroemeriaceae, an important clade of the Austral floristic realm

### *Abstract:*

The Austral floristic realm comprises 16 families that are restricted to South America and Australasia. An important member of this realm is the Alstroemeriaceae, with 200 species in four genera, *Alstroemeria*, *Bomarea* and *Luzuriaga* in South America, *Drymophila* and the remaining *Luzuriaga* in Australia, Tasmania and New Zealand. Evolutionary studies on the Alstroemeriaceae have included few species and have suffered from a lack of phylogenetic resolution due to limited signal in the DNA regions sequenced. In this study we will test the hypothesis that the oldest divergence(s) in Alstroemeriaceae date(s) back to the break-up of East Gondwana. We will answer two questions: What is the evolutionary relationship between *Alstroemeria* and *Bomarea*, and how was their divergence affected by the uplift of the Andes? What is the history of the *Alstroemeria* subclades that are restricted to the Brazilian shield region and the Chilean and Peruvian/Ecuadorian chains of the Andes? The chloroplast DNA regions *ndhF*, *rbcL*, and the nuclear ITS have been sequenced for 80 species of Alstroemeriaceae. Preliminary analyses have been performed including some Colchicaceae species as outgroups. A molecular clock run has been done using the chloroplast matrices and some *Smilax* fossils as calibration points. The results show that *Alstroemeria* is embedded in *Bomarea*, and their divergence is dated to 17 My ago, which coincides with the main Andean uplift. Alstroemeriaceae apparently entered South America from Antarctica twice; one event each in *Luzuriageae* and *Alstroemerieae*, and then spread north to Mexico and northeast to Brazil and the Guianas.

## Hong Chen

*Affiliation:*

DSMZ Braunschweig

*Scientific field of research:*

Evolutionary genomics

*Study system:*

aquatic *Sphingomonadaceae*

*Title:*

Analysis of the population substructure of aquatic *Sphingomonadaceae* by MLSA

Hong Chen, Mareike Jogler, Jörg Overmann

*Abstract:*

The role of recombination, adaptation and selection in shaping bacterial diversity was assessed using aquatic members of the *Sphingomonadaceae* (*Alphaproteobacteria*) as a model group. Our multilocus sequence analysis (MLSA) targets a set of 9 housekeeping genes (*atpD*, *dnaK*, *EF-G*, *EF-Tu*, *gap*, *groEL*, *gyrB*, *recA*, *rpoB*) in *Sphingomonadaceae* and was used to elucidate the population structure and the significance of recombination events in this group. The new MLSA primers were designed based on all available genome sequences of 5 strains of *Sphingomonadaceae* and 2 strains of the closest phylogenetically related genus *Erythrobacter*, 95 strains of *Sphingomonadaceae* were isolated from Starnbergersee and Walchensee, and subjected to the novel MLSA approach. Based on their rRNA gene sequences, these strains fall into 15 different phylogenetic groups. Multiple isolate were available for all major phlotypes. While 16S rRNA gene sequences were identical for certain members of one 16S rRNA group, the tree of the concatenated sequences of 9 housekeeping genes indicated a significant genomic divergence between the different strains. Based on the frequency of sequence divergence the isolated *Sphingomonadaceae* represent a clonal population, Most significantly, MLSA revealed the presence of distinct subclusters among individual 16S rRNA groups, suggesting different selection pressure between subclusters and the existence of distinct evolutionary units despite the identical or very similar 16S rRNA gene sequences.

## **Davide M. Dominoni**

*Affiliation:*

Max Planck Institute for Ornithology, Vogelwarte Radolfzell

*Scientific field of research:*

Evolutionary biology

*Study system:*

Blackbirds (*Turdus merula*)

*Title:*

Chronobiology of urban life: activity patterns of European blackbirds *Turdus merula* along an urban/rural gradient

D. M. Dominoni and J. Partecke

*Abstract:*

Across much of the world, urban areas are growing faster than any other land cover type. Animals which have successfully settled in these man-made ecosystems have to cope with novel environmental conditions compared to their forest conspecifics. One of the most apparent urban-specific environmental factors is artificial light at night. While there is no doubt that photoperiod i.e. the light fraction of a 24 h day is one of the driving forces regulating life cycles of plants and animals, nothing is known about the effects of this so called ‘light pollution’ in urban environments on the behaviour, physiology, and brain functions of animals. Previous studies, however, support the idea of a stimulatory effect by artificial night light. Urban birds exposed to higher light irradiance initiated their morning chorus earlier than birds living in rural areas. Even changes in the seasonal organization of annual events such as reproduction in urban populations have been tried to explain by increased night light irradiance. To elucidate the biological significance of artificial night light we quantified daily activity pattern of urban and rural individuals along an urban/rural gradient in Munich, Germany, with the use of an automated telemetry system. Simultaneously we tagged the same individuals with micro light loggers to measure light irradiance to which the individuals are exposed. In our talk we will report on the effects of light irradiance and noise levels on the daily activity profiles of urban and rural European blackbirds and finally will discuss the ecological and evolutionary consequences.

## **Adriana Dorado**

### *Affiliation:*

EES Program, LMU Munich

### *Scientific field of research:*

Behavioral ecology of birds

### *Study system:*

Blue tit (*Cyanistes caeruleus*)

### *Title:*

Sleep behaviour in blue tits (*Cyanistes caeruleus*): sex and temperature effect

### *Abstract:*

Sleep is an energy conservation mechanism linked with metabolic rate. It is used for almost all the animals. Environmental factors and sex might affect the variability within and among species in sleep duration. However, little is known about sleep behavior and the variables related with it, especially in wild animals. In birds, temperature related with metabolic rates might affect variables such as sleep duration. Other variables like the sex could affect behaviors like peeking, which consists in awake phases during the sleep time. Blue tits are an ideal study system because are very common in the wild and accept easily artificial nestboxes in the forest to roosting during the winter. Therefore, we wanted to test the effect of sex and temperature in sleep habits in four different winter months. We found differences between sexes in the early breeding season in sleep duration and awake phases, probably due to the differences of the role of the sexes. On the other hand, while temperature increases the sleep duration decreases. That is possibly related to the metabolic rate which increases at low temperatures in birds. In conclusion, females and males have different functions and necessities to receive the breeding season and we can found evidence in the sleep behaviour. In addition, we cannot definitely conclude that temperature changes triggered the decrease in sleep duration. Light intensity (day length), as well might affect the sleep behaviour in blue tits.

**Thomas D'Souza**

*Affiliation:*

Animal Evolutionary Ecology, Tübingen University

*Scientific field of research:*

Evolution of sex

*Study system:*

Freshwater planarians

*Title:*

Evolution in a box: Tools to improve teaching of evolution at high schools

*Abstract:*

In Germany, "Evolution" is often addressed in a purely historical context. On the one hand, it is one of the few disciplines in biology that is consistently explained starting from its historical discovery by Darwin and other 19th century scientists. On the other hand, it is often reduced to a mere narrative of the genealogy of life. In both cases, pupils, students and the general public obtain the impression of a discipline that consists of nothing more than a theory that has been conceptualized a long time ago and has remained largely unchanged since. Although it explains our distant ancestry, it has little relevance for present-day processes and modern humans, which are "not evolving anyway". Here we present some ideas to improve the teaching of evolution in high schools as a part of the educational concept "Tübingen in Evolution, Evolution in Tübingen" within the framework of the Volkswagen Foundation initiative "Curriculum evolutionary biology". In didactic courses students have developed school activities which aim at illustrating concepts of evolutionary biology in a vivid and active manner. Importantly, these school activities can be easily incorporated in any existent biology curricula at school. Topics include so far human evolution, cultural evolution and construction of phylogenies based on fossil records. These activities are also part of courses and advanced trainings for teachers and students to achieve a wide circulation.

**Thomas D'Souza and Nico Michiels**

*Title:*

Tübingen in Evolution, Evolution in Tübingen

*Abstract:*

The goal of this programme is two-pronged. First, it aims at achieving a better understanding of evolutionary biology by the general public by aiming at improved school education, better education of teachers and a permanent, public lecture series. Second, it promotes “evolutionary thinking” as an academic soft skill for university students outside regular evolutionary teaching programmes. This involves (1) assuring that evolution is used as the unifying theme throughout biology courses, (2) offering courses specifically aimed at students from other fields, (3) organising high-level seminars by international speakers that bridge gaps between disciplines, and (4) offering financial encouragement for student projects that involve interdisciplinary cooperation on evolutionary topics.

## Daniel Dreesmann

### *Affiliation:*

Johannes Gutenberg University, Mainz

### *Scientific field of research:*

Science education, science communication

### *Title:*

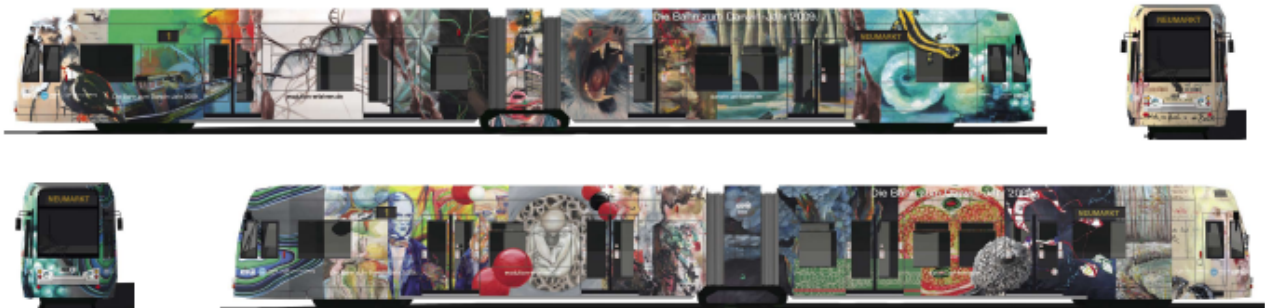
A Streetcar named Darwin - Bringing evolutionary biology before the general public.

Daniel Dreesmann<sup>1,3</sup>, Silke Leverkus<sup>2</sup>, Volker Saul

<sup>1</sup>Institut für Genetik, <sup>2</sup>Institut für Kunst und Kunsttheorie, Universität zu Köln; <sup>3</sup>present address: AG Didaktik der Biologie, Institut für Zoologie, Johannes Gutenberg-Universität Mainz.

### *Abstract:*

Celebrating Charles Darwin's 200th birthday as well as the 150th anniversary of the first edition of "On the Origin of Species", our project used public transportation in Cologne to pique streetcar riders' curiosities for evolution. During their daily commute they should be attracted by colorful artwork and become interested in Darwin-related themes such as evolution and medicine, the evolution of birds and "evolution on our doorstep" which presents research projects carried out around Cologne and in the river Rhine. 20 art students worked more than six months to transform an ordinary streetcar model into a rolling piece of art. During this time of intensive artistic work and discussions about how to communicate evolutionary biology through paintings and drawings to the general public, the streetcar underwent its own evolutionary process. Its final result is a streetcar that is covered inside and out with digitalized artwork printed on a very thin adhesive membrane. This analog-to-digital transition was a true chance to play with motifs in such a way that small paintings could be enlarged – e.g. to visualize the strokes of a brush – and large paintings diminished. The project "Evolution erfahren – Die Bahn zum Darwin-Jahr" was funded by the VolkswagenStiftung through the ideas competition "Evolution today". Please visit [www.evolution-erfahren.de](http://www.evolution-erfahren.de) for pictures and photographs.



## **Johannes Engelken**

*Affiliation:*

Pompeu Fabra University, Barcelona, Spain

*Scientific field of research:*

Human evolutionary genetics

*Study system:*

Modern human populations

*Title:*

Local adaptation of modern humans to micronutrient deficiencies

Johannes Engelken\*‡, Elena Carnero\*, Kun Tang † , Jaume Bertranpetit\*, Mark Stoneking ‡ , Elena Bosch\*

\*Institute of Evolutionary Biology (UPF-CSIC), Pompeu Fabra University, Barcelona, Spain. † PICB Institute for Computational Biology, Shanghai Institutes for Biological Sciences, Chinese Academy of Sciences, Shanghai, China. ‡ Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany

*Abstract:*

During their Out-of-Africa migration and following spread across the globe during the last 100,000 years, human populations were exposed to new environments, unfamiliar diets and different diseases. From an evolutionary point of view, local natural selection may have contributed substantially to the present distribution of human genetic diversity. We hypothesize that certain human genes involved in micronutrient metabolism may have been under natural selection as an adaptation to worldwide micronutrient deficiencies which are known from agriculture as well as from different human populations. Over the last years, genome-wide genotyping and mRNA expression data representing different human populations have become available from cell lines provided by the public HapMap and HGDP projects. We are using these datasets of genetic variation as well as our own resequencing data to detangle the complex genetic patterns of selective sweeps around a number of candidate loci and to identify mRNA expression Quantitative Trait Loci (eQTL). We are following up on potential functional variants in tissue samples, using mainly mRNA expression and protein expression as molecular phenotypes. Our general goal is to characterize evolutionary consequences of pre-historic challenges to the diet of different human populations.

## **Natalia Filipowicz**

*Affiliation:*

Systematic Botany and Mycology, LMU Munich

*Scientific field of research:*

Systematics, biogeography and evolution of angiosperms

*Study system:*

Angiosperms (Solanaceae, Cucurbitaceae)

*Title:*

The worldwide holoparasitic lineage Apodanthaceae confidently placed in the Cucurbitales

Natalia Filipowicz and Susanne S. Renner

*Abstract:*

Apodanthaceae, a clade of c. 19 holoparasitic species classified in three genera (one of them never validly published) and growing in the Americas, Africa, the Near East, and Australia, is one of only two “unplaced” plant families in the latest classification of flowering plants. One reason why Apodanthaceae have remained unplaced is lateral gene transfer between these parasites and their hosts. We performed phylogenetic analyses of 15 accessions representing species from the USA, Chile, and Australia, and a matrix of 190 mitochondrial *matR* sequences from species in 39 of the 66 orders and 95 of the c. 450 families of flowering plants. Apodanthaceae place together with the seven families of Cucurbitales, and this relationship had 100% bootstrap support at the codon level, and 99% at the nucleotide level. Lateral transfer of *matR* between parasites and hosts (which had been suspected in earlier studies) can be excluded because all accessions of apodanths cluster together, rather than with their respective hosts. Apodanthaceae and Cucurbitales moreover share several non-synonymous substitutions not found in other angiosperms. Within Apodanthaceae, the *matR* phylogeny agrees with geography, such that the New World species are sisters to each other, while the Australian accessions form a separate clade.

**Iris Fischer**

*Affiliation:*

Evolutionary Biology & EES Program, LMU Munich

*Scientific field of research:*

Molecular evolution, adaptation

*Study system:*

Wild tomato

*Title:*

The role of the *Asr* gene family in adaptation to drought in wild tomatoes

*Abstract:*

While the threat of climate change becomes more and more concrete, the understanding of drought adaptation mechanisms in plant is becoming a burning issue in term of food safety. In that context, wild tomato species that originated from South America are a valuable model to study the evolution of drought tolerance because they grow in a large range of environments, from mesic to extremely arid. The aim of this study was a better understanding of the role of the *Asr* gene family in the drought adaptation of to closely related species of wild tomatoes: *Solanum chilense* and *Solanum peruvianum*. We sequenced five members of the *Asr* gene family *Asr1*, *Asr2*, *Asr3*, *Asr4* and *Asr5* in several populations of *S. chilense* and *S. peruvianum*. The studied populations were collected in contrasted habitats regarding to water availability to be able to detect local adaptation phenomena. Our results show that the *Asr* members were submitted to contrasted selective pressures. In particular, while *Asr1* appears to be mostly submitted to purifying selection, *Asr4* is involved in local adaptation to dry environments in the *S. chilense* populations.

**Susanne Franssen**

*Affiliation:*

Institute for Evolution and Biodiversity, University of Münster

*Scientific field of research:*

Evolutionary bioinformatics, evolutionary genomics

*Study system:*

Seagrasses (marine angiosperms), legumes

*Title:*

Practical insights from the computational analysis of next generation sequencing reads for a transcriptome database of *Pisum sativum*, a legume model plant

*Abstract:*

Next generation sequencing technologies provide a promising opportunity for non-model organisms to enter the field of evolutionary genomics. EST data sets generated with the longer read NGS technologies, i.e. Roche/454 have already been successfully employed in various higher plant transcriptome sequencing projects. In those projects it is always crucial to establish a reliable and preferably comprehensive backbone of the transcriptome of the study organism, which is affected by library preparation methods as well as strategies for de novo assembly. In this study 450 Megabases of EST reads were generated for the garden pea, *Pisum sativum*, a biochemical model plant with a large genome, 4300 Mb, and no genomic reference available. NGS with the Roche/454 platform was used for various aerial tissue samples, evaluated and a variety of approaches, including normalisation, alternative sequencing technologies, saturation estimation and diverse assembly strategies were evaluated. A comparison between a first and a second pass assembly revealed a significant number of chimeras in the latter. Several of these cases seem to arise because, in the absence of a backbone genome, paralogs cannot be distinguished e.g. from alleles. Data from various leaf libraries indicates that normalization allows partial recovery of expression strength aside the desired effect of increased coverage. Based on theoretical and biological considerations it is concluded that the sequence reads in the database tag the vast majority of transcripts in the aerial tissues. Insights gained from this study assist in establishing a reference transcriptome of the marine angiosperm *Zostera marina*, providing the basis for deciphering heat adaptations of this ecosystem engineering species at evolutionary time scales.

## **Nijuscha Gruhn**

### *Affiliation:*

Institut für Angewandte Genetik, Freie Universität Berlin

### *Scientific field of research:*

Evolution of signaling systems

### *Study system:*

Plants

### *Title:*

Cytokinin perception in *Physcomitrella patens*: Insights into the evolution of phytohormone signaling

### *Abstract:*

The signaling pathway of the phytohormone cytokinin, is based on the two-component signaling system of bacteria and is well characterized in higher plants. However, virtually nothing is known about the evolution of this signaling system. *Physcomitrella patens* is the most basal organism containing all the components for cytokinin signaling and thus can serve as a link between the well-characterized seed plants and the potential origin of this signaling system in green algae. In *Physcomitrella patens* the effect of cytokinin on the transition of the filamental growth stage (protonema) to the leaf like structure (gametophore) is used as a reliable bioassay though its molecular principle is completely obscure. In *Physcomitrella patens* the first step of the cytokinin signaling cascade, as derived from the current model, is represented by three cytokinin binding receptors (*PpCREs*). For investigating the receptors binding to different types of cytokinin, isolated cDNAs coding for *PpCRE1* and *PpCRE2* (all attempts to clone *PpCRE3* were unsuccessful) are expressed in *E.coli*. Cytokinins binding to the receptor and subsequent competition experiments will show binding capacities of the receptors. A further step to investigate cytokinin perception is the construction of stable transformants, overexpressing a cytokinin receptor fused to GFP. Monitoring these lines will show where cytokinin perception takes place in the cell, as well as overexpressing the receptor might result in an enhanced sensitivity to cytokinin. Simultaneously created tobacco plants expressing *PpCRE::GFP* shed light on where cytokinin perception takes place in the cell. For localization of the expression pattern throughout the plant, promoter::reporter fusions for both cloned receptors are in the progress of selecting stable transformants.

**Torsten Günther**

*Affiliation:*

University of Hohenheim

*Scientific field of research:*

Computational population genetics

*Study system:*

*Arabidopsis thaliana*

*Title:*

Methods for natural selection mapping in plants

*Abstract:*

Current next-generation sequencing projects provide sufficiently large datasets for the genome-wide detection of natural selection in many species. Genome-wide scans were able to detect new candidate regions for selection as well as previously identified target genes in humans and other model species. However, unbiased and time-efficient methods are required for the analysis of genome-wide datasets. We present methods to analyze the signature of positive and purifying selection in plant genomes. These methods were tested on simulated datasets under various complex demographic models to assess their power on empirical data. Additionally, we applied the tests to genome-wide SNP and sequence data from *Arabidopsis thaliana* and found some interesting patterns in particular populations.

## Tanja Haus

*Affiliation:*

German Primate Center, Göttingen

*Scientific field of research:*

Hybridization in primates

*Study system:*

Primates

*Title:*

Impact of hybridization on the evolution of green monkeys (*Chlorocebus* spp.)

Tanja Haus, Christian Roos and Dietmar Zinner

*Abstract:*

Green monkeys (*Chlorocebus*) are widely distributed in sub-Saharan Africa. Currently at least 6 species are recognized and hybridization is known from species in Ethiopia and Uganda. Several recent genetic studies of primates, for example of baboons (*Papio*) and macaques (*Macaca*), indicated that hybridization and introgression events are important factors in primate evolution. Green monkeys are most likely an excellent model to examine such processes and the impact of genetic exchange among taxa on primate evolution. Within this project we investigate the molecular phylogeny of green monkeys and the impact of natural hybridization on speciation processes in two contact zones in West and East Africa. We collected faecal samples along the Volta River in Ghana and Burkina Faso in the contact zone of the species *Chlorocebus sabaesus* and *C. tantalus*. In Ethiopia we will collect data in hybrid zones of *C. aethiops*, *C. pygerythrus* and *C. djamdjamensis*. We are analyzing the molecular phylogeny and population genetic structures using different loci of mitochondrial and nuclear DNA. Here we will present first data of green monkey populations in Ghana and Burkina Faso collected between January and March 2010.

## **Emanuel Heitlinger**

### *Affiliation:*

University of Edinburgh, Scotland / Karlsruhe Institute of Technology

### *Scientific field of research:*

Host-parasite interactions, evolutionary transcriptomics

### *Study system:*

Swimbladder-nematode *Anguillicoloides crassus* and two different eel-species.

### *Title:*

The transcriptome of *Anguillicoloides crassus* sampled by pyrosequencing

### *Abstract:*

Currently “next generation” sequencing technologies are considerably expanding the toolbox of researchers working on non-model organisms. Here, work on *Anguillicoloides crassus*, a nematode parasite of freshwater eels, which was introduced from Asia to Europe early in the 1980s is presented. The possible divergence between Asian and European populations is investigated using high throughput 454-pyrosequencing of the nematode’s transcriptome. Emphasis is put on the assembly (different assembly statistics resulting from different assembly algorithms and parameters) as a prerequisite for all downstream analyses. Furthermore protein-prediction based on similarity and de novo methods as well as annotation with GO terms, EC numbers and KEGG pathways are outlined. Identification of Single Nucleotide Polymorphisms (SNPs) from this dataset will provide a wealth of new markers for population-genetic studies. In addition analysis of gene expression using digital transcriptomics (tag-sequencing) or mRNA-seq (direct sequencing of cDNA) on an Illumina Solexa platform is enabled by providing an outline of the transcriptome to map reads generated on this platform. Our experimental design using cross-infection experiments combined with this second technology is briefly presented. Based on the divergence of both sequence and gene expression levels combined with inferences drawn from functional annotation, possible adaptation to the new host and environment should be tested.

## **Corinna Hopfen**

*Affiliation:*

Institute of Population Genetics, University of Veterinary Medicine, Vienna

*Scientific field of research:*

Evo-devo genetics

*Study system:*

*Drosophila*

*Title:*

Genetic dissection of morphological evolution in *Drosophila*

Corinna Hopfen, Alistair P McGregor

*Abstract:*

A central question in evolutionary biology is to understand how morphology evolves. Recently, considerable progress has been made in identifying the molecular changes underlying variation in many traits. Nevertheless, many aspects of morphological evolution remain poorly understood, such as the molecular basis of variation in complex traits like organ size and shape, and the contribution of standing genetic variation to inter-specific differences. The *Drosophila melanogaster* species complex provides many morphological traits like eye size as well as the male external genitalia, which are highly diverged between closely related *Drosophila* sister species. For instance, the morphologies of the posterior genital lobes, claspers and anal plates of male *Drosophila* vary dramatically between species and therefore serve as excellent model traits to address evolutionary questions. In addition, also eye size differs in almost 20% between species. This study is aiming to uncover the molecular genetic basis of inter-specific morphological differences using Quantitative Trait Mapping, in order to broaden our knowledge of how morphology evolves between species.

## **Anja Hörger**

### *Affiliation:*

Evolutionary Biology, LMU Munich

### *Scientific field of research:*

Host-parasite interactions

### *Study system:*

Wild tomatoes (*Solanum peruvianum*, *Solanum chilense*) and their pathogens  
*Pseudomonas syringae*, *Cladosporium fulvum* and *Phytophthora infestans*

### *Title:*

Evolution of pathogen resistance pathways in wild tomato

### *Abstract:*

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 the evolution of several downstream genes involved in two different defense response pathways in populations of a wild tomato species (*Solanum peruvianum*) from South America. Different evolutionary patterns were observed in these genes. Molecules that potentially interact directly with pathogen ligands appeared to be subject to balancing selection. However, we found evidence for strong purifying selection at downstream loci, which are involved in signal transmission and thus show a high degree of connectivity. We discovered that one candidate locus, the Rcr3 gene, is a member of a multi-gene family. We developed functional assays to reveal the evolutionary history of different Rcr3-copies by linking the observed sequence variation to functional differences during the defense response.

## Susanne Horn

### *Affiliation:*

Max Planck Institute for Evolutionary Anthropology, Leipzig

### *Scientific field of research:*

Evolutionary genetics

### *Study system:*

Beavers (Castoridae)

### *Title:*

Evolutionary genetics of beavers (Castoridae)

Susanne Horn<sup>1</sup>, Anne Karin Hufthammer<sup>2</sup>, Norbert Benecke<sup>3</sup>, Charles Schouwenburg<sup>4</sup>, Borut Toskan<sup>5</sup>, Aslak Ermala<sup>6</sup>, Ronny Wolf<sup>7</sup>, Walter Durka<sup>8</sup>, Michael Hofreiter<sup>1,9</sup>

<sup>1</sup> Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany; <sup>2</sup> Bergen Museum of Natural History, Norway; <sup>3</sup> DAINST, Berlin, Germany; <sup>4</sup> Zwartewaal, Netherlands; <sup>5</sup> ZRC SAZU, Slovenia; <sup>6</sup> Finnish Game and Fisheries Research Institute, Finland; <sup>7</sup> University of Leipzig; <sup>8</sup> UFZ Halle, Germany; <sup>9</sup> University of York, UK.

### *Abstract:*

Evolutionary processes shaped the diversity of beavers (Castoridae) for around 40 million years. A variety of Castorids existed at these times, however only the genus *Castor* is still present today. From about 6 million years ago onwards, the genus *Castor* diverged into two separate species, the Eurasian beaver (*C. fiber*) and the North American beaver (*C. canadensis*). In order to estimate the timing for this speciation, mitochondrial genomes were sequenced for several Eurasian beavers as well as one North American specimen. This large set of sequence data shall be used to improve the divergence time estimates on the phylogenetic tree of rodents. In more recent times, a major influence on the Eurasian beaver populations has been made by humans. *C. fiber* was hunted extensively to make use of its fur and meat. Thus, only the genetic analysis of ancient beavers can explain the development of today's phylogeographic structure and allows to assess the genetic diversity of beavers that has been lost during the population bottleneck. Ancient DNA techniques were used for analyzing beaver bone and tooth samples, excavated at historical sites. Using these DNA sequences, we were able to identify potential colonization routes taken by beavers in Central and Northern Europe after the end of the last glacial maximum, around 10'000 years ago. These recolonization patterns help to explain the phylogeographic pattern in extant and extinct beaver populations. Furthermore, new ancient DNA haplotypes could be identified. They clearly show a high genetic diversity in ancient beavers, which were lost during the population bottleneck.

## **Gunther Jansen**

### *Affiliation:*

Christian-Albrechts University of Kiel

### *Scientific field of research:*

Host-parasite interactions, evolutionary medicine, evolutionary ecology, genomics, genetics, microbiology

### *Study system:*

*C. elegans* (host), *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Escherichia coli*, *Bacillus thuringiensis*

### *Title:*

The importance of evolutionary reservoirs for emergent infectious disease

### *Abstract:*

Recent epidemiological observations suggest that diseases such as leishmaniasis, tuberculosis and malaria are on the rise again, despite seemingly successful efforts to eradicate them. The re-emergence of these diseases is often linked to coinfection with HIV or to patients treated with immunosuppressive drugs. Theoretical models confirm that diseases may break out in a population after the causative agent has passed through an adaptive stage in immunocompromised hosts. However, these predictions have not been tested empirically. I propose to address these ideas using an empirical model system for emergent disease. In an experimental evolution setup, I infect artificially immunocompromised *Caenorhabditis elegans* worms (via knock-outs of central immunity genes) with several opportunistic bacteria such as *Staphylococcus*, *Pseudomonas*, *Escherichia* and *Bacillus*. This will yield evolutionary material that can be analysed phenotypically, genetically and genomically across pathogen species and across type of immunocompromisation. The insights I gain will allow me to investigate the mechanisms and dynamics of virulence evolution, pathogen emergence, and finally construct empiry-driven epidemiological models.

## **Mareike Jogler**

*Affiliation:*

DSMZ Braunschweig

*Scientific field of research:*

Bacterial diversity

*Study system:*

Planktonic freshwater bacteria

*Title:*

Bacterial speciation - planktonic freshwater bacteria as a model system

Mareike Jogler, Helge Siemens, Hong Chen and Jörg Overmann

*Abstract:*

The role of recombination, adaptation and selection in shaping bacterial diversity was elucidated by searching for different ecotypes within groups of closely related bacterial lineages (up to 100 % 16S rRNA gene sequence identity). Members of the family *Sphingomonadaceae* constituted an abundant fraction of the *Alphaproteobacteria* in the oligotrophic, alpine Walchensee and the mesotrophic, prealpine Starnberger See. Of these, two phylogenetically tight subgroups of *Sphingomonadaceae*, relatives of *Sandarakinorhabdus limnophila* as well as the novel lineage G1A, were identified by a seasonal clone library as the dominant *Sphingomonadaceae*. These two dominant groups were found to be physiologically active throughout the year by DGGE. In parallel, a large number of *Sphingomonadaceae* could be recovered in pure culture by a high throughput cultivation approach followed by a PCR based *Sphingomonadaceae* screening. Among them were 8 isolates corresponding to the *S. limnophila*-cluster whereas 65 isolates were related to the G1A-cluster. Based on their dominance and year-round activity *in situ* and the availability of several independent pure culture isolates, these two bacterial groups will be used as a model system to elucidate the presence of different ecotypes by qPCR. Their specific ecological niches will be identified by physiological characterisation and *in situ* growth test.

## **Katharina Jörger**

*Affiliation:*

Bavarian State Collection of Zoology, Munich

*Scientific field of research:*

Molecular phylogenetics and biogeography

*Study system:*

Acochlidia (Gastropoda)

*Title:*

Uncovering enigmas from the sand: Molecular phylogeny and evolution of Acochlidia (Heterobranchia, Gastropoda)

*Abstract:*

The Acochlidia are an enigmatic group of heterobranch gastropods, mainly inhabiting marine sands worldwide. Being a small group with only 28 valid species, these slugs are morphologically highly aberrant and diverse, comprising a series of unusual characters (e.g. occurrence secondary gonochorism, lack of copulatory organs, dagger-shaped radulae). While most inhabit the marine mesopsammon, some show adaptations to brackish waters or even truly conquered limnic systems. To explain this and other major events in acochlidian evolution a robust phylogenetic hypothesis is needed. While morphological analyses face the problem of a high degree of convergent development due to adaptations to the similar (interstitial) habitat, molecular markers provide a dataset independent from direct ecological pressures. This study presents a first molecular phylogeny of the Acochlidia based on four markers (nuclear 18S, 28S-sequence and mitochondrial 16S and CoI), leading to a good resolution at all taxonomic levels. Fast evolving mitochondrial markers uncovered a high degree of cryptic species within similar habitats and little geographic distance and on the other hand confirmed species with large-range distribution. Two major lineages (Microhedyllacea and Hedylopsacea) developed two opposite trends of reproduction, both interpreted as special adaptations to a spatially limited and unstable habitat. Based on the presented phylogenetic hypothesis the invasion of limnic systems in Acochlidia is discussed.

**Nadine Klauke**

*Affiliation:*

Department of Evolutionary Biology and Ecology, University of Freiburg

*Scientific field of research:*

Behavioral ecology of birds

*Study system:*

El Oro parakeet (*Pyrrhura orcesi*)

*Title:*

Cooperative breeding – are multiple strategies evolutionary stable?

Nadine Klauke, Tobias Mika, Marie Lucas, Gernot Segelbacher, H. Martin Schaefer

*Abstract:*

The El Oro Parakeet (*Pyrrhura orcesi*) is an endemic parakeet species of Southern Ecuador. During my first field season, I demonstrated that this parakeet breeds cooperatively, a behavior thought to be atypical in parrots. I carried out behavioral observations with nest cameras installed at artificial nest boxes as well as genetic analyses with microsatellite markers. Groups consist of up to eight individuals with predominantly males, but also females helping in provisioning the offspring. The relatedness within flocks is variable most likely due to changing flock composition between breeding seasons. Clutch sizes of up to eight eggs in flocks containing at least two females may indicate that more than one female lays eggs in one nest. So far only one male per flock fathered the offspring. Manipulating nest site availability suggests that this is not a limiting ecological factor leading to cooperative breeding. Instead, cooperative behavior may be explicable by direct benefits such as access to potential mates and gaining experience to breed, but this has to be further evaluated during my project.

## **Enrico König**

### *Affiliation:*

Carl von Ossietzky University of Oldenburg

### *Scientific field of research:*

Host-parasite interactions, molecular evolution, genetics

### *Study system:*

Frog skin peptides, amphibians

### *Title:*

The peptide based defence system in anuran amphibians

### *Abstract:*

Antimicrobial peptides (AMPs) are common weapons against pathogens. They are widely distributed in the animal kingdom as a part of the innate immune system. The hypervariable peptide domain of the AMP gene of frogs was shown to underlie positive selection leading by far to the highest known diversity of antimicrobial peptides. Though, the AMP gene retained a conserved signal sequence. The similarity of the signal peptides indicates a common ancestry of this gene which duplicated several times during evolution of Neobatrachia (“higher frogs”). In previous studies I showed that there are apparently two more signal peptide motifs in “archaic frogs.” However, the neobatrachian signal motif can also be found in other peptide precursors, particularly such encoding neuropeptides which have mammalian counterparts (e.g., bradykinins, dermorphins). Even precursors of the first gene encoded low molecular weight antioxidants recently identified from *Babina pleuraden* (Ranidae) show high similarity to the neobatrachian signal motif. Here I want to present new insights into the peptide based defence system of anuran amphibians which seems to be highly adaptive in order to protect their skin against biological (predators, microorganisms) and non-biological (UV radiation) harms.

**Susanne Kühnel**

*Affiliation:*

Friedrich Schiller University, Jena

*Scientific field of research:*

Evolutionary reproductive morphology, amphibians

*Study system:*

Caecilian amphibians

*Title:*

Evolutionary reproductive morphology of caecilian amphibians

*Abstract:*

Extremely variable life histories and modes of parity make caecilians an ideal model group for evolutionary reproductive morphology studies. Exceptional among amphibians all caecilians practise internal fertilisation with the everted male cloaca aiding as a unique copulatory organ (i.e. phalloseum or phallus). Since research on caecilian cloacal morphology mostly concentrates on males, we present the first single-species study on general and functional morphology aspects of the female cloaca in an oviparous caecilian amphibian (*Ichthyophis cf. kohtaoensis*). Combined with conventional histology we introduced recent techniques such as 3D-reconstruction and soft tissue SR $\mu$ CT-scans to the research field of evolutionary and comparative genital morphology. All females were similar in their overall cloacal structure with differences in size and histology associated with the reproductive cycle. In contrast to previous studies the female cloaca could be divided in two distinct regions, similar to the conditions found in males. The cranial part contains urogenital pockets, which may have a distinct function during oviposition. As a stunning novel feature, the caudal cloacal part possess dorsolateral blind sacs at its onset, which resemble a minute reflection of those known in males of *Ichthyophis* and other species. Finally, the comparative investigation of caecilian copulatory organs in the context of a novel comparative study will give important insight into the evolution of reproduction and life history. The multi-level approach as currently used is the key to fully understand the link between genital morphology and the evolution of reproductive modes in this fascinating but neglected group of tetrapods.

## **Miriam Linnenbrink**

*Affiliation:*

Institute for Experimental Medicine, Christian-Albrechts University of Kiel

*Scientific field of research:*

Evolutionary genomics

*Study system:*

House mouse

*Title:*

Expression variation at *B4galnt2* is associated with a bleeding disorder in house mice – Which evolutionary forces govern this process?

*Abstract:*

The *B4galnt2* gene is a conserved N-acetylgalactosaminyltransferase displaying a gastrointestinal epithelial cell-specific expression pattern in most mammals. In house mice, two highly divergent alleles segregate in natural populations and display complex signatures of selection. One allele class confers a gastrointestinal epithelial cell-specific expression pattern as seen in other mammals, while a second allele class confers a blood vessel expression pattern and is associated with a phenotype in mice that closely resembles a common human bleeding disorder, von Willebrand disease. Previous work showed that different local populations of *Mus musculus domesticus* display dramatic differences in the frequency of these alleles due to the recent action of natural selection. To further understand the nature of these forces, we are currently conducting a fine-scale analysis of allele frequencies across Europe. In addition, to determine whether alternative *B4galnt2* alleles have been maintained by long-term balancing selection, we have performed a population survey of the gene region in a close relative of house mice, *M. spretus*. Our preliminary results indicate that although alternative *B4galnt2* alleles have been maintained since the common ancestor of the *M. musculus* species complex and *M. spretus*, widespread differentiation is present at *B4galnt2* due to local selective pressures.

**Michael Matschiner**

*Affiliation:*

University of Basel, Switzerland

*Scientific field of research:*

Molecular evolution

*Study system:*

Notothenioidei (Antarctic fishes)

*Title:*

A new dating of the notothenioid radiation

*Abstract:*

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

## **Mamadou Mboup**

*Affiliation:*

LMU Munich

*Scientific field of research:*

Evolutionary biology

*Study system:*

Tomato

*Title:*

Evidence of genetic recombination in wheat yellow rust populations of a Chinese oversummering area

*Abstract:*

Wheat yellow rust (*Puccinia striiformis* f.sp. tritici) (PST) has been described as a strongly clonal species in both European and Australian populations, with very limited molecular diversity but rapidly evolving virulences. Contrastingly, marked genetic diversity has been reported in Chinese PST populations. To test whether such variability could originate from oversummering areas, we assessed the diversity of virulence and molecular markers (AFLP and SSR) using 412 PST isolates from the highlands of Tianshui county in Gansu province. Very marked phenotypic and genotypic diversity (38% and 89%, respectively) was found. No genetic structure dependent on the sites sampled ( $F_{st} = 0.004$ ) or altitude distribution ( $F_{st} = 0.0098$ ) was detected, indicating important gene flow at the county scale. This study also revealed genetic recombination between molecular markers and thus strongly suggests the existence of a sexual or parasexual cycle in PST in Tianshui county. The observations of higher rates of sexual spore production in genotypes originating from Tianshui are the very first elements suggestive of the existence of a sexual cycle in this species.

## **Mariana Mondragón-Palomino**

### *Affiliation:*

Department of Genetics, Friedrich Schiller University, Jena

### *Scientific field of research:*

Plant molecular evolution and development

### *Study system:*

Plants

### *Title:*

How to make thousands of different orchid flowers?

### *Abstract:*

With nearly 30,000 species, the orchid family is one of the largest plant groups and its unique variety of flower forms has intrigued scientists for centuries. This major feature and the importance of specific flower characteristics and plant-pollinator interactions make of the Orchidaceae a key group for investigating the genetic basis of morphological diversity. Goethe considered orchids as ‘monstrous lilies,’ while Darwin and others hypothesized about the mechanisms behind their particular flower morphology. However, relatively little is known about the genetics of orchid morphological diversity. Our project approaches this question by determining how changes in the number, sequence and expression of developmental regulatory genes resulted in the formation of orchid-specific flower structures. We study class B MADS-box genes because in angiosperms, they encode transcription factors essential for the development of the perianth. We isolated 25 class B MADS-box genes from a representative group of species and characterized their molecular evolution, pattern of expression and the proteins they encode. The molecular phylogeny of these genes showed that there are four well-supported ancient clades of orchid-specific *DEF*-like class B genes. This finding contrasts with the fact most angiosperms have a single *DEF*-like gene or duplication is relatively recent and species-specific. Based on this phylogeny and the patterns of expression documented in the literature, we developed the ‘orchid code.’ This model considers the identity of the perianth organs is specified by the combinatorial interaction of four *DEF*-like MADS-box genes. We tested the hypotheses derived from the ‘orchid code’ by characterizing the patterns of evolution and expression of the genes we isolated. Here, I discuss these computational and experimental analyses and consider the contribution of gene families to the emergence of morphological novelties during evolution.

## **Hendrik Müller**

*Affiliation:*

Institut für Spezielle Zoologie, Friedrich Schiller University, Jena

*Scientific field of research:*

Evolutionary developmental morphology

*Study system:*

Plethodontid salamanders

*Title:*

Did lungless salamanders re-evolve an aquatic larva?

*Abstract:*

Dollo's Law dictates that structures once lost during evolution can not be regained in the same form; in short, evolution is irreversible. This notion has recently been challenged by reports of the re-evolution of wings in stick insects and other such instances. More interesting even are reports of re-evolved life history traits such as the re-evolution of egg laying from viviparous ancestors in a boid snake or the re-evolution of a tadpole larva in marsupial frogs. Another case in point are plethodontid or lungless salamanders of the genus *Desmognathus*. Phylogenetic evidence suggests that some members of this genus re-evolved an aquatic larval stage from direct developing ancestors. This is highly remarkable because direct development, where known, dramatically alters embryonic development and usually leads to a deletion of larva specific characters from the ontogeny, which would rule out heterochronic shifts in hatching time as a most likely mechanism for regaining an aquatic larva. To address these questions, I study various plethodontid salamanders from different evolutionary lineages, covering species with a primary aquatic larva, species that potentially re-evolved an aquatic larva and direct developing species. My work combines classical morphological techniques like histology and clearing and differential staining with modern imaging techniques such as synchrotron radiation CT scanning and computerized 3D reconstructions, as well as immunostaining and in situ hybridisation.

**Lena Müller**

*Affiliation:*

Evolutionary and Functional Genomics & EES Program, LMU Munich

*Scientific field of research:*

Evolutionary genomics

*Study system:*

*Drosophila melanogaster*

*Title:*

Gene expression variation in natural populations of *Drosophila*

*Abstract:*

Recent advances in genomic technologies have enabled global analyses of gene expression variation among individuals of a species. A surprising finding has been that many species harbour vast amounts of gene expression variation. The goal of this project is the evolutionary and functional analysis of genes showing significant expression variation within and between populations of the fruit fly *Drosophila melanogaster*. The objectives include: 1) microarray experiments to determine gene expression variation in two natural populations, 2) population genetic analyses of coding and regulatory sequences to elucidate the roles of selection, drift, and demography in the maintenance of gene expression variation, and 3) transgenic experiments to functionally test the effects of putative *cis*-regulatory variants on gene expression. So far, we have used microarrays to identify genes showing significant expression differences between adult females from an African and a European population of *D. melanogaster*. The differentially-expressed genes include those with functions in insecticide resistance and proteolysis. Although several of the genes with the greatest expression divergence between populations show the same expression pattern in adult males, the vast majority show a difference only in females. This suggests that sex-specific regulatory adaptation has occurred in response to environmental change.

**Vladislav Nachev**

*Affiliation:*

Humboldt University

*Scientific field of research:*

Virtual pollination ecology

*Study system:*

Neotropical nectar-feeding bats

*Title:*

Cognition-mediated coevolution: discrimination of nectar concentrations in *Glossophaga*

*Abstract:*

From a plant's perspective optimizing the energetic contents of the nectar reward for effective attraction of pollinators poses the so-called Plant Dilemma: even in the absence of costs for nectar production, the plant should not provide rewards that are too profitable for the pollinator, because this might decrease pollen dispersal rate. This effect can be caused by an increase in the number of revisits to the same flower, which leads to geitonogamy, or by a decrease in visitation rate to profitable nectar sources because fewer visits are needed to satisfy the energetic needs of the forager. In order to estimate the fitness losses due to these effects and the general capacity of glossophagine bats to discriminate between nectar concentrations, we conducted a two-alternative free choice experiment with a population of wild *Glossophaga commissarisi*. Bats were marked with RFID tags and their visits to an array of artificial plants (feeders) were recorded individually. From the relative visitation rates to feeders with different nectar concentrations, we calculated individual psychometric functions. We also performed a virtual selection pressure analysis: nectar concentrations were encoded with a virtual genome and virtual pollen transfer and reproductive success were calculated using individual bat visit sequences. In order to estimate the fitness loss due to revisits, we calculated the selection differentials with and without allowing self-pollination and compared them to the expected evolution under genetic drift. Within the assumptions of the model, the fitness losses were found consistent with the Plant Dilemma, but negligible in magnitude.

**Lisha Naduvilezhath**

*Affiliation:*

Evolutionary Biology & EES Program, LMU Munich

*Scientific field of research:*

Theoretical population genetics

*Study system:*

Wild tomato (*Solanum chilense* and *S. peruvianum*)

*Title:*

Estimating parameters of different demographic models

*Abstract:*

We developed a novel composite likelihood method (Jaatha) to estimate demographic parameters such as divergence time, population mutation rates, and migration. We have applied Jaatha to a set of demographic models each with a few and many loci. These different simulation scenarios and comparisons to other methods show that our method gives reasonably reliable results, is fast compared to other available software, and flexible in demographic model choice. The results of using Jaatha on the two recently diverged wild tomato species *Solanum chilense* and *S. peruvianum* will also be discussed.

**Lars Nauheimer**

*Affiliation:*

Systematic Botany and Mycology & EES Program, LMU Munich

*Scientific field of research:*

Plant systematics and biogeography

*Study system:*

*Alocasia* (Araceae)

*Title:*

Biogeography of *Alocasia* (Araceae): colonization of the Malay Archipelago

*Abstract:*

*Alocasia* is a genus of Araceae comprising c. 85 species distributed from Sri Lanka to subtropical Australia. Most species are lowland perhumid to everwet forest understorey herbs, although a few grow on exposed sites or at elevations above 1000 m. *Alocasia* is most diverse on Borneo (c. 40 species), the Philippines (c. 18), and New Guinea (c. 12). Rather few species occur in continental Asia and only a single indigenous species occurs in Australia. Molecular clock analyses based on a fossil-calibrated chloroplast and nuclear DNA dataset (>5000 nucleotides) imply divergence from *Leucocasia* (1 species) on the Laurasian continent in the Oligocene. The topology so far suggests repeated dispersal in the Late Miocene between continental Asia, the islands of the Sunda shelf and the Philippines, and a single dispersal to the islands of Wallacea, New Guinea, and to the Australian continent. This fits with the Miocene climate changing from cool/dry to warm/wet, enabling everwet forest, and with it *Alocasia*, to expand into the Malay Archipelago. Most crown group radiations date to the Pliocene. At least three species occur in Java, Sumatra, and the Malay Peninsula, illustrating possible across-island gene flow. Based on herbarium collections, we have begun climate niche modeling for a few well-collected species.

**Catalina Olano Marín**

*Affiliation:*

EES Program, LMU Munich

*Scientific field of research:*

Plant systematics

*Study system:*

Plants (hemiparasites)

*Title:*

Authentication of Radix Astragali based on PCR-RFLP and phylogenetic relationships of Chinese *Astragalus* species using DNA sequence analysis

*Abstract:*

During centuries the Chinese medicine Radix Astragali has been widely used due to its therapeutic value. Although the official source of the medicine comes from the root of *Astragalus mongholicus* some other *Astragalus* species are often marketed either as sources or as adulterants, and thus, the therapeutic effects of *A. mongholicus* are not achieved. This situation could be due to problematic infrageneric taxonomy and species delimitation of the genus. It is thus important to assess the phylogenetic relationships, as well as the identification and authentication of the *Astragalus* species related to Radix Astragali. PCR-restriction fragment length polymorphism (PCR-RFLP) analysis was applied to the Internal Transcribed Spacer region (ITS1, 5.8S rRNA, ITS2) for the identification of *A. mongholicus*. For this analysis, two distinctive sites which are recognized by the restriction endonucleases *FspI* (NsbI) and *RasI* (Csp6I) were identified. This method provides effective and accurate identification of *A. mongholicus*. The phylogenetic relationships among the species were determined using GenBank ITS sequences of thirty taxa of *Astragalus*.

## **Francesco Paparazzo**

*Affiliation:*

Evolutionary Biology & EES Program, LMU Munich

*Scientific field of research:*

Host-parasite interactions

*Study system:*

*Drosophila*

*Title:*

Host parasite coevolution in *Drosophila melanogaster*

*Abstract:*

The goal of the project is to gain insight into the evolution of the innate immunity genes in *Drosophila melanogaster*. We develop population genetics methods to detect genes involved in host-parasite coevolution and that have been under recent selection. We are particularly interested in the type of selection acting on these genes and in the distinction of the resulting coevolutionary scenarios (e.g. trench warfare vs. arms race). Therefore, we plan to infect *Drosophila melanogaster* populations coming from distinct localities (Africa, Asia and Europe) with the fungus *Beauveria bassiana*. Then we perform microarray experiments to investigate the transcriptional response to infection and to identify immunity genes which present expression patterns indicative of natural selection. We sequence the candidate genes to obtain DNA polymorphisms from our populations and we apply our statistical methods to these data and to polymorphism data obtained from previous genome scans.

## **Pavlos Pavlidis**

*Affiliation:*

Evolutionary Biology, LMU Munich

*Scientific field of research:*

Evolutionary genomics

*Title:*

msABC: a modification of Hudson's ms to infer demographic history using multi-locus SNP data

Pavlos Pavlidis, Stefan Laurent, and Wolfgang Stephan

Demographic inference aims at revealing the past population size changes that a population has experienced. Furthermore, it is important for detecting selection because it comprises the null hypothesis. Recently, Approximate Bayesian Computation (ABC) approaches provide a simple, and robust framework, that can be used in order to infer the demographic history of a single or multiple populations using SNP datasets and coalescent simulations. We present here msABC, a coalescent-based software that facilitates the simulation of multi-locus data, suitable for an ABC analysis. msABC is based on Hudson's ms algorithm, which is used extensively for simulating neutral demographic histories of populations. The flexibility of the original algorithm has been extended so that sample size may vary among loci, missing data can be incorporated in simulations and calculations, and a multitude of summary statistics for single or multiple populations is generated. The source code of msABC is available at <http://bio.lmu.de/~pavlidis/msabc>.

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*Title:*

Detection and fine-mapping of selective sweeps in the human genome

Johannes Engelken and Pavlos Pavlidis

*Abstract:*

The recent availability of dense, genome-wide polymorphism data from different human populations together with improved statistical tools have led to the identification of several hundred candidate loci as putative targets of positive selection. For a small subset of these loci, functional polymorphisms have been identified which affect traits like skin color or lactase persistence and hereby suggest a biological explanation for the observed genomic patterns. Here, we examine how different statistical tests perform on detecting and fine-mapping positive selection in seven such loci from the human genome. Among these, different polymorphisms at the OCA2/HERC2 locus have been demonstrated to have a strong association with eye color variation in Europeans and independently, with skin color in Asians.. In the case of the LCT locus, a regulatory polymorphism linked to

the persistence of lactose tolerance to persist into adulthood has been included in our comparison. Specifically, we scrutinize the performance of linkage disequilibrium-based and site frequency spectrum-based statistical tests to confirm and to fine-map selective sweeps in these loci. Additionally, we examine the performance of combining those methods into a machine learning framework. Neutral demographic scenarios are included into the analysis as null hypothesis. By examining the behavior of the tests in the neutral scenarios we obtain a cutoff value, and alternatively in the case of the machine learning framework, we train the algorithm to detect the neutral class. We hope that these efforts will help facilitate the identification of functional variants in genomic regions under positive selection.

## **Pleuni Pennings**

*Affiliation:*

LMU Munich

*Scientific field of research:*

Population genetics, theory, resistance

*Study system:*

Ants, HIV

*Title:*

Non adherence and the evolution of drug resistance

*Abstract:*

Drug resistance is a major problem in diseases such as cancer, malaria and HIV and despite strategies to avoid resistance (such as combination therapy) resistance still occurs and many questions remain. One question is why non-adherence (when a patient doesn't take his drugs as prescribed) sometimes increases and sometimes decreases the risk of evolution of resistance. In principle, non-adherence can both slow down the evolution of resistance, because selection pressure decreases, or it can speed up the evolution of resistance, because the evolving population (e.g., the virus population) will grow, leading to more genetic variation on which selection can act. Whether the net result of non-adherence is slower or faster evolution must therefore depend on factors such as drug or virus characteristics, but it is not yet understood how. HIV is an ideal model to study the effect of the level of adherence on the evolution of drug resistance for two reasons: 1) because a patient usually gets infected with HIV once and patients stay infected for life. An HIV strain therefore evolves within a patient for many years, independently from HIV strains in other patients. Every patient therefore represents an independent evolutionary history of a viral population. 2) The second reason for studying HIV is that there are good data available on patient adherence, on drug characteristics, and resistance mutations. I will combine stochastic modeling approaches and data-analysis to reach a better understanding of adherence-resistance relationships. The results will allow for design of better treatment strategies.

## **Ina Pokorny**

### *Affiliation:*

Evolutionary Biology, University of Potsdam

### *Scientific field of research:*

Basic and applied research on MHC in different vertebrates

### *Study system:*

Ducks, tigers, amphibians

### *Title:*

MHC variability in captive and wild Indian tigers

### *Abstract:*

Indian tigers are endangered, and therefore the study of adaptive genetic variation could be essential to gain information on functionally important genes for further conservation management. Here we present the first results of ongoing analyses of MHC class I and MHC DRB genes in wild and captive tigers from India. We were able to amplify alpha-1 and alpha-2 domain of MHC class I and beta-1 domain of MHC class II DRB genes. We detected high variability in peptide binding sites and give evidence that positive selection is acting on these functional important sites. Phylogenetic analysis revealed that trans-species evolution is acting on MHC in tigers and Felidae relatives. Tigers showed a low MHC variability, especially among DRB genes, which is comparable to that of other endangered big cats. Captive and wild tigers do not significantly differ in MHC variability, but four alleles appeared in wild tigers and were absent in zoo populations. Northern populations of tiger exhibit one allele more than tigers from Central India. We further successfully amplified MHC DRB alleles from scat samples. Non-invasive sampling of endangered species with low individual densities and big home ranges becomes more and more important. Our first results lay the basis for further more detailed analysis of MHC variability in Indian tiger populations.

## Sylvia Ritter

### *Affiliation:*

Helmholtz-Centre for Environmental Research – UFZ

### *Scientific field of research:*

Evolutionary biology of social parasitic butterflies

### *Study system:*

*Phengaris* (butterfly) - *Myrmica* (ants) parasite-host model system

### *Title:*

Undiscovered diversity within *Phengaris nausithous* and *P. teleius*? Evidence for the existence of cryptic species within an endangered butterfly species.

Sylvia Ritter, Josef Settele, Stefan Michalski, Walter Durka

### *Abstract:*

Cryptic speciation in morphologically well defined species is a fundamental problem of taxonomy, ecology, and conservation. DNA sequence divergence analysis of the mitochondrial marker gene Cytochrome Oxidase I (COI) is a tool often used to resolve inter- and intraspecific phylogenetic relationships. A high COI divergence within well defined species may indicate morphologically hardly detectable cryptic speciation and provide an essential knowledge for decision-making in nature conservation, e.g. population re-introduction programs. The myrmecophilous, highly socially parasitic butterfly species of the genus *Phengaris* (*Maculinea*) are of high scientific (host-parasite model system) and nature conservation (European Habitats' Directive) interests. In a previous molecular genetic study on the genus level cryptic speciation was hypothesized in *Phengaris nausithous* and *P. teleius* (Als et al. 2004), two butterfly species which experience a dramatic decrease of populations in Europe mostly because of a loss of their habitats. In this study we present the phylogenetic relationships within both species based on the DNA-sequence of the mitochondrial molecular marker gene Cytochrome Oxidase I (COI). The comprehensive sample set for each species includes around 30 populations each, from their whole Palaearctic distributional range. Despite similar distributional ranges the two species differ in the degree of genetic differentiation among regions, which may indicate ongoing speciation processes in one of the species.

**Olivia Roth**

*Affiliation:*

Leibniz Institute for Marine Sciences IFM-GEOMAR, Kiel

*Scientific field of research:*

Host-parasite interactions

*Study system:*

The pipefish *Syngnathus typhle*

*Title:*

Evolutionary costs and benefits of trans-generational immune priming in a sex-role reversed fish

*Abstract:*

The transfer of genetic information across generations is a prerequisite of evolution. However, information can also be transferred to offspring non-genetically. Such trans-generational effects are of particular relevance in host-parasite interactions, where vertebrate mothers transfer antibodies to their offspring via eggs, blood or milk. Given the fitness costs and prevalence of parasites, such trans-generational immune priming may profoundly affect coevolutionary dynamics. The transfer of immunity from mothers to offspring is consistent with parental investment theory, because mothers invest more into rearing their offspring than fathers. However, in a species like *Syngnathus typhle* where males breed eggs in a placenta-like brood pouch (sex-role reversed), male investment is high. Thus, males and females may transfer immune components to the offspring. This prerequisite would give us an ideal system to study genetic and phenotypic determinants and their interaction of parasite resistance on both, paternal and maternal side. An activation of the immune defense through the transfer of immunity is likely to be traded-off with other life-history traits, hence, costs for both, parents and offspring are to be expected. We therefore predict trans-generational immune priming to be less beneficial under a genetically constant parasite regime than under rapidly changing parasite genotypes.

## **Philipp Schiffer**

### *Affiliation:*

Zoological Institute, University of Cologne

### *Scientific field of research:*

Evolution of sex and speciation

### *Study system:*

Nematoda

### *Title:*

Evolution in parthenogenetic organisms – a multiplex analysis of inter- and intra- specific variation in the nematode Genus *Panagrolaimus*

### *Abstract:*

It stands to question whether or not parthenogenetic reproduction allows the establishment of genetically distinct populations due to variation and selection as in gonochoristic species and if it is thus possible (and necessary) to assign species status to closely related parthenogenetic strains. Intra- or inter-specific variation, however, cannot be addressed straight forward in parthenogenetic organisms, as the Biological Species Concept (BSC) cannot be applied and the Morphological Species Concept (MSC) is rendered dubious due to recently revealed cases of cryptic speciation in many taxa. Biologists, therefore, resort to the Phylogenetic Species Concept (PSC). Until recently this concept suffered from pitfalls caused by divergent single gene genealogies and 'universal' markers, which actually turned out to be not generally applicable. However, employing Next Generation Sequencing (NGS) it is now possible to overcome such limitations by generating a much broader genetic data base. In this study I will investigate species status within a group of parthenogenetic nematodes from the genus *Panagrolaimus* - where several phylogenetic 'standard' markers had turned out to be non-informative. Morphologically extremely similar roundworms of this cosmopolitan genus can be found in sandy and dry top soil. Therefore, in a multiplex Illumina assay I will sequence full mitochondrial genomes of several parthenogenetic individuals from this taxon - originating from different locations - as well as closely related sexual representatives. In addition, I plan to carry out a morphological analysis. This should yield information concerning not only genus phylogeny but also intra- and inter- species relationships between closely related parthenogenetic organisms.

## **Martin Schmelz**

*Affiliation:*

Max Planck Institute for Evolutionary Anthropology, Leipzig

*Scientific field of research:*

Social cognition in great apes

*Study system:*

Non-invasive behavioral tests on captive great apes (chimpanzees) at the Zoo Leipzig

*Title:*

Chimpanzees think about what others are thinking

Martin Schmelz, Josep Call & Michael Tomasello

*Abstract:*

If chimpanzees are faced with two opaque boards on a table, in the context of searching for food, they do not choose the one lying flat (because if food was under there it would not be lying flat), but rather they choose the slanted one - presumably inferring that some unperceived food underneath is causing the slant (Call, 2007). Here we demonstrate that chimpanzees know that other chimpanzees in the same situation will make a similar inference. In a back and forth foraging game, when their competitor had chosen before them, chimpanzees tended to avoid the slanted board on the assumption that the competitor had already chosen it. Chimpanzees can determine the inferences a conspecific is likely to make and then adjust their competitive strategies accordingly.

## Patrizia Sebastian

### *Affiliation:*

Systematic Botany and Mycology & EES Program, LMU Munich

### *Scientific field of research:*

Molecular phylogenetics and biogeography

### *Study system:*

Cucurbitaceae (Cucumis & Sicyos)

### *Title:*

Melon and cucumber originated, and likely were domesticated, in India, not Africa: evidence from wild relatives, ancestral area reconstruction, and known centers of plant domestication

Patrizia Sebastian<sup>1</sup>, Hanno Schaefer<sup>2</sup>, Ian R. Telford<sup>3</sup>, Susanne S. Renner<sup>1</sup>

<sup>1</sup>Department of Biology, University of Munich, Germany; <sup>2</sup>Imperial College London, Silwood Park Campus, Ascot, United Kingdom. <sup>3</sup>N.C.W. Beadle Herbarium, The University of New England, Armidale, NSW, Australia

### *Abstract:*

*Cucumis sativus* (cucumber), the 6<sup>th</sup> angiosperm to have its complete genome sequenced, and *Cucumis melo* (honeymelon), are among the most important vegetable crops worldwide. Their wild relatives, geographic origin, and place(s) of domestication are unclear. One recent molecular study suggested an African origin of *C. melo* (Ghebretinsae et al., 2007), while another inferred that *C. melo* is sister to an Australian/Asian clade that includes *C. sativus* (Renner et al., 2007). Using six plastid and nuclear markers, we sequenced 104 relevant herbarium and fresh collections of *Cucumis* from Africa, Asia, and Australia. The results reveal that melon and cucumber have numerous previously overlooked species-level relatives in India, Indochina, Australia, and around the Indian Ocean (including East Africa). Range reconstruction using maximum likelihood suggests Asia as the most likely ancestral area for the most recent common ancestor of melon and cucumber, and both species have extant wild progenitors in Himalayan India. Based on a molecular clock, the common ancestor of *C. melo* and its Indian and Australian sister species diverged from the remaining Asian/Australian *Cucumis* species 11±4 Ma. These results imply that the search for crossable wild species related to melon and cucumber from now on should concentrate on their newly identified relatives in Asia and Australia, instead of supposed “wild melons” in sub-Saharan Africa or the Middle East. The Indo-Gangetic plain is a well-known center for crop domestication, and the oldest *C. melo* seeds, dated to 2200-1700 BC, have been reported from the Indus Valley.

## **Charlotte Störmer**

### *Affiliation:*

Zentrum für Philosophie und Grundlagen der Wissenschaft, University of Gießen

### *Scientific field of research:*

Human life-history evolution

### *Study system:*

Historic (18<sup>th</sup> and 19<sup>th</sup> centuries) human population of the Krummhörn region (Ostfriesland)

### *Title:*

Sex differences in the consequences of early-life exposure to epidemiological stress – a life-history approach

### *Abstract:*

Exposure to infectious disease in early life has been suggested to have a negative effect on later-life survival, possibly through the induction of inflammatory responses. Although a life-course perspective emphasizes the importance of both survival and reproduction for individual fitness, to date no studies have investigated whether early-life exposure to infectious disease has an impact on reproduction as it has been suggested for later survival. To address this question I have used family reconstitution data from a historical (18<sup>th</sup> and 19<sup>th</sup> century) human population in the Krummhörn (Germany) comparing survival and reproduction between an exposed and a non-exposed group. The exposed group comprised those exposed to a high infectious disease load during prenatal and early postnatal development. The results show a marked sex difference in the impact of early-life exposure to infectious disease. Exposed females show no effect on their life expectancy but significantly reduced fertility (number of children). For exposed males, however, the effect on survival is opponent over time: mortality is increased during childhood but decreased in late adulthood. Above that, exposed males reproduce earlier and have a smaller proportion of surviving children. Accordingly, this study does not support former studies indicating a negative association between early-life disease load and later survival. I argue that due to differences in male and female life strategies males in general are more vulnerable especially early in life. Hence, i.e. adverse environmental conditions may have a stronger effect on male survivability and reproductive performance.

## **Aurelien Tellier**

*Affiliation:*

Evolutionary Biology, LMU Munich

*Scientific field of research:*

Population genetics and host-parasite interactions

*Study system:*

Wild tomato species

*Title:*

Demography, population history and selection in wild tomato species

Aurélien Tellier and Wolfgang Stephan

*Abstract:*

A key question in evolution is to study how species adapt to different abiotic and biotic environments. More specifically, population geneticists aim to reveal genes under Darwinian selection underlying these adaptations. However, since the seminal work of Kimura on the neutral theory of evolution, various demographic and random historical events are known to create pattern of genetic polymorphism similar to those expected under selection. Our general objective is thus to disentangle the consequence on polymorphism of demographic events acting at a whole genome scale from that of selection acting at a given target locus. Our biological models are four wild tomato species *Solanum* sp. found in South-America. Populations of these species are found in various fragmented habitats ranging from costal deserts to the high altitude of the Andes Mountains reflecting possible genetic adaptations to drought or cold. First, we infer from sequence data parameters of life history traits such as seed bank, and of population history such as migration rates among populations and species expansion. This is realized for each species using a Bayesian analysis framework. Second, we study the level of purifying and positive selection in seven genes in our four species. We correlate the strength of selection to stress conditions in different abiotic environments.

**Dr. Arndt Telschow**

*Affiliation:*

Institute for Evolution and Biodiversity, University of Münster

*Scientific field of research:*

Theoretical biology, bioinformatics

*Study system:*

*Wolbachia & Nasonia*

*Title:*

Horizontal gene transfer between *Wolbachia*, *Nasonia*, and Pox-viruses

Arndt Telschow, Andrew Moore, Andreas Schueler, Erich Bornberg-Bauer

*Abstract:*

As part of the *Nasonia* genome project, we annotated the protein domains of *Nasonia vitripennis* using HMMER2 and domain models obtained from Pfam A and B. Protein domains and their properties were compared to 17 fully sequenced arthropod genomes consisting of 12 *Drosophila* species as well as *Apis mellifera*, *Anopheles gambiae*, *Aedes aegypti*, *Tribolium castaneum*, and *Daphnia pulex* (Werren et al. 2010, Science). While the global properties of *Nasonia* do not differ much from the other arthropods, the study of protein domain arrangements in *Nasonia* relative to other organisms has uncovered an intriguing case of possible ancient horizontal gene transfer involving pox viruses, *Wolbachia* and *Nasonia*: thirteen ankyrin repeat bearing proteins in the *Nasonia* genome also contain a C-terminal PRANC (Pox proteins Repeats of ANkyrin - C terminal) domain. The PRANC domain was previously only known in pox-viruses. Screening of other genomes uncovered a second source of ANK-PRANC bearing genes in *Wolbachia* and some related *Rickettsia*. A phylogenetic analysis of the PRANC-domain sequences clearly indicates that the PRANC domain containing proteins underwent amplification and divergence in *Nasonia* subsequent to one or more horizontal acquisition events. *Nasonia* and *Wolbachia* PRANCs are more similar to each other relative to pox virus PRANCs. The most likely explanation therefore is that the *Nasonia* acquired an ANK-PRANC protein from *Wolbachia* by horizontal gene transfer.

## Francisco Javier Velásquez Puentes

*Affiliation:*

EES Program, LMU Munich

*Scientific field of research:*

Phylogeography

*Study system:*

Birds

*Title:*

Diversification of *Myadestes ralloides* (Passeriformes, Turdidae) through the Andes in Colombia

*Abstract:*

The Andean complex harbors an enormous diversity of bird species. This is due in part to the geographical features and historical events which promoted the diversification of several species. The species *Myadestes ralloides* (Passeriformes, Turdidae) is a common tropical bird widely distributed through the Andean complex. In this study, we wanted to know firstly the relationship of *M. ralloides* with its Central American relatives (*Myadestes melanops* and *Myadestes coloratus*) and the relationship among different populations of *M. ralloides*. Secondly, we wanted to establish if geographical factors such as the valleys which divide the Andean mountains in Colombia are important barriers against gene flow. And thirdly, we wanted to know if historical factors such as the Pleistocene glaciations affected the diversification of this species as a response to the repeated compression and expansion of the Andean vegetation layers. In order to answer these questions we used the ATPasa6&8 mitochondrial gene. We obtained genealogical reconstructions and also performed population genetic analyses. Firstly, our results suggest an unresolved monophyly of *M. ralloides* with its Central American relatives. Secondly, we found several important geographical barriers against gene flow, such as the Magdalena valley which separates the eastern slope from the central slope in Colombia. Finally, climatic changes during the Pleistocene probably did not affect the historical demography of Colombian populations of *M. ralloides*. This study demonstrates the importance of the Colombian Andean region in terms of the evolutionary processes which promote the diversification of Andean bird species and contribute to studies of phylogeography in montane bird taxa.

## **Vera Weisbecker**

*Affiliation:*

Friedrich Schiller University, Jena / Cambridge University, England

*Scientific field of research:*

Mammalian brain evo-devo

*Study system:*

Mammals

*Title:*

A comparative anatomist's approach to neuroscience

*Abstract:*

Modern neurosciences are largely concerned with cellular and physiological details of primarily human brain morphology and function. However, mammalian brain evolution exhibits striking regularities that provide insights into the developmental and structural properties of the human brain. As a consequence, diverse neuroscientific disciplines - language evolution theory to computational connectivity research - draw heavily on comparative-anatomical and developmental research of mammalian brain evolution. My research focuses on some of the current paradigms of mammalian brain evolution and development. In the last year, I have published critical appraisals of the mechanistic "late equals large"-hypothesis, which posits that mammalian neurogenesis is highly conserved and translates into a developmental constraint on mammalian brain partition patterns. My re-analysis of the available data shows that neither is neurogenesis particularly conservative, nor does it reflect on relative brain partition size. My second focus has been the evolution of brain size across mammals. I showed that basal metabolic rate, which has previously been considered an indispensable correlate of mammalian brain size, is not required for the growth of a large brain. Furthermore, I demonstrated that mammalian brain size evolution interacts more tightly with brain development (particularly neonatal brain maturity) than previously assumed. I am currently collecting and CT-scanning mammalian developmental series for developmental research on the development of mammalian brain size and partitions. In addition, I am running palaeontological projects on the evolution of brain size in early mammals and their predecessors.

## **Ricardo Wilches**

### *Affiliation:*

Evolutionary Biology & EES Program, LMU Munich

### *Scientific field of research:*

Population genetics, adaptive evolution

### *Study system:*

*Drosophila melanogaster*

### *Title:*

The putative role of an X-linked candidate gene expression regulator on cold adaptation in *Drosophila melanogaster* as revealed by selection mapping and gene expression experiments

### *Abstract:*

Genome-wide genetic variation surveys reveal regions with polymorphism patterns that cannot be explained by an assumed genetic null model (i.e., neutrality and demography). These outlier regions are likely to bear the footprints of past selective events. Identifying the causes of these events leading to adaptive evolution is central to interpreting the species' ecological and evolutionary traits. I have chosen to study in detail the polymorphism patterns of one such outlier X-linked regions previously identified in European *Drosophila melanogaster* surveys. The region also co-localizes with a recently found quantitative trait locus (QTL) associated with recovery after cold stress exposure in the same population. I found a pattern of polymorphism that can be explained by a selective event (sweep) that occurred in an ancestral African population and subsequently spread to Europe. This sweep falls into a 3.5 kb-long intergene region, which has a likely role as gene expression regulation sequence. Therefore two genes in the vicinity of this region became candidate genes to study gene expression differences between populations and under chill comma recovery conditions. My ongoing research suggests that the expression of one such gene is enhanced during chill comma recovery in European flies.

This finding can be taken as preliminary evidence of an adaptive role of cis-regulatory sequences on the adaptation of *Drosophila* to temperate zone climate conditions.

## **Lothar Wissler**

### *Affiliation:*

Institute for Evolution and Biodiversity, University of Münster

### *Scientific field of research:*

Evolutionary bioinformatics

### *Study system:*

Plants

### *Title:*

Back to the sea twice: The molecular basis of seagrass adaptation to marine life

### *Abstract:*

Seagrasses are a polyphyletic group of monocotyledonous angiosperms that have adapted to a completely submerged lifestyle in marine waters. Here, we exploit two collections of expressed sequence tags (ESTs) of two wide-spread and ecologically important seagrass species, the Mediterranean seagrass *Posidonia oceanica* (L.) Delile and eelgrass *Zostera marina* L., which have independently evolved from terrestrial ancestors to fully marine existence. This replicated yet independent evolutionary history facilitates the identification of traits that have evolved in parallel and were thus instrumental for adaptation to a marine habitat. By using orthologous gene sequences from moss, six terrestrial, and the two seagrasses *Z. marina* and *P. oceanica*, we identified those genes which evolved at an accelerated rate in seagrass branches of the phylogenetic tree. Of all 171 analyzed orthologous gene clusters, 35% indicated signs of distinct evolutionary rates, and 34 genes (20%) showed evidence for positive selection in seagrasses. Characterization of these positively selected genes using the Gene Ontology (GO) uncovered that significantly more genes than expected by chance are localized in chloroplasts or are structural constituents of ribosomes. Additionally, results indicate that genes involved in the processes of carbon fixation and photosynthesis (mostly concerning light harvesting and non photochemical quenching) have been positively selected. However, no genes conferring tolerance to higher levels of salinity could be identified.

**Meike Wittmann**

*Affiliation:*

EES Program, LMU Munich

*Scientific field of research:*

Theoretical evolutionary ecology

*Study system:*

*Daphnia*

*Title:*

Can *Daphnia lumholtzi* invade European lakes? The role of stochasticity and life-history evolution in biological invasions

Meike Wittmann, Jonathan M. Jeschke, Christian Laforsch & Wilfried Gabriel

*Abstract:*

In spite of all research effort to identify characteristics of successful invaders and invulnerable communities, biological invasions remain largely unpredictable. Because introduced populations are almost always small initially after their introduction, demographic stochasticity and the characteristics of the introduced individuals play a major role in determining whether a population can establish or goes extinct. Furthermore, introduced species can adapt to new environments, both by phenotypic plasticity and through evolutionary processes. These factors can be incorporated into an individual-based model, which tracks the fates of individuals in a population rather than abundances of homogeneous classes of individuals. We illustrate the approach using the example of *Daphnia lumholtzi*, a cladoceran that is native to the Palearctic and invasive in North America. To investigate whether *D. lumholtzi* could also potentially invade European lakes, we developed an individual-based simulation model for the dynamics of native and introduced *Daphnia* that takes into account individual variation and stochasticity in life-history events, phenotypic plasticity and predation. Because life-history strategies in the model are heritable and cause differential reproductive success, evolution of *Daphnia* life histories can emerge from the model and influence the outcome of the introduction. The model is parameterized with information from the literature and predation experiments. By simulating introduction events, we can derive testable predictions on how the invasion success of *Daphnia lumholtzi* depends on the characteristics of the introduced clone and biotic (e.g. predation pressure) as well as abiotic (e.g. temperature) conditions.

**Katharina C. Wollenberg**

*Affiliation:*

OEB, Harvard University, USA

*Scientific field of research:*

Lineage diversification, phylogeography

*Study system:*

*Anolis* lizards

*Title:*

Inferring lineage diversification in a widespread species of *Anolis*

K. C. Wollenberg & J. B. Losos

*Abstract:*

The Caribbean Greater Antilles are thought to host *in situ* speciation. The widespread anole species *Anolis cybotes* inhabits the Greater Antillean island of Hispaniola. *Anolis cybotes* has previously been found to show high intraspecific differentiation, and that diversification among the trunk-ground anoles of the *cybotes*-group species is explained by adaptation to different habitat types (Glor et al., 2003). We inferred whether lineage diversification among populations of *A. cybotes* is equally explicable by habitat type and whether geomorphology plays a role in promoting these high levels of divergence. Two transects were sampled (i) one transecting Hispaniola in the East and (ii) one along the border between Dominican Republic and Haiti. Transect (i) was characterized by uniform habitat type and a uniform topography, while (ii) was characterized by a wide range of habitats allocated to complex geomorphology. A preliminary phylogeny of ~200 sampled specimens showed high additional genetic variation among populations. Geomorphology significantly explained the prevalence of different clades, levels of morphological divergence (of the toepads, skeleton and dewlap), and differences in niche utilization by *A. cybotes*. We did not find an association of habitat types with altitude along the sampled transects. While different subclades were indeed found in different habitat types, habitat type however did not explain most morphological variation in *A. cybotes*. This suggests, that geomorphology is a main predictor of morphological and genetic diversity. Skeletal and dewlap morphology covaried with altitude in paraphyletic clades, which furthermore suggests that these similarities evolved convergently.

**Daniel Živkovic**

*Affiliation:*

Evolutionary Biology, LMU Munich

*Scientific field of research:*

Theoretical population genetics

*Title:*

Analytical results on the allele frequency spectrum for time-varying population size based on diffusion theory

*Abstract:*

The allele frequency spectrum has attracted a great deal of attention for the simultaneous inference of the demographic and adaptive history of populations. In a recent study, Evans et al. developed a forward diffusion equation describing the allele frequency spectrum, when the population is subject to size changes and selection. From the diffusion equation, the authors derived a system of ordinary differential equations (ODEs) for the moments in a Wright-Fisher diffusion with varying population size and constant selection, but did not find a rigorous solution for this set of ODEs. Here, we present an explicit solution for this system of ODEs with variable population size, but without selection. Then, we use this result to derive the frequency spectrum of a sample for time-varying population size. We relate the obtained forward-in-time-solution for the allele frequency spectrum under variable population size to the backwards-in-time-solution by Griffiths and Tavaré that was previously derived via coalescent theory. In conclusion, we discuss the applicability of the theoretical results to the analysis of nucleotide polymorphism data.