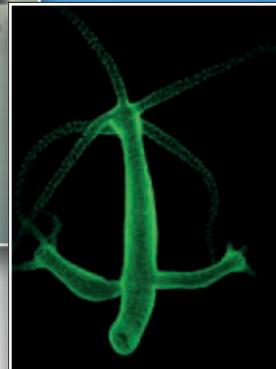
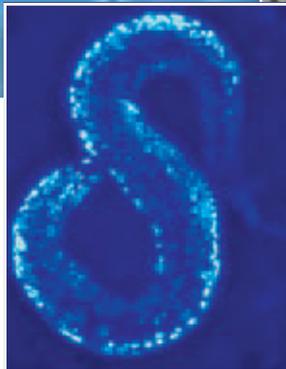


ABSTRACTS



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109<sup>th</sup> ANNUAL MEETING of the GERMAN  
ZOOLOGICAL SOCIETY  
Deutsche Zoologische Gesellschaft

14–17 September 2016 | UNIVERSITY OF KIEL



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**109th ANNUAL MEETING of the  
GERMAN ZOOLOGICAL SOCIETY (DZG)**  
14–17 September 2016

Abstracts

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## INTRODUCTORY LECTURE

### **History of Zoology in Kiel**

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The Zoological Institute of Kiel University traces its origins to 1775, when the Danish entomologist Johann Christian Fabricius became the first Professor for Natural Sciences, Economy and Cameral Sciences in Kiel. This coincided with the opening of the Zoological Museum, where Fabricius founded the zoological collection in Kiel and started the modern entomological research in describing more than 9000 insect species and developing new classification concepts for insects.

In the 19th century the zoological research expanded to many fields as anatomy, ecology, systematics and evolutionary research. One major focus became the marine science.

Since the appointment of Karl August Moebius as the first "real" professor for Zoology in 1868, members of the Institute have been responsible for some major advances in marine zoology, as well as the realization of many of today's prominent marine expeditions. For example, it was in this Institute that Karl August Moebius discovered the principles of biological interactions defining the term "Biocenosis". Viktor Hensen coined the term "Plankton" and started a revolutionary research on this field. Adolf Remane discovered one of the last unknown habitats, the Mesopsammon and defined the criteria of homology.

Famous expeditions with a strong participation of Kiel zoologists were the Plankton Expedition (1899), the German Deep Sea Expedition (1898-1899) or the German South Polar Expedition (1901-1903).

## KEY NOTE

### **Darwin's blind spot: the microbial making of a species**

\*S. Bordenstein<sup>1</sup>

<sup>1</sup>Vanderbilt University, Departments of Biological Sciences and Pathology, Microbiology, & Immunology, Nashville, TN, USA

Unprecedented attention to our microbial world has in part turned the fields of zoology and botany inward—toward a new awareness and understanding of the universality and complexity of host-microbiota relationships. Here, I present our laboratory's work on the origin of animal species in light of this conceptual shift. Specifically, we ask how do closely related host species vary in their bacterial symbiont communities? Does host evolutionary history affect microbiota differences between species? And what is the role of the microbiota in reproductive isolation and animal speciation? Overall, answers to these questions indicate that the composition and functional effects of an animal's microbial community can be closely allied with host evolution, even across wide-ranging timescales and in diverse animal systems reared under controlled conditions. Appreciation of the microbiota's role in animal speciation will provide a better understanding of what Darwin dubbed the "mystery of mysteries" in *The Origin of Species*.

## PLENARY TALKS

### **Science along the stem: New perspectives from deep time on the origin and early evolution of phenotypes**

\* G. S. Bever<sup>1</sup>

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Evolutionary theory predicts that transformations in phenotypic characters involve a period of ancestral polymorphism wherein the probability of either the primitive or derived condition being expressed is relatively high. The periods of high variability circumscribed by changes in developmental potential may be extremely restricted in both time and space, especially when selection is strong, and may even be limited to a single ancestral population. In such cases, the probability of sampling fossils from within one of these “zones of variability” is so low that the resultant variation is unlikely to directly influence broad patterns of evolutionary change as communicated on a taxonomically inclusive tree. If, however, an evolving developmental network maintains its potential for high phenotypic variation over a significant period of geological time then the probability of sampling fossils from within this zone increases, as does its potential influence on our perception of evolutionary history.

The hypothesis that extended zones of variability exist often enough to significantly affect our macroevolutionary view of the fossil record makes certain testable predictions. First, if the potential to express variation is controlled in part by phylogenetically informative transformations in the upstream architecture of the involved developmental pathways than polymorphism levels, when examined across a clade of extant species, should have phylogenetic structure. Second, characters more recently evolved and thus diagnostic of more exclusive clades should express higher levels of polymorphism within extant species than characters that evolved at deeper positions on the tree. Third, as fossils are sampled successively closer in time and tree space to the evolutionary origin of a character, the probability increases that those fossils are drawn from within a zone of variability translating to increased homoplasy in the early history of that character.

Empirical data drawn from multiple extant vertebrate lineages support the conclusion that the first and second predictions are frequently, if not consistently, met. In addition, a survey of tetrapod phylogeny produces a host of characters that conform to the pattern of the third prediction indicating that conserved variability is significantly affecting our view of evolutionary history based on the fossil record. This hypothesis provides new opportunities for integrating morphology, development, systematics, and the fossil record to address long-standing problems in evolutionary biology.

### **How to eat without a mouth or gut: symbioses between chemosynthetic bacteria and gutless marine worms**

\* N. Dubilier<sup>1</sup>

<sup>1</sup>Max Planck Institute for Marine Microbiology Director of the Symbiosis Department, Bremen, Germany

Marine worms without a mouth or gut were first discovered nearly 40 years ago in coral reef sediments, but the mystery of how they gain their nutrition was not solved until large communities of gutless invertebrates were discovered in 1977 at hydrothermal vents in the deep sea. We now know that these animals gain their nutrition from chemosynthetic bacteria that fix carbon dioxide into organic compounds, as in photosynthesis, but using reduced compounds such as sulfide or methane as energy sources instead of sunlight. Chemosynthetic symbioses occur worldwide and have evolved multiple times from numerous bacterial lineages and at least nine animal groups (Dubilier et al. 2008. *Nature Rev Microbiol*). In my talk, I will present an overview of the research in my lab on these symbioses and describe how new tools that range from in situ instruments for measuring environmental parameters to lab-based methods such as 'omics' and single cell imaging, provide the opportunity to understand symbiotic associations in their environmental and ecological context.

### **Systems neurobiology of the *Platynereis* larva**

\*G. Jékely<sup>1</sup>

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Abstract: Precise neuronal synaptic connectivity and its modulation by chemical signaling are ultimately responsible for the circuit dynamics controlling effector activity during behavior. We currently have little information on the complete synaptic connectivity (connectome) of entire neuronal circuits and how these are modulated. The establishment of new, small, relatively simple model organisms could greatly benefit neuroscience by allowing whole-body connectomics and by expanding the range of nervous system phenomena that can be studied. We work on the larval stages of the marine annelid *Platynereis dumerilii* that has recently emerged as a powerful experimental system for the study of neural circuits and neuromodulation in a whole-body context. We use connectomics, neurogenetics, activity imaging, and behavioral experiments to understand how circuits influence behavior and physiology in the planktonic larvae of *Platynereis*. By studying different larval stages, we can also gain insights into how circuit maturation influences larval behavior during development.

### **Genomics of parallel evolution and speciation during repeated adaptive radiations in cichlid fishes**

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Genome-wide data reveal an often highly heterogeneous pattern of genomic divergence during speciation. Disentangling the dynamic effects of divergent selection and gene flow from the stochastic effects of a population's demographic history remains difficult. Cases of recent sympatric speciation seem promising in this regard, since selection had to be strong enough to overcome gene flow and may thus leave distinct signatures in the genome, while the confounding effect of genetic drift is usually assumed to be negligible. Midas cichlid fishes (*Amphilophus* sp.) inhabiting small and isolated crater lakes in Nicaragua form young (only < 2 - 22,000 years old) and monophyletic flocks of endemic species and no geographic barriers exist in these lakes. Thus, sympatric ecological speciation is the most likely mode of speciation. Moreover, Midas cichlids provide natural replicates of this process and several species seem to be at different stages of the speciation continuum. Based on a comprehensive RADseq data set (of > 700 individuals) from the source population and the crater lakes to (i) infer the demographic history of the speciation processes of small-scale radiations of Midas cichlids based on the joint site frequency spectrum and full-likelihood coalescent simulations and (ii) take this information into account when describing their differentiation at a genomic level. Overall, we find evidence for colonizations by small founder populations, speciation in sympatry, and document a highly heterogeneous landscape of genomic differentiation. Particular focus was on patterns of differentiation in previously identified QTLs with an emphasis on finding genes and mutations that underlie adaptive traits (such as body shape, coloration, dentition and lips) involved in ecological speciation in these repeated adaptive radiations.

### **Growing up and growing old: links across life history stages**

\*P. Monaghan<sup>1</sup>

<sup>1</sup>University of Glasgow Institute of Biodiversity, Animal Health and Comparative Medicine, College of Medicine, Veterinary and Life Sciences Glasgow, GB

Understanding the determinants of variation in ageing and longevity is a topic of great interest to both scientists and society. Even within species, there is considerable inter-individual variation in the rate of deterioration in later life. Some of this variation is genetic in origin, but environmental conditions play an important role. We know that environmental conditions during growth and development can influence a diverse range of morphological, physiological and behavioural traits, with long term consequences for reproductive performance, the rate of senescence, and longevity. In some circumstances, the developmental environment may induce adaptive changes that enable the organism to perform best given the prevailing conditions, and early life advantages may be traded-off against late life costs. I will illustrate these effects with examples drawn from our research on a range of vertebrate species, studied both in the laboratory and in the field. I will discuss whole organism outcomes and underlying mechanistic processes, and illustrate long term effects attributable to pre-

natal, juvenile and adult life conditions. Multiple mechanistic processes underlie these phenotypic effects and their consequences, including changes to hormonal systems, oxidative stress and rates of telomere erosion, which are linked to faster senescence and shorter lifespan. I will focus particularly on the tempo of growth and stress exposure in early life, discuss both direct and indirect environmental effects and how the interaction between conditions experienced early and later in life can influence individual outcomes. I will also discuss whether or not these phenotypic effects are an adaptive response to a given set of circumstances.

### **The Human Sleep Project: Investigating Sleep in the Real World**

\*Till Roenneberg<sup>1</sup>

<sup>1</sup>Ludwig-Maximilians-Universität Munich, Institute of Medical Psychology, Human Chronobiology/  
Munich Center for Neurosciences - Brain & Mind, München, Germany

Over the past century, modern sleep research and sleep medicine have made remarkable progress with the help of new technologies (from the first EEG to recent advances in genetic and molecular biology). For example, the neuronal pathways important for the initiation and maintenance of sleep have been described, and we are accumulating the first insights into the genetic and molecular basis of sleep.

Despite these significant advances in the elucidating the mechanisms of sleep, we are only beginning to understand the nature of sleep in real life. We still lack answers to some of the most fundamental questions, e.g., what makes good, high quality sleep, and how much sleep is optimal for an individual. In the *Human Sleep Project*, we try to step back in our approaches to answer these basic questions. We have developed methods over the past years that allow easy measurement of sleep, based on simple activity recordings, and will use these in a world-wide exploration of sleep in everyday life. We will record activity/sleep from people, who live without electricity, from those in industrialised urban settings, from those living at the equator and those living close to the poles, from people at the western to the eastern borders of timezones etc.

We are building an internet platform, which allows easy uploads from devices that are worn already by many people around the globe. The database of this platform will be fed by these “walk-in” participants, by data collected on exhibitions and experiments, but also by all the activity data that have been collected over the past decades in sleep-labs (for some days before subjects come to the lab).

Here, I report about our newly developed methods, the first insights and results of the *Human Sleep Project*, and the future strategies to elucidate the function of sleep by real-life measurements that go far beyond actimetry.

## PRICE GIVING CEREMONY

### **Werner-Rathmayer-Preis to Nora Siefert**

#### **A genetic investigation of Carinthian bespectacled sheep**

\*N. Siefert<sup>1</sup>

<sup>1</sup>Wilhelm-Raabe-Schule Hannover: Landessiegerin Jugend forscht Niedersachsen und Werner-Rathmayer-Preisträgerin 2016

The old, resilient and frugal Carinthian bespectacled sheep (Kärntner Brillenschaf) is an endangered domestic breed. The conservation of such traditional breeds is desirable because of their suitability for extensive farming and for providing a valuable source of genetic variation in order to enlarge modern breeds' gene pools. The Organic Garden of the Peiner Comprehensive School owns a small flock of four specimens. These individuals were investigated for purity and their suitability for breeding. Attention was paid to genotypic diversity. Buccal swab samples from all four Carinthian bespectacled sheep were taken in order to compare genotypes at eight selected Short Tandem Repeats (STRs) loci. At some of the loci, private microsatellite alleles of the Carinthian breed are known. Alleles were identified by first tagging the PCR products with a fluorescent marker. The fluorescent fragments were then separated on a 6% polyacrylamid gel.

The obtained banding patterns of the four specimens differed at several loci. Three different private alleles could be identified in three of the specimens, in the fourth individual, further two private alleles were detected. This points towards a high variability within the flock and that close genetic relationships among the four sheep are unlikely. The result can be used as basis for selective breeding with this flock and may thus contribute to the conservation of the Carinthian bespectacled sheep.

### **Karl-Ritter-von-Frisch Medaille to Diethard Tautz**

#### **The origin of new genes and evolutionary innovations**

\*D. Tautz<sup>1</sup>

<sup>1</sup>Max-Planck Institute for Evolutionary Biology, August-Thienemann-Straße 2, 24306 Plön

The genetic mechanisms that lead to the generation of evolutionary innovations have been discussed since almost 100 years. Early evidence showed that gene duplications with diversification must play a role, but later an additional emphasis was placed on changes in regulatory evolution. Recently it has become clear that new genetic information can also arise out of random DNA sequences and that this mechanism is actually very active. However, it remains a challenge to judge how much it has contributed to innovations throughout evolution. We have developed a conceptual framework called phylostratigraphy that allows to harness the ever increasing amount of genome sequence information to address the role of new genes in evolutionary transitions. In my presentation, I will discuss the concept of punctuated evolution and the origin of new gene functions through de novo evolution. I will conclude with an outlook of how we can understand the integration of new gene functions within existing networks to create new traits. A key to this are the new insights that come from understanding the genetic architecture of quantitative traits.

## TOPICAL SESSIONS

### Behavioural Biology – invited talks

#### **New insights into family life: why fathers stay, mothers are so caring and offspring get spoiled.**

\*S. Steiger<sup>1</sup>

<sup>1</sup>University of Ulm, Ulm, Germany

Scientists have long been fascinated by the fact that parents of some animals go to great lengths to increase survival and growth of their offspring, usually at a cost to their own survival and reproduction. They invest time and energy to feed their young, to carry them around, or to protect them from parasites, desiccation and other environmental hazards. However, the classical view that saw the family as harmoniously bound radically changed during the last decades and the current view is one of conflict of interests between all family members. For example, each parent stands to gain if the other one invests more. But why do the family units then not break down more often? I will present new insights into family life evolution, thereby illustrating (1) which additional factors can promote the evolution of male participation in care, (2) why it is not necessarily against a mother's interest that she is investing more, (3) how communication can resolve conflicts between the parents and (4) that the evolution of parental care can be a self-reinforcing process.

**Keywords:** family life, parental care, burying beetles

#### **Comparative Bioacoustics: Differences in the emotional communication across mammals**

\*M. Scheumann<sup>1</sup>

<sup>1</sup>University of Veterinary Medicine Hanover, Institute of Zoology, Hannover, Germany

Darwin (1872) first postulated that vocal emotional communication follows similar rules in humans and non-human animals. Current empirical studies provide initial support for cross-taxa affect-coding rules, but also contrary results were found. This might be explained by different methodological approaches across species. Thus, cross-taxa comparisons and comparative approaches investigating several species in a similar experimental design are needed. Here, I will present my research on implicit and explicit cross-taxa vocal emotional perception and cross-taxa affect-coding rules. Using an implicit approach, results of event-related brain potentials suggest that early automatic emotional processing may be influenced by evolutionary retained mechanisms, but the attentional orienting is mainly modulated by the prior experience. Also in explicit tasks, voice-induced cross-taxa emotional perception is shaped more by experience-dependent cognitive mechanisms than by cross-taxa affect-coding rules. Investigating the existence of a universal affect-coding rule, infants of different mammalian species were exposed to contexts of low and high affect-intensity, using the same experimental design. Across species no consistent changes of acoustic parameters between contexts of different affect-intensity were found. Thus, these results do not support a general universal affect-coding rule across mammals instead they lead to the question to what extent emotional perception is dependent on individualized experience and to what extent affect-coding rules in mammals are evolutionary shaped by socio-ecological factors (e.g., breeding system, social system).

**Keywords:** emotion, bioacoustics, mammals

## Behavioural Biology – oral presentations

### OP-BB-01

#### Frequency dependency of vertical sound source localisation of the parasitoid fly *Emblemasoma auditrix* (Diptera: Sarcophagidae)

\*N. Tron<sup>1</sup>, R. Lakes-Harlan<sup>1</sup>

<sup>1</sup>Justus-Liebig University, Department of Animal Physiology, Gießen, Germany

Acoustically directed movement in the three dimensional space is a complex task performed notably by birds, bats and some insect species. The precision of acoustic orientation depends on directionality of the hearing system as well as on the auditory behaviour. The fly *Emblemasoma auditrix* is a parasitoid of the singing cicada *Okanagana rimosa* and locates its host acoustically. *E. auditrix* can locate the position of an acoustic target in azimuth and elevation already from its resting position (Tron et al., 2015).

What is the cue for detection of elevated sound sources? Laser Doppler vibrometric measurements indicate that the vibration of the tympanal membrane depends on the elevation of the sound source. Therefore, we hypothesize that manipulation of the frequency content of the sound signal (calling song of *O. rimosa*) should cause differences on the phonotactic localization behaviour. Therefore, the calling song was filtered and presented to *E. auditrix* in an experimental field setup. The phonotactic behaviour was filmed and analysed for different parts of approach (start, flight, and landing).

The results show that the flies have different body angles directly at take-off, a different accuracy during flight and a different landing precision, when tested with the frequency manipulated calling songs.

In conclusion, we proposed that the flies use the frequency composition of a signal as a mechanism to improve the sound source localisation. Further studies are needed to show how the information is encoded in the nervous system and how the frequency filtering is archived, e.g. with “body related transfer functions”, despite the small size of the fly.

Tron, N., Beuter, L.-K. and Lakes-Harlan, R. (2015). *Ecol. Entomol.* 40:707-716.

**Keywords:** phonotaxis, directional hearing, host finding

### OP-BB-02

#### Intraspecific competition alters patch choice from a distance in a parasitic wasp

L. Pfeiffer<sup>1</sup>, J. Ruther<sup>1</sup>, \*J. Stöckl<sup>1</sup>

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Most species of parasitoid wasps are rather time limited than egg limited, as females die before they can deposit all their eggs. Direct and indirect competition with conspecific females is one of the key factors influencing the time allocation strategies of parasitic wasps. However, long-range decisions in the pursuit of resources are rarely considered in these studies. Wasps of the genus *Leptopilina* can detect the presence of conspecific females on a host patch from a distance by the volatile compound (-)-iridomyrmecin released by the females on the host patch. Consequently, females avoid such host patches during foraging and prefer host patches without competition.

Here we show that the avoidance behaviour of *Leptopilina heterotoma* is not innate, but triggered by the experience of intraspecific competition. If females were kept isolated from other females they did not avoid host patches with conspecifics. But when females were kept in groups of five females they consistently showed the avoidance behaviour. For this it was irrelevant, whether the females could oviposit during the encounter of the conspecific females or not. Females could use olfactory, visual, and tactile stimuli to detect the presence of conspecific females. We show, that only the combination of both olfactory and visual/tactile stimuli can trigger the avoidance behaviour. Furthermore, we could show, that females only react to the iridomyrmecin produced by *Leptopilina*, but not to compounds produced by other parasitic wasps attacking the same hosts.

Our results show, that parasitic wasps can adapt their patch choice strategy to the density of conspecific competitors and underlines the importance of avoidance of competition as a factor for host patch selection.

**Keywords:** Parasitic wasp, patch choice, competition

OP-BB-03

**Personality affects mate choice in a monogamous cichlid, *Pelvicachromis pulcher***

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Behavioural plasticity allows individuals to adapt to changing environmental conditions. Nonetheless, there is increasing evidence for the existence of consistent individual differences in behaviour over time and/or contexts, i.e. personality differences. Yet, little is known about the evolution and adaptive value of being consistent in a varying world. Here, we investigated the hypothesis that individual personality is subject to sexual selection in the monogamous, biparental cichlid *Pelvicachromis pulcher*. Individuals of this species form territories and defend them against conspecifics. Therefore, a high level of aggression is thought to signal parental ability (i.e. territory defense, protection of the offspring) and is expected to be an important personality trait in mate choice.

Level and consistency of aggression were assessed for males and females using mirror tests. Females were then allowed to observe two males, a low and a high aggression male, during interactions with mirrors. Subsequent female mate preferences were measured. Male level of aggression in interaction with behavioural consistency significantly influenced female preferences. Also, female consistency in aggression positively influenced their preference for high aggression males. Our results show that personality and predictability are important traits that can affect mate choice and can be sexually selected.

**Keywords:** personality, aggression, mate choice

OP-BB-04

**Gestural development of chimpanzees (*Pan troglodytes*) in the wild is influenced by interactional experiences and maternal proximity**

\*M. Fröhlich<sup>1</sup>, G. Müller<sup>1</sup>, C. Zeiträg<sup>1</sup>, R. M. Wittig<sup>2</sup>, S. Pika<sup>1</sup>

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**Introduction:** The comparative approach presents one of the most powerful tools to draw conclusions about language precursors and adaptations. Understanding communicative development of great apes can reveal crucial insights into the cognitive abilities underlying signal usage. However, little is known about the ontogeny of ape gestural signalling in the wild and the extent to which it relies upon the social and physical environment.

**Objectives:** The aim of the present study was to examine the influence of interactional experience and maternal proximity on the gestural development of chimpanzees (*Pan troglodytes*) living in two communities in the wild (Taï South, Côte d'Ivoire; Kanyawara, Uganda). Specifically, we asked whether context, interaction rates, and maternal proximity affected gestural frequency, series and repertoire.

**Methods:** To target this aim, we used a novel combination of video recordings and focal scans obtained from eleven infants aged 9-69 months during 1145 hours of observation. This resulted in a total of 1120 coded interactions in the contexts of food sharing, joint travel and social play, and 4516 scan sample points.

**Results:** Overall, we found that social play comprised the majority of gesture cases, gestural series and gesture types. While gestural frequency and repertoire was larger with more interactional experience with conspecifics, surprisingly the opposite effect was found for interaction rates with mothers. In addition, we found that maternal proximity, but also sex and study site had a profound influence on gestural production.

**Conclusion:** We conclude that gestural development relies heavily on interactional experiences with peers, which provides further support for gestural acquisition via the learning mechanism of 'social negotiation' in great apes.

**Keywords:** communication, development, great ape

**OP-BB-05**

**Spatial learning using the electric sense in weakly electric fish (*Gnathonemus petersii*)**

\*S. N. Jung<sup>1</sup>, S. Künzel<sup>1</sup>, J. Engelmann<sup>1</sup>

<sup>1</sup>University, Biology, Bielefeld, Germany

Navigation is an important task for finding mates, food and shelter for animals that travel over longer distances such as fish, birds, mammals and many insect species. To navigate through an environment spatial information must be stored and accessed in a fixed frame of reference: i.e., egocentric and/or allocentric. The former is a body-centered reference; the latter is a world-based reference that makes use of landmarks independent of the animal's position. Here, we investigated which behavioral strategies the weakly electric fish use for spatial navigation. Interestingly, these fish rely on a near-range sensory system for navigation; i.e, electrolocation. Thus, to create any form of cognitive map, they need to actively visit and sample the environment.

We developed a spatial memory task, where fish had to find one out of 15 locations in a circular arena. Animals were videotaped (IR illumination) and their electric organ discharges (EODs) were recorded. The food rewarded location was marked with a metal pyramid at a distance of 10 cm and remained constant during learning. We extracted various behavioral parameters such as the trajectories, sampling density, time spent, number of errors per trial. All animals successfully learned the rewarded location over 3-6 sessions. Once fish showed that they reliably had learned ( $p < 0.05$ , binominal test in 2 consecutive sessions) we performed test sessions addressing the use of ego- versus allocentric mechanisms. For both conditions the fish were able to learn the new target location within one session, indicating that fish can switch between behavioral strategies if one fails. Doing additional experiments we are now investigating which of the two behavioral strategies is the most salient one.

**Keywords:** spatial learning, weakly electric fish, active sensing

**OP-BB-06**

**Modulation of breeding activities in wild and domesticated canaries**

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Changes in photoperiod play a major role in the timing of seasonal reproduction in most vertebrates, including birds. Direct environmental stimuli such as temperature, rainfall or availability of food are thought to be important for fine-tuning breeding activities. In (wild) island canaries (*Serinus canaria*), we previously have shown that breeding may occur up to six weeks before the usual onset of the breeding season when exposed to favourable environmental cues as represented by growing green vegetation under short-day conditions. We now provide evidence from long-term observations that in the absence of stimulatory supplementary cues under natural day conditions, the onset of breeding fully depends on photoperiod alone, suggesting that there is no carry-over effect from early breeding activities of the previous breeding season. Further, domesticated canaries are able to skip an entire breeding season when favourable environmental cues are missing, resulting in a lack of breeding activities during 16 months, but birds are fully receptive to photoperiodic stimulation in the subsequent winter period. Thus, both wild and domesticated canaries show a remarkable plasticity in the integration of environmental stimuli in order to find a suitable breeding window. Moreover, under natural conditions birds may even use different habitats depending on whether environmental conditions are suitable for breeding.

**Keywords:** breeding season, environmental cue, songbirds

**OP-BB-07**

**Individual recognition in wild greater sac-winged bats (*Saccopteryx bilineata*): evidence from a playback experiment with a violation-of-expectation paradigm**

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The ability to recognize conspecifics individually plays a crucial role in shaping animal societies and is considered to be cognitively more advanced than class-level recognition (e.g. discriminating familiar vs. unfamiliar conspecifics). Under natural conditions, vocal individual recognition has predominantly been studied in primates, despite its importance for other mammalian taxa. Here, we present experimental evidence that wild bats, *Saccopteryx bilineata*, can recognize individual group members using voice cues in distress calls. Bats produce distress calls when being caught by a predator, and distress calls often attract conspecifics. We conducted a distress call playback experiment in direct vicinity of the bats' day-roost during which we simulated predation events that were either plausible or physically impossible (violation-of-expectation paradigm). Bats approached the speaker broadcasting distress calls of group members only when the simulated scenario was plausible (when the stimulus donor had already left the roost), but never when the simulated scenario was physically impossible (when the stimulus donor was still perched among the focal bats). Thus, distress calls only elicited a relevant behavioral response (phonotaxis) when the expectation about the signaler's position was not violated. The lack of responsiveness when conflicting information was presented (i.e. the physical presence of an individual in one place and its voice in another place) strongly suggests that *S. bilineata* is capable of recognizing individual conspecifics based on voice cues in distress calls. Interestingly, conflicting information did not seem to enhance general alertness or vigilance (as e.g. in primates and meerkats); however, these behaviors are difficult to quantify in roosting bats and, therefore, might have been overlooked.

**Keywords:** individual recognition, social vocalization, playback experiment

**OP-BB-08**

**Identifying enemies - a no-brainer?**

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Elaborate division of labor is stable only when groups can be closed off to the outside. In eusocial species with often thousands of individuals per colony, the discrimination of nestmates from non-nestmates is thus a crucial process that needs to be precise and quick. Discrimination is based on colony-specific blends of cuticular chemicals. These are "labels" that are evaluated by e.g. guards at a nest entrance, in what is often described as a label-template-matching process. The template is thought to be a neural representation of the average colony label, stored in the memory. However, recent findings challenge such a simple picture. One open question is whether the template is actually located in the brain or whether decisions are already made in the neural periphery, e.g. the antennae, to increase processing speed. Another challenge to classical models is that recognition seems to be asymmetric, since individuals react to novel cues only, leading to the notion that non-nestmates, rather than nestmates, are recognised. Further, some authors suggest that nestmate recognition is based on collective decisions in groups that single workers cannot achieve on their own. I will present data from behavioral and chemical experiments on ants to test the different hypotheses that have been put forward. Our experiments exploiting natural and experimentally manipulated label variation support asymmetric recognition with a focus on aggression being triggered by unfamiliar labels. However, some simple behavioral experiments using the mandible opening response indicate that the picture is indeed not so simple. Multiple synergistic processes seem to be at play, potentially with separate recognition of non-nestmates and nestmates.

**Keywords:** nestmate recognition, ants, label-template matching

## Behavioural Biology – posters

### PP-BB-01

#### ***Behavioral, and bioenergetics, and morphological characteristics of the ant lion larvae with respectively obligatory (sit-and-wait) and facultative pit building strategies under natural and laboratorial conditions (Myrmeleontidae, Neuroptera, Insecta***

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In order to assess and to compare the often contradictorily discussed prey capture strategies of the antlion larvae (Myrmeleontidae), we carried out both field and laboratory research. The main objective was to prove the independent occurrences of both obligatory and facultative pit construction behavior among antlion larvae. These comparisons occurred through the measurement of different pit parameters, and energetic rates, and prey use rates, and morphological aspects as well. We used exclusively the L3 larval instar of both foraging strategies namely the obligatory and facultative pit construction strategies. The data were collected under different research conditions and prey capture regimes: pit building; locomotion; prey capture. The results show significant differences between larvae from both strategies, under field and under laboratory conditions as well, e.g. the sit-and-wait larvae had more extraction rates than the facultative pit builders. Similarly, larvae with the obligatory funnel building strategy built larger funnel than the ones from the other foraging strategy. Sit-and-wait larvae showed higher body mass increasing rates, but lower body mass losses than the facultative ones. However, the mass loss and increasing profiles were similar. It became clear that the locomotion of the larvae is associated with higher energy costs in both strategies compared to the funnel construction costs. Further differences exist with respect to the length of the locomotor extremities, the tooth pattern in the inner side of the mandible, the construction of the mandible and the head capsule width. All investigated characteristics exhibit constancy and homogeneity within the respective strategies.

**Keywords:** Pit building behavior, Antlion larvae, Prey capture strategy

### PP-BB-02

#### **Social influences during adolescence modify adult mating behaviour in zebra finches (*Taeniopygia guttata*) - consequences for reproductive success**

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In zebra finches the social rearing environment during adolescence strongly affects the adult sexual behaviour of males. Individuals grown up in groups with juveniles only sing more to females than individuals grown up in mixed-age groups with juveniles and adults or in juvenile pairs, and discriminate most between females without a mate and females with a mate. When tested for their aggressive behaviour towards conspecifics in competition contexts, males reared in juvenile groups and mixed-age groups show more aggressive attacks towards opponents than males reared in juvenile pairs, and a more discriminating pattern of aggression towards male and female conspecifics. The differences in behavioural frequencies and strategies suggest that male zebra finches differ in their ability to appropriately address behaviour towards conspecifics according to their social background, which might be essential for survival and successful reproduction. In order to verify this, we investigated the reproductive success of males in a mate restricted breeding experiment with female shortage. We will present whether males with varying adolescent social experiences differ in their pairing success, the percentage of in pair or extra pair paternities, the number of fertilized eggs, the number of hatchlings or the number of fledglings they produce. In addition, we will present survival data of offspring until adulthood.

**Keywords:** social environment, adolescence, adult behaviour & reproduction

**PP-BB-03**

**Feeding-type composition changes with group size in a socially foraging spider**

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In groups of socially foraging animals, feeding behaviour may change with group size in response to varying cost-benefit trade-offs. Numerous studies have described group-size effects on group-average feeding behaviour, particularly emphasizing an increase in scrounging incidence for larger groups, where individuals (scroungers) feed from the food sources others (producers) discovered. However, individual variation in feeding behaviour remains unconsidered in the vast majority of these studies even though theoretical models predict individuals to specialize in feeding tactic and anticipate higher scrounger-type frequencies in larger groups. We combined group-level and individual-level analyses of group-size effects on social foraging in the subsocial spider *Australomisidia ergandros*. Lending novel experimental support to model predictions, we found that individuals specialize in feeding tactic and that higher scrounging and lower producing incidence in larger groups were mediated through shifts in the ratio of feeding types.

**Keywords:** behavioural type, group size, social foraging

**PP-BB-04**

**How accurate are Census Data? - Estimating Colony Size of Galapagos Sea Lions**

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Population monitoring is vital for conservation and management. However, simple counts of animals can be misleading and this problem is exacerbated in seals (pinnipeds) where individuals spend much time foraging away from colonies. We analyzed a 13-year-series of census data of Galapagos sea lions (*Zalophus wollebaeki*) from the colony of Caamaño, an islet in the center of the Galapagos archipelago where a large proportion of animals was individually marked. Based on regular resighting efforts during the cold, reproductive (cold-R; August to January) and the warm, non-reproductive (warm-nR; February to May) season, we document changes in numbers for different sex and age classes. During the cold-R season the number of adults increased as the number of newborn pups increased. Numbers were larger in the morning and evening than around mid-day and not significantly influenced by tide levels. More adults frequented the colony during the warm-nR season than the cold-R season. Raw counts suggested a decline in numbers over the 13 years, but Lincoln-Petersen (LP-) estimates (assuming a closed population) did not support that conclusion. Raw counts and LP estimates were not significantly correlated, demonstrating the overwhelming importance of variability in attendance patterns of individuals. The probability of observing a given adult in the colony varied between 16% (mean for cold-R season) and 23% (warm-nR season) and may be much less for independent 2 to 4 year olds. Dependent juveniles (up to the age of about 2 years) are observed much more frequently ashore (35% during the cold-R and 50% during the warm-nR seasons). Simple counts underestimate real population size by a factor of 4-6 and may lead to erroneous conclusions about trends in population size.

**Keywords:** Population monitoring, Lincoln-Petersen estimate, Galapagos sea lion

**PP-BB-05**

**Studying the role personality plays in house mouse social networks.**

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Behavioural patterns which are consistent and stable over time are defined as personalities. Personalities are heritable; however, they are also influenced by environmental factors, including social environment. Structure in social environment influences the access individuals have to resources such as territory, nutrition and potential mates. House mice (*Mus musculus domesticus*) have a hierarchical social system, in which dominant males defend resources and restrict access to subordinate individuals. This may result in non-random associations, which may affect individual fitness. The role individuals play in a social network should be influenced by their personality. In order to study the role individuals with different personality types play within their social environment, we tracked small populations of house mice in semi-natural enclosures using RFID tags on all adult individuals and antennae on nest boxes. Throughout the experiment, we measured behavioural traits at regular intervals and collected DNA samples for parentage analysis. Antenna reads were used to measure social interactions between individuals, before and after behavioural tests, as well as behavioural scores from the tests themselves, we aim to ascertain the role personality plays in social networks and how this influences individual fitness.

**Keywords:** Personality, Fitness, House Mouse

**PP-BB-06**

**Separate effects of selection for high productivity and genetic strain on fearfulness and sociality in laying hens**

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Productivity and genotype have been implicated in differences in fearfulness and stress reactivity in layers but their relative contributions have not been fully explored. We aimed to determine the separate effects of these factors on fearfulness and sociality. Therefore, we used 80 hens from a 2x2 group design, with two white and two brown layer lines which differed in laying performance (200 vs. 300 eggs/y) within colours, respectively. Fearfulness and sociality were measured using six different test paradigms (visual cliff, emergence from a box, social approach, novel object, mirror approach, tonic immobility). The data from the tests were analysed using a GLM with genetic background (white/brown) and productivity level (high/low) and their interaction as explanatory variables.

Highly productive lines were consistently and significantly less social than less productive lines and white were more social than brown layers (e.g. social approach test: mean times to reach conspecifics 11s vs. 37s for white vs brown layers (GLM:  $F_{1,73}=29.17$ ,  $p<0.0001$ ); 36s vs. 14s for high vs. low productivity (GLM:  $F_{1,73}=25.03$ ,  $p<0.0001$ )).

Genetic background but not productivity had a significant effect on fearfulness, with white layers being more fearful (e.g., time to end tonic immobility: 321s vs. 182s for white vs. brown layers (GLM:  $F_{1,73}=14.47$ ,  $p<0.001$ )).

Our results show that genetic strains and selection for productivity can affect different dimensions of behavior differently. This needs to be taken into account when characterising the effects of genotype on behavioural traits. The impact of unintentional changes in behavior that accompany intense selection pressure on productivity deserves further study e.g. effects on welfare or function.

**Keywords:** Chicken, Sociality, Selection

PP-BB-07

**Disentangling the mechanism of kin recognition in zebra finches**

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Recognising close relatives, i.e. kin, is crucial to avoid inbreeding. Olfactory cues are used to recognise kin in many vertebrate species, including zebra finches. In a previous study we have shown that prior association isn't necessary for olfactory kin recognition, indicating that zebra finch females use phenotype matching to recognise kin. Whether females use their own odour as a template (self-referent phenotype matching), or a family odour learned during the nestling period (family-referent phenotype matching) is unknown yet. This study aimed to disentangle the two potential mechanisms. We conducted a mating experiment to test whether females hatched from fostered eggs show a different mating preference than females that grew up in their natal nest. We formed groups of five individuals, consisting of two females and three males, each. Males and females in each group were unfamiliar. The experiment consisted of two different conditions: The first experimental condition contained one female and her genetic brother. In the second experimental condition each group contained one female, which hatched from a cross-fostered egg and was therefore exposed to another family odour after hatching, plus a genetic brother and a foster brother, i.e. male offspring of the foster parents. If females recognise kin based on self-referent phenotype matching, we expect females to generally avoid mating with their unfamiliar brother. If females use the family odour learned early in life, we expect females from fostered eggs to show a different mating preference.

We observed pair bonding, analysed the reproductive success and determined the mate of each female by genetic parentage analysis. The results of the experiment will be presented and discussed.

**Keywords:** kin recognition, phenotype matching, zebra finch

PP-BB-08

**The role of spatial extra- versus intramaze cues on cannabinergic impairment of spatial memory retrieval in the zebrafish**

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**Introduction:** The vertebrate endocannabinoid system is crucially involved in acquisition of and retrieval from spatial memory. There are two different spatial learning strategies: A) egocentric and B) allocentric. The first depends on the location of objects in space relative to the body axis. The latter one relies on the location of one object with respect to other objects and it is more sensitive to cannabinoid interference than the first one, suggesting the involvement of different neuronal substrates. The teleost lateral pallium of the telencephalon is heavily involved in spatial learning and memory and it shows rich expression of the cannabinoid receptor CB1.

**Objective:** This study aimed at investigating the role of extra- versus intramaze cues (flags) on cannabinergic impairment of retrieval from zebrafish spatial memory.

**Methods:** For acquisition of spatial memory, two groups of zebrafish were trained in a hole-board task. The setup was equipped for A) with extramaze cues only, for B) intramaze cues were additionally introduced. After reaching a constant behavioral level, we exposed the animals to the CB1 agonist THC ( $\Delta^9$ -tetrahydrocannabinol) before testing for memory retrieval.

**Results:** Depending on the extramaze cues, animals decreased the time to find the baited food hole, while intramaze cues improved acquisition learning. THC treatment impaired memory retrieval in group A), while this effect was less pronounced in B).

**Conclusions:** Associating a direct indicator (flag) of a food spot involves a spatial learning strategy differing from a pure allocentric orienting performance, being independent of the endocannabinoid system, supporting the participation of another neuronal basis.

**Keywords:** Zebrafish, Spatial Memory, Endocannabinoid System

PP-BB-09

**Raider of the lost coin: Object detection within substrate in the weakly electric fish  
*Gnathonemus petersii***

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The mormyrid weakly electric fish *Gnathonemus petersii* is able to find food items (insect larvae) that are buried in the substrate using multiple senses, including olfaction, and both passive and active electrical sensing. During active electrolocation the fish detect objects by perceiving object-evoked changes in a self-generated electric field. While many experiments have investigated this sense, the majority have focused on object detection in open water.

We investigated the limits of object detection within substrate by determining firstly, the minimal detectable size of aluminium coins buried in gravel and secondly, the depth threshold, at which the fish were able to detect living and dead insect larvae within the ground.

In experiment one, three *G. petersii* were trained to associate an aluminium coin (Ø 22 mm, 2 mm) with a food reward and were subsequently tested to determine whether they were able to detect a coin of a particular diameter (between 22 - 4 mm) when buried 0.5 cm deep in one of four alternative gravel-filled cups. In experiment two, three other individuals were tasked with finding a single *Chironomidae* larva (living/dead) buried at varying depths in one of two gravel filled cups. Controls were conducted to test which senses were involved in the detection.

The results show that all fish were able to detect the 6 mm coin within the substrate and one individual was even able to find the 4 mm coin. Furthermore, preliminary results reveal that the fish dug for the larva up to a depth of at least 2.5 cm.

Although the substrate consisted of isolating material, which was only interspersed with conductive water *Gnathonemus petersii* was able to detect objects very efficiently, even finding items not much bigger than the surrounding gravel stones.

**Keywords:** *Gnathonemus petersii*, electrolocation, prey detection

PP-BB-10

**Optical illusions cause fish confusion: Kanizsa figures, subjective contours and two different size illusions in *Chiloscyllium griseum* and *Chromis chromis*.**

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How illusions are perceived in both vertebrates and invertebrates has been the focus of a number of recent studies in a wide variety of species. Juvenile bamboo sharks (*Chiloscyllium griseum*) were tested for their ability to perceive subjective, illusory contours and size illusions. Individuals were able to discriminate Kanizsa figures from alternate stimuli, and between subjective, illusory contours in >75% of all tests, suggesting perceptual information processing mechanisms such as 'filling-in' and '(a)modal completion'. However, inter-species variation in the perception of size illusions refer to the way animals focus their visual attention on presented scenes or sets of stimuli: bamboo sharks were not deceived by Müller-Lyer illusions but displayed side preferences or chose by chance. Similarly, sharks were neither deceived by Ebbinghaus circles nor variations of the Delboeuf illusion. Instead, they appeared to choose according to assimilation effects. In contrast to sharks, Damselfish (*Chromis chromis*) were tricked by the Ebbinghaus circles as they tended to perceive larger surrounding circles decrease the size estimation of central circles and vice versa. They perceive the Ebbinghaus illusion as a contrast illusion, because they seem to take global aspects such as relative size of the surrounding elements into consideration. Thus, their size perception appears to be distorted away from the surrounding context. However, effects of perceptual information processing mechanisms such as 'perceptual grouping' and 'local' or 'global' visual perception are considered to be present in neural visual processing and associative interpretation of optical illusions in *Chiloscyllium griseum* as well as in *Chromis chromis*.

**Keywords:** Optical Illusions, *Chiloscyllium griseum*, *Chromis chromis*

PP-BB-11

**Color vision and visual memory formation in *Camponotus blandus***

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Recent behavioral studies suggest that ants can detect and discriminate colors, independent of brightness levels. However, the contradictory information on the spectral organization of the ants' visual system (dichromacy vs. trichromacy) based on physiological, molecular and behavioral data of previous studies asks for a detailed behavioral analysis of the ant's color vision ability in the context of visual orientation. We therefore aimed to investigate the color preference, learning and memory performance of *Camponotus blandus* ants under controlled laboratory conditions in more detail.

Freely walking foragers were trained individually to discriminate a combination of different monochromatic light stimuli (365 nm, 450 nm and 528 nm) of a constant intensity in an associative learning paradigm presented in dual choice experiments. Subsequently, they were tested in several non-rewarded control tests where the intensities of target and distractor stimuli were randomly changed.

The results showed that *C. blandus* workers exhibit a strong innate preference for ultraviolet (UV, 365 nm) over blue (450 nm) and green (528 nm) light. Initially, the learning performance of the workers was influenced by innate color preferences. They could significantly discriminate 365 nm from 528 nm and 450 nm, and vice versa, irrespective of intensity changes. However, they failed to distinguish between 450 nm and 528 nm. Overall, the results showed that *C. blandus* workers can discriminate colors irrespective of intensity changes. We, now, discuss several possibilities why color discrimination is constricted in the mid- and long wavelength part of the light spectrum.

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**Keywords:** Color learning, Color memory, Ant

PP-BB-12

**Social interactions in a pulse-type weakly electric fish only rely on passive reception of electric communication signals**

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**Introduction:** Mormyrid weakly electric fish discharge sequences of electric signals to actively sense their environment and to communicate with conspecifics. These functions are mediated by different types of dermal electroreceptor organs, which are mormyromasts for active electrolocation and knollenorgans for electrocommunication. Our behavioral experiments reliably demonstrated attraction of the weakly electric fish *Mormyrus rume* towards a mobile dummy fish equipped with electrodes emitting playback of electrical discharge patterns. Both, signaling patterns and motor behaviors displayed in response to playback signals, reflect social interactions between individuals.

**Objective:** This study aimed to show that social interactions among weakly electric fish can be mediated solely by passive reception of electrical communication signals.

**Materials & methods:** By moving a playback emitting dummy along a predefined trajectory within an electrically transparent tube under infrared light, we excluded vision and hydrodynamic cues as factors that could initiate interactive behaviors between *M. rume* and the dummy. Additionally, some fish were electrically silenced to control for active electrolocation.

**Results:** Upon detection of playback signals, a prolonged period of electrical silence, followed by a characteristic discharge pattern, was induced in the receiving animals. Fish followed the dummy on stereotypical swimming trajectories. These behaviors were absent in control trials without playback. Trajectories of silenced fish were similar to those observed in intact fish.

**Conclusion:** Electric signaling alone suffices as a key stimulus to induce social behaviors and interactions among weakly electric fish.

**Keywords:** Playback, Electrocommunication, Sensory perception

**PP-BB-13**

**Group dynamics in electric fish: Electric and motor-interactions in mixed and natural groups of *Mormyrus rume* (Mormyridae, Teleostei)**

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The weakly electric fish *Mormyrus rume* produces brief, pulse-type electric organ discharges (EODs) that are used for active electrolocation and electrocommunication. The inter-discharge intervals (IDIs) are most eminent for electrocommunication and their temporal variations are related to different behavioural reactions and contexts. Thus, the electrosensory system is crucially involved in the formation, behaviour and coherence of social groups.

This study aims to reveal characteristics of social interactions and electrical communication in small groups of *M. rume*.

We measured group sizes, swimming trajectories and synchronisation of electric discharges between group members while they moved from a sheltered into an open field area in order to quantify group and social behaviour of *M. rume*. Furthermore, animals of the group were systematically replaced by a dummy fish emitting electrical playback signals, which were previously recorded in a corresponding group situation.

Animals swimming in groups frequently synchronised their EOD- activity when leaving the sheltered area. The dummy initiated following behaviour when integrated into a group. Fish were recruited from the sheltered area and synchronised their discharges with the playback patterns of the dummy comparable to situations with conspecifics only.

Conclusions:

An electro-communicating dummy can initiate electric and motor social behaviours in small groups of *M. rume*.

**Keywords:** Group dynamics, Electrocommunication, Synchronisation

**PP-BB-14**

**«The Red and the Black»: a colour morph story in a tropical bird**

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Evolution promotes phenotypes that best match environmental conditions, thereby limiting intra-specific phenotypic variation. Still, some species show distinct discrete phenotypes. These so-called morphs do not only vary in appearance and genetic background, but also in their behavioural and physiological traits. This suggests that one morph is better adapted under given environmental conditions while the other morph is better adapted under other conditions. However, how differences between morphs vary in a changing environment (*e.g.*, because of climate change), and how this relates to individual fitness remains largely unexplored. Gouldian finches (*Erythrura gouldiae*) present two major colour morphs, the red- and the black-headed birds, which coexist throughout their entire geographic range. Some studies have already highlighted significant physiological and behavioural differences between both colour morphs. However, how colour morphs differ under challenging conditions, such as under hot conditions, has not been yet investigated. This is important, as the temperatures in the native tropical habitat of Gouldian finches are expected to increase in the next decades, which may favour one of the two morphs at the expense of the other. Here, we simulated a heat wave, and conducted several behavioural tests to highlight morph-specific differences before, during and after this heat wave. Our aim was to examine whether behavioural variations between morphs persisted under challenging conditions and could explain polymorphic stability within this species.

**Keywords:** Colour polymorphism, Behavioural ecology, Gouldian finch

PP-BB-15

**Differential functioning of genital titillators in tettigoniid bushcrickets**

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**Introduction:** In some bushcricket species males bear sclerotized genitalia, the titillators. The number and shape of these titillators differ largely depending on the species. Previously, we supposed the paired titillators in *Metrioptera roeselii* to stimulate the female resulting in suppressed resistance and ensured spermatophore attachment.

**Objectives:** We compared the titillator function during mating between three species to test whether their manipulation yielded similar or different outcomes. We analyzed the following hypotheses: titillators could stimulate the females, assist in spermatophore transfer or help to maintain the mating position.

**Materials & methods:** To test the utilization of these structures during mating, we shortened titillators in *Pholidoptera littoralis* and covered the titillator with glue in *Letana inflata* to modify the surface. Moreover, we used synchrotron-based X-ray cineradiography of mating couples in *Metrioptera roeselii*.

**Results:** Shortening the titillators in *Ph. littoralis* resulted in males slipping out of the mating position, which suggests that here titillators have an anchoring function. In *L. inflata*, the manipulation of the male's titillator led to female resistance behaviour during the mating and resulted in several failed matings. The titillator of *L. inflata* seems to be critical for suppressing the females' resistance. With the X-ray live-movies, it was the first time that we were able to show the movement of titillators inside females of *Metrioptera roeselii*.

**Conclusion:** Bushcricket titillators have different functions depending on the species; they might stimulate females to suppress female resistance and assure proper spermatophore attachment; in one species it is used as anchor.

**Keywords:** Tettigoniidae, titillators, stimulatory devices

PP-BB-16

**Fitness consequences of zebra finch personality**

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Animal personality describes behavioural differences between individuals that are consistent across time and contexts. Especially the evolutionary mechanisms generating and maintaining individual differences are of great interest. The fitness consequences of animal personality are a crucial research topic as they could help to explain how variation in personality traits is maintained in a population. Previous research has provided some evidence for co-variation between animal personality and fitness parameters such as reproductive success and survival.

In this study, we have developed a standardized test battery comprising three personality traits. We measured **aggression** towards a mirror, **exploration** in a novel environment and **fearlessness** in a tonic immobility test in a captive population of wild-type zebra finches (*Taeniopygia guttata*). We established bi-directional selection lines on each of these three traits to study their genetic and environmental causes as well as the covariation with fitness.

We hypothesized that lines selected for 'high' trait values (bolder behaviors) would invest more in reproduction than 'low' selected lines.

We tested the effect of trait and direction of selection on reproductive parameters over three generations. The lines did not differ significantly in the number of clutches or hatching success, but in fecundity, with 'bold' lines laying more eggs. Furthermore, lines selected for bolder behaviors (more aggressive, less fearful) had a higher juvenile survival to nutritional independence. To conclude, differences in fitness in our selection lines fit to the pace-of-life hypothesis with 'bolder' personality types reproducing more intensely.

**Keywords:** animal personality, selection line, reproductive success

**PP-BB-17**

**Surface wave perception in Crocodiles**

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Crocodiles can sense capillary water surface waves with their integumentary sensory organs (ISOs). The ISOs - located mainly on the jaws - are sensitive to water surface waves elicited by prey, predators or conspecifics. The aim of our study was to determine the frequency and amplitude content of natural surface wave stimuli and whether and to what precision crocodiles can discriminate and locate different types of wave stimuli. Using operant conditioning, crocodiles were trained to show an oriented response to a certain surface wave stimulus, produced by blowing air onto the water surface. To investigate their surface wave discrimination abilities a second unrewarded wave stimulus was presented. If single-frequency wave stimuli were presented, frequency discrimination limens were 0.04 at 40 Hz and 0.1 at 15 Hz. Frequency changes (e.g. from 40 to 38.5 Hz) within a wave train were also recognized. Nile crocodiles determined the direction and - roughly - the distance to a surface wave source even in the presence of an interfering surface wave stimulus.

**Keywords:** Crocodile, Surface wave, Mechanoreception

**PP-BB-18**

**Habitat selection and nesting behaviour of hedgehogs (*Erinaceus europaeus*) in an urban area measured by telemetry and GPS tracking**

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This study investigated habitat selection and movement behaviour of the European hedgehog (*Erinaceus europaeus*) in the Treptower Park, an urban park in Berlin of 88 ha in size. The park was mapped with regard to sealing, meadows, shrubbery density, ground-cover plants and tree counts. From August until October 2015, hedgehogs were monitored using combined VHF radio tags and GPS devices. In total, 57 hedgehogs (34 ♀, 23 ♂) were found. 20 individuals (12 ♀, 8 ♂) were tracked by VHF telemetry, 7 of the 20 individuals (4 ♀, 3 ♂) were additionally monitored by GPS devices. 48 nests of 17 individuals (11 ♀, 6 ♂) were detected by VHF tracking, with observed non-simultaneous nest sharing (♂♂; ♂♀). Often nests were located in small patches of vegetation types which differed from the classified surrounding area. Shrubberies with detected nests had a larger circumference compared to those without nests. Nest locations had shorter distances to meadows than randomly placed nest locations. Based on nocturnal 5-minutes-GPS locations, home range size varied widely depending on specific location, and study time (♀: 5-15 ha ♂: 5-25 ha). Home range sizes and covered distances per night did not differ significantly between females and males. Home range overlaps between female and male hedgehogs were significantly smaller than between females. Preferred habitats during the day (inactivity) were bushes of high density, while at night (activity) the preferred habitat was meadow. The presence of ground-cover plants resulted in 1.5 times higher use of females than of males. In summary, the preferred hedgehog areas appeared to be patchy with alternating meadows and heterogeneous shelter vegetation of high and low densities offering long edges for nesting locations.

**Keywords:** Hedgehog, Habitat analysis, Nest situation

PP-BB-19

**Mating patterns between two geographically and genetically distant populations in the haplochromine cichlid *Astatotilapia burtoni***

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The event of speciation and the understanding of how it is driven by selection is a ubiquitous topic in biology. Reproductive isolation may evolve as a by-product of the accumulation of differences between two geographically distant populations. The radiation of East African cichlids in Lake Tanganyika is an important model for studying patterns of speciation. Here, we focus on mating patterns in a haplochromine species, *Astatotilapia burtoni*, which occurs within Lake Tanganyika and surrounding rivers. We use two experimental setups involving two geographically and genetically distant lake populations to assess the level of reproductive isolation. In the first experiment, where only visual cues were considered, the number of eggs laid next to each male serves as a measure of female preference. The second experiment allows direct contact between males and females (i.e. all cues available), and mate choice is determined via genetic paternity testing. The results of these experiments allow us to infer at which stage of the speciation continuum the populations are resting.

**Keywords:** female choice, reproductive isolation, sexual selection

PP-BB-20

**To prefer or not to prefer - plasticity in the sex pheromone response of *Nasonia vitripennis* females**

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**Introduction:** The response of *Nasonia vitripennis* (*Nv*) females to the male sex pheromone is plastic: after mating they are no longer attracted. The behavioral switch is independent of sperm transfer, but the underlying neurophysiological mechanism is unknown. It is also unclear whether the switch is irreversible or whether females can regain the pheromone preference by reward learning. The neuromodulators octopamine (OA) and dopamine (DA) are known to be involved in reward learning (OA) and aversion learning (DA) of insects.

**Objectives:** We tested two hypotheses: (1) The behavioral switch in *Nv* females is regulated similarly to aversion learning and thus DA is involved in this process. (2) After reward learning, mated *Nv* females regain the preference for the male sex pheromone and OA is involved in this process.

**Materials & methods:** We studied the pheromone response of conditioned and unconditioned *Nv* females in olfactometer bioassays. We investigated the role of catecholamines by treating females with the OA receptor antagonist mianserin or the DA receptor antagonist chlorpromazine.

**Results:** Mated females treated with chlorpromazine prior to mating were still attracted to the male sex pheromone. This effect was absent in females treated with mianserin. Mated females exposed to the male sex pheromone during oviposition (=reward) preferred the pheromone in subsequent olfactometer tests but did not so when treated with mianserin. Chlorpromazine did not impair reward learning in *Nv* females.

**Conclusion:** The behavioral switch in mated *Nv* females is not irreversible, but the pheromone response can be regained by reward learning. Results suggest that DA and OA are antagonistically involved in the loss and regain of the pheromone preference.

**Keywords:** parasitoid wasp, learning, catecholamines

PP-BB-21

**OBJECT DETECTION IN EXPLORATION LEARNING THROUGH ELECTROLOCATION|: the action-perception loop in *Gnathonemus petersii*.**

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The generation of purposeful and goal-oriented behavior depends on an animals' ability to perceive and extract sensory information from its environment. Thus an animals' behavior is an interactive process of action and perception in which the corollaries of the ongoing behavior alter the sensory signals that in turn lead to a suitable motor response. Given a certain task at hand, the animal tends to adapt their behavior in order to maximize the probability of obtaining a positive result. Undoubtedly this kind of learning requires a fine interpolation between the motor act and the resulting sensory information.

Active electroreception evolved independently in African and American electric fish and it is based on the selective tuning of electroreceptors to the waveform of the self-emitted electric field generated by the activation of an electric organ (EO). One of the selective advantages afforded by the electric sense is that it enables animals to detect objects in dark aquatic environments.

Here we show the detection and approach trajectories made by the African fish *Gnathonemus petersii* to reach a metal cube in a freely moving two choice paradigm. The change at the behavioral level in the fish, leads to a better use of the surrounded space and to a refined paths, reducing the number of failures. This is given by maximizing the use of information obtained by eliminating any ambiguities regarding which option to choose. The use of several motors patterns observed at the beginning of training is filtered to those that provide information about the task, this also leads to changes in the frequency in which the fish obtain the data (eg e-scans) and the information obtained itself (electric images).

**Keywords:** electric sense, object detection, action-perception loop

PP-BB-22

**Object-location paired-associates learning in a basal primate (*Microcebus murinus*).**

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In order to embed the cognition of a basal primate into the evolution of primate intelligence, we investigated object-location paired-associates learning in the grey mouse lemur (*Microcebus murinus*). We trained 15 individuals in the highly standardized CANTAB dPAL task: subjects had to memorize three paired-associates between pictorial stimuli and their rewarded location on a touchscreen and to correctly respond to them in the presence of a distracting stimulus. A total of 5 subjects could successfully be trained to reach an *a priori* learning criterion (>80% correct choices in 2 consecutive sessions). Successful young adults (<4 years; N=3) needed between 2 and 3 months of daily training (1 session/day; 36 trials/session), whereas successful old adults (>6 years; N=2) needed substantially longer (5/9.5 months). We further compared the performance data of *M. murinus* to that of a human sample (male adults, N=12). As expected, human subjects generally performed much better (i.e. learned faster; 2-5 sessions) than mouse lemurs, but their error profiles helped to interpret performance in mouse lemurs and suggest that at least 4 of the 5 successful individuals used a spatial, hippocampus-based strategy for dPAL, while one individual might have solved the task using a conditional strategy. To our best knowledge, this is the first empiric evidence for standardized object-location paired-associates learning in a basal primate. By allowing the direct comparison of cognitive data from mice to man, the touchscreen-based, standardized dPAL protocol provides a unique tool for comparative research on the evolution of intelligence.

Funding: EC-FP7/2007-2013/no278486 "DEVELAGE"

**Keywords:** grey mouse lemur, CANTAB dPAL, touchscreen

**PP-BB-24**

**Animal personality and speciation in coral reef fishes**

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**Introduction:** Tropical reef fishes are spectacularly diverse, yet little is known about speciation in these animals.

**Question:** Here, we focus on the Caribbean hamlets (*Hypoplectrus* spp, Serranidae) to explore whether animal personality has played a role in this recent evolutionary radiation. Several hamlets have been hypothesised to behave like aggressive mimics, whereby they mimic the behaviour of resembling non-predatory reef fishes in order to gain access to deceived prey.

**Methods:** Focusing on the mimic-model pair formed by the butter hamlet (*H. unicolor*) and the four-eye butterflyfish (*Chaetodon capistratus*), we conducted repeated behavioural observations ( $n=206$ ) of aggressive mimicry and mating in tagged individuals of a natural population, to investigate whether this behaviour can be considered a personality trait, and whether it is linked to mate choice.

**Results:** Our observations indicate that this behaviour varies consistently among individuals, and that mate choice is weakly assortative with respect to this trait.

**Conclusion:** Our study establishes an important link between ecology, personality, and reproductive isolation.

**Keywords:** aggressive mimicry, mate choice, behavioural syndrome

## Developmental Biology – invited talks

### Zebrafish Germline Development: Its Evolution and Biophysics

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**Introduction:** Germ cells are the precursors to gametes. The germline is therefore essential to initiate the next generation. In the zebrafish, primordial germ cells (PGCs) are specified during embryogenesis by RNA granules termed germ plasm. The current model of germ plasm evolution proposes its independent origin in different animal lineages.

**Objectives:** Continuous fertility is a vital prerequisite for evolution. The invention of independent mechanisms to establish the reproductive cell lineage is therefore difficult to bring in line with evolution.

**Materials & methods:** Using forward genetics in zebrafish, we isolated several years ago Bucky ball (Buc) as the first germ plasm organizer specific to vertebrates. Similarly, *Drosophila* Oskar (Osk) was discovered to organize germ plasm, but is restricted to insect genomes supporting the independent origin of germ plasm during animal evolution.

**Results:** Here, we show that *Drosophila* Osk and zebrafish Buc act as functional homologs. Fascinatingly, both proteins induced PGCs in zebrafish suggesting that they act through a common biochemical network. However, Osk and Buc did not share homologous sequences, but still bound to conserved germ plasm components. Moreover, bioinformatic predictions showed that Osk and Buc encode intrinsically disordered proteins, which quickly change their sequence during evolution.

**Conclusion:** Our findings suggest that Buc is an Osk homolog, which exerts its conserved role through biophysical similarities. Osk and Buc might represent a first example for proteins classified as “novel”, which are functional homologs in distant species.

### Systems biology of vertebrate development

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How an initially homogenous population of cells self-organizes to form patterned embryos and tissues is a long-standing mystery in the field of developmental biology. The prominent reaction-diffusion model postulates that patterns emerge under the influence of poorly diffusive activators and highly diffusive inhibitors. We have found biophysical evidence demonstrating differential diffusivity of the activator Nodal and the inhibitor Lefty, which pattern the germ layers during early vertebrate development. We focus on three major questions to understand how this reaction-diffusion system transforms a uniform field of cells into an embryo: First, how is the differential diffusivity of Nodal and Lefty achieved? Second, how does this reaction-diffusion system adapt to tissue size? Third, how does the Nodal/Lefty reaction-diffusion system self-organize? I will present the results from our recent quantitative experiments and mathematical modeling using developing zebrafish and mouse embryonic stem cells as model systems to address these questions.

## Developmental Biology – oral presentations

### OP-DB-01

#### Functional evolution of a morphogenetic gradient

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While it is well established that gradients of diffusible morphogens produce complex pattern during development, their role as drivers in morphological evolution has remained speculative, largely due to the challenge of quantifying their activities in species outside of select genetic model organisms. One of the most intensely studied examples is the gradient of Bone Morphogenetic Protein (BMP) signaling in fly embryos. In flies like *Megaselia abdita* (Phoridae), the BMP gradient specifies two widely conserved extraembryonic membranes, the serosa and amnion, but in *Drosophila melanogaster*, BMP signaling specifies a single membrane, the amnioserosa. The BMP gradient of *Megaselia* broadens during early gastrulation but is static at the corresponding *Drosophila* stage. We were able to show that the later, broad BMP gradient specifies amnion in *Megaselia* and is driven by a positive feedback circuit that intensifies BMP signaling during early gastrulation at the edge of the germ rudiment. In *Megaselia*, this feedback circuit depends on *dorsocross* (*doc*) and *doc*-dependent expression of *eiger* (*egr*) whereas in *Drosophila*, it depends on *zerknüllt* (*zen*), which activates *doc* and *egr* expression, thereby restricting positive feedback to the dorsal midline during gastrulation. The observed differences between *Megaselia* and *Drosophila* suggest that the ancestral use of the positive feedback circuit was to promote amnion specification. Thus, we demonstrate that spatio-temporal changes in morphogen gradients can drive organismal evolution.

**Keywords:** Bone Morphogenetic Protein, evolutionary development, flies

### OP-DB-02

#### Shared gene expression profile during dorso-ventral patterning in cephalopods and chordates

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1. The bilaterian dorso-ventral (DV) body axis is established by bone morphogenetic proteins (BMPs). In protostomes BMP signaling genes are primarily expressed on the dorsal side, while the expression domains of their antagonists such as *Chordin* are located on the ventral side. In chordates, the BMPs are expressed ventrally, while the expression domains of their antagonists are located dorsally. This situation has been interpreted as a consequence of DV axis inversion that occurred during early chordate evolution. In general, bilaterians possess a pronounced antero-posterior (AP) axis with the exception of scaphopod and cephalopod mollusks having an elongated DV axis. To date the molecular basis of DV axis formation is still poorly studied in the Mollusca, however, it is known that *Bmp2/4* is expressed in the dorsal shell field of various gastropods and a bivalve.

2. In this study we assessed how BMP signaling genes and their antagonists are expressed in bilaterians with pronounced DV body axes.

3. The expression patterns of selected BMP signaling genes and their antagonists were investigated in representatives of three additional molluscan clades: the conchiferans *Antalis entalis* (a scaphopod) and *Idiosepius notoides* (a cephalopod), and the aculiferan *Acanthochitona crinita* (a polyplacophoran).

4. While the above-mentioned genes are expressed in a typical protostome-like manner in the polyplacophoran, a chordate-like mode of expression is found in the scaphopod and the cephalopod.

5. Our study suggests that certain BMP signaling genes and their antagonists have been recruited into the formation of the DV axis in an inverted fashion in cephalopods and scaphopods. This might explain the extremely pronounced DV body axes of scaphopods and cephalopods, in contrast to the pronounced AP axes of the majority of other protostomes.

**Keywords:** evolution, development, mollusk

**OP-DB-03**

***foxQ2* - a novel regulator for arthropod head and brain development**

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The insect head is composed of several segments and an anterior non-segmental tissue. While pattern formation of the segmented part of the body is well understood in *Drosophila*, patterning of the anterior non-segmental region remains enigmatic. We use the red flour beetle *Tribolium castaneum* as model for head development because of its insect typical non-involuting larval head. Previously, we have tested a number of candidate genes assumed to play a role in head patterning based on data from *Drosophila* and the vertebrate neural plate. However, this candidate gene approach will miss novel players of head patterning.

In order to identify such novel genes, we screened the data of the ongoing genome wide RNAi screen *iBeetle* for head phenotypes. We found *Tc-foxq2* to be annotated in the with a highly specific head phenotype where the labrum was missing. We show that *Tc-foxq2* is specifically expressed in the anterior pre-segmental region of the head in line with data from other metazoans. RNAi experiments showed that *Tc-foxq2* is an upstream player within the anterior head gene regulatory network, forming a conserved patterning unit with *Tc-six3*. Heat-shock induced misexpression was used to further refine the regulatory network. Finally, using in vivo imaging reporter lines that visualize the brain we show that embryonic knock down of *Tc-foxq2* function leads to defects in the central body and the mushroom bodies.

With this work we provide the first functional characterization of this gene in Arthropods and reveal a crucial upstream function in anterior patterning.

**Keywords:** insect head, insect brain, foxQ2

**OP-DB-04**

**The bulbus organ of *Parasteatoda tepidariorum* - precise maneuvers with a numb structure? Revisited.**

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Male spiders evolved a unique structure for sperm transfer: the bulbus, a pipette like organ to take up, store and transfer sperm under terrestrial conditions. The bulbus organ is situated on the last segment of the second appendage pair of the spider, the pedipalp. During the last instar before the adult moult it develops within the tarsus segment, but many aspects of its ontogenesis are unclear. The morphology of the bulbus organ ranges from a simple pear-shaped protrusion to extremely complex, sclerite equipped structures, and there is no known reversal to plesiomorphic sperm transfer modes. Despite its complexity and disparity, the bulbus organ is apparently not equipped with any nervous tissue and thus is believed to be entirely numb. However, a recent study identifies a single bulbus nerve in a single spider species. Thus, it is currently unclear whether bulbus innervation exists in other species as well. In our lab we investigate the development and morphology of the common house spider *Parasteatoda tepidariorum*. We study the structure of the bulbus in adult stages and its formation during postembryonic stages, using high resolution imaging techniques. Therefore, we use a multi method approach with three dimensional imaging through micro CT with high brilliance bench and synchrotron radiation sources, immunohistochemistry combined with CLSM and ultra-structure analysis with TEM. We focus on the development of the primordium of the bulbus and its transformation during moulting with a special focus on a possible presence of innervation. This work will provide an in-depth view of the structure and possible innervation of a bulbus of the complex, sclerite equipped type.

**Keywords:** Spider, Pedipalp, Synchrotron  $\mu$ CT

**OP-DB-05**

**The evolution of social behaviors in an insect society**

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Organisms can assemble into advanced societies that exhibit a most sophisticated level of biological organization. In social insects, workers can integrate their rich behavioral repertoire to the extent that they become a single functional unit. Collaboration among the hundreds and even millions of society members has resulted in the emergence of properties that make societies far better adapted to the environment and very successful in ecological terms. In honeybees, a genetically encoded program specifies a worker's brain during development, ensuring the social behaviors that have evolved over the last 60 to 75 million years. We have, however, little understanding of the mechanisms the insect brain employ and have evolved to control the behaviors and social interactions. We have identified candidate genes of an evolved developmental program in worker brains using RNAseq approaches. We are currently studying the function of those genes using CRISPR/Cas9 derived and transgenic methods. We will measure the impact of these brain perturbations on worker behaviors in the social environment of a colony by using an automatic behavioral annotation and tracking system. Our study seeks to link the evolution of the worker's development program with the well adapted properties emerging at the level of the society.

**Keywords:** social organization, development, brain

**OP-DB-06**

**Evolution of stem cells and cancer: lessons from early-branching metazoans.**

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Stem cells emerged in evolution at the point of transition to stable multicellularity. This increase in hierarchical complexity requires robust mechanisms to maintain tissue homeostasis, and dynamically interact with the environment and symbiotic partners. Dysfunction of stem cell activity is expected to lead to cancer formation, and to undermine (meta-)organism integrity. Recently we provided the first evidence for naturally occurring bona fide cancer in early-branching metazoans (Domazet-Lošo, Klimovich *et al.*, 2014). In two species of the freshwater cnidarian *Hydra* female-restricted germ-line stem cells were found to have lost their sensitivity to environmental signals, became unable to undergo differentiation and apoptosis, and gained metastasis-like invasive phenotype. Comparative transcriptomic analysis revealed that multiple gene regulatory networks are dysregulated in the tumor. Among them, signaling pathways controlling apoptosis are impaired, conferring cell-death resistance to tumor cells. Moreover, the expression of several oncogenes, well-known to drive tumorigenesis in vertebrates, is greatly disturbed. Notably, the disturbance of gene expression and loss of tissue homeostasis go side by side with dramatic change in host-associated microbiome composition. Our findings suggest that the evolutionary origin of spontaneous cancers dates back to the origin of multicellular life, and revisits differentiation arrest and resistance to apoptosis as fundamental mechanisms of cancerogenesis. Finally, the study points to the essential role of stably associated microbiota in maintaining tissue homeostasis and organism integrity.

**Keywords:** cancer, apoptosis, microbiome

## Developmental Biology – posters

### PP-DB-01

#### Identification of a novel Gene required for maintaining differentiation states in telotrophic *Tribolium castaneum* oogenesis

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**Introduction:** The beetle *Tribolium* represents telotrophic ovaries, which differ fundamentally from the polytrophic ovary of *Drosophila*. In *Drosophila*, the spatial and temporal association of germline stem cells and somatic stem cells makes it difficult to analyse somatic cell lineages. In *Tribolium*, however, systemic RNAi allows examining somatic cell fates independently of the germ line.

**Objectives:** To identify genes that affect the follicle cell lineages, we participated in a genome-wide RNAi screen (iBeetle).

**Material & methods:** Ovary phenotypes were analysed by different molecular markers

**Results:** Depletion of TC003132 - a putative casein kinase II substrate - results in severe phenotypes. Upon adult RNAi, encapsulation and alignment of egg-chambers is disturbed and ovarioles are depleted of follicle cells, including central pre-follicular cells. In addition, the so-called somatic-plug - a group of small somatic cells located at the posterior end of the tropharium - is dispersed. As monitored by Eya expression, central pre-follicular cells become disorganized and cease mitosis, which eventually results in the loss of somatic lineages.

TC003132 RNAi also affects the differentiation of germ-line derived cells, as we observed “nurse-cell-like” behaviour of otherwise arrested pro-oocytes. While it remains to be elucidated as to whether these cells still have pro-oocyte fates, it is tempting to speculate that in the absence of TC003132 pro-oocyte fate is omitted and germ-line cells trans-differentiate into nurse-cells.

**Conclusion:** Our results indicate a key function for TC003132 in maintaining the differentiation state of the germ-line and somatic cell-lineages in telotrophic *Tribolium* oogenesis.

**Keywords:** Oogenesis, Differentiation, *Tribolium castaneum*

### PP-DB-02

#### FGFs in *Hydra*

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Signaling by fibroblast growth factors (FGFs) and their receptors (FGFRs) is essential in many developmental processes in animals, e.g. patterning, morphogenesis and organogenesis, differentiation, cell proliferation or migration (1). FGFRs and their ligands are highly conserved and already exist in the ancestral phylum Cnidaria (2, 3). Although the model organism *Hydra* lacks distinct organs, FGFR signaling is crucial. It controls morphogenesis of the polyps, namely, detachment of the vegetative buds (4,5). Kringelchen (FGFRa), one of two known FGFRs in *Hydra*, controls boundary formation and tissue constriction in late budding stages by targeting at least two downstream pathways (4, 5). A highly dynamic expression pattern of this receptor tyrosine kinase suggests additional, yet unrevealed functions. Four potential *Hydra* FGFR ligands (FGFa, FGFC, FGFE and FGFF) were recently isolated and pilot experiments carried out to obtain a first glimpse into their function(s) (6). First results suggest that the *Hydra* FGFs, and particularly FGFC and FGFF, might play a role in the selective guidance of cells as well as in cell differentiation.

(1) Thisse and Thisse, 2005; (2) Rebscher et al., 2009; (3) Oulion et al., 2012; (4) Sudhop et al., 2004; (5) Hasse et al., 2014; (6) Lange et al., 2014

**Keywords:** boundary formation, signaling, differentiation

**PP-DB-03**

**Tissue separation during bud detachment in *Hydra vulgaris***

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The separation of cells and tissues is a hallmark during embryonic development. It is mainly controlled by apical constriction of cells and requires a rearrangement of the actin cytoskeleton and the establishment of cortical actomyosin complexes, which leads to boundary formation and tissue separation by mechanical forces (1). RhoA- GTPase, activated by FGFR, (2) acts upstream of the Rho-associated-kinase (ROCK) (3) and is able to initiate and control rearrangement of the actin cytoskeleton and actomyosin contractility. The knowledge of intracellular signaling pathways during the process of tissue separation in our model organism *Hydra* is limited and has to be investigated in the future. In the small fresh water polyp *Hydra vulgaris* the FGFR- signaling is known to control the bud detachment (4 and 5). In the last phases of budding (stages 8-10) a strong lateral accumulation of F-actin in constricting cells at the bud base is detectable. The final phase of bud detachment depends on the activity of MEK-ERK and Rho-ROCK signaling in cells at the bud base. With different inhibitors we can interfere the Rho pathway and so we are able to inhibit the accumulation of F-actin at the bud base. Our conclusion is that via FGFR activated RhoA and thereby also the Rho-ROCK-pathway are basic modules for F-actin accumulation during the final phases of budding. Which intracellular mechanisms are involved in the formation of F-actin accumulation and how the final separation of the tissue during bud detachment in *Hydra* takes place is the major goal of this project.

**Keywords:** Actin cytoskeleton, Cnidaria, Morphogenesis

**PP-DB-04**

**Early decisions in the limb primordium - the outside-in leg phenotype of the novel *Tribolium* gene *Tc-flipflop***

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The general bauplan of the leg is highly conserved among arthropods. Cytological and molecular processes involved in leg development are well studied in the fruit fly *Drosophila melanogaster* where they originate from initially invaginated imaginal discs. Other than in *Drosophila* but similar to vertebrate embryos, *Tribolium* develops everted limb buds during embryogenesis. Cell proliferation and cell shape changes contribute to the distal outgrowth of a leg. However, the molecular processes directing the evagination of the limb buds are yet to be determined. To better understand early steps of leg development in *Tribolium* we analyse *Tc-flipflop*, a newly discovered gene in the iBeetle screen. RNAi-knockdown of *Tc-flipflop* results in a variety of phenotypic traits. Most prominently, appendages grow inwards the larval body rather than evert. This phenotype can already be detected as early as limb buds start to form. *Tc-flipflop* and its paralog *Tc-flipflop2* represent evolutionary non-conserved genes and therefore, their involvement in a known pathway is not evident. Our findings that *Tc-RhoGEF2* RNAi results in a phenotype similar to that of *Tc-flipflop* RNAi, indicate Rho-associated signalling pathways to be involved in the early evaginating limb bud. We further analyse the role of *Tc-flipflop* as well as other candidate genes involved in appendage-eversion at the molecular and cellular level to better understand this crucial aspect of appendage formation.

**Keywords:** appendage development, tissue shaping, RNA interference

PP-DB-05

**Gene expression patterning of the collar cord in the hemichordate *Balanoglossus*: Support for independent evolution of tubular nervous systems in Deuterostomia?**

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Comparative gene expression analyses have revealed that the neural tube of chordate deuterostomes and the ventral nerve cord of polychaete protostomes exhibit a highly similar mediolateral architecture. On that basis, a likewise complex CNS has been proposed in the urbilaterian. Hemichordate enteropneusts, a group of non-chordate deuterostomes, possess a much less complex nervous system, yet a part of the dorsal nerve cord forms a hollow tube resembling the neural tube of chordates. Putative homology of this collar cord and the chordate neural tube is supported by ultrastructural resemblances. However, recent gene expression analyses are less conclusive and revealed contradicting results. The majority of data has been collected from *Saccoglossus kowalevskii*, a species showing a derived mode of development. In order to clarify this issue, we investigated the expression of neuronal regionalization genes in the indirect developing enteropneust *Balanoglossus misakiensis*. We focused on the development of the collar cord and studied anteroposterior (*six3/6*, *otx*, *engrailed*) and mediolateral (*pax6*, *dlx*, *nk2.1/2.2*) patterning genes. Expression analysis shows that the tubular collar cord of *B. misakiensis* is positioned anteroposteriorly in a region corresponding to the vertebrate midbrain. However, mediolateral patterning of *pax6*, *dlx*, and *nk2.1/2.2* is completely aberrant and has no corresponding domains in the chordate neural tube, neither in the midbrain region nor in the trunk. Under consideration of all available data (morphology, gene expression, and phylogenomic analyses), putative homology of the collar cord and chordate neural tube is evaluated.

**Keywords:** nervous system evolution, neural tube, deuterostomes

PP-DB-06

**Bioelectrical polarity is linked to cytoskeletal polarity in ovarian follicle cells of the *Drosophila* mutant *gurken***

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Bioelectrical signals are involved in the generation of cell polarity as well as in cytoskeletal dynamics. For studying possible connections between electrochemical gradients, tissue polarity and the cytoskeletal organization, *Drosophila* oogenesis is a suitable model system. Through interactions between soma and germ line cells, the transforming growth factor homolog Gurken (Grk) establishes both the anteroposterior and dorsoventral axes. In the follicular epithelium of wild type (WT) and *grk* mutant follicles, we have observed stage-specific gradients of intracellular pH ( $pH_i$ ) and membrane potentials ( $V_{mem}$ ) using the fluorescent pH-indicator 5-CFDA,AM and the potentiometric dye DiBAC<sub>4</sub>(3). We also compared WT and *grk* mutant follicles in their cytoskeletal organization using rhodamine-phalloidin and antibodies against acetylated  $\alpha$ -tubulin. Concerning the  $pH_i$  and  $V_{mem}$  patterns, differences first become obvious during mid-oogenesis when the respective dorsoventral gradients are established in WT, but not in *grk* follicle cells. In accordance with bioelectrical differences, *grk* follicle cells also exhibit some cytoskeletal differences. In WT follicle cells, the basal microfilament and microtubule patterns are both more or less cell-autonomously organized, whereas in *grk* follicle cells these cytoskeletal elements are characterized by coordinated transcellular patterns. The striking alignment of microfilaments perpendicular to microtubules in *grk* follicle cells points to a predominant role of microfilaments in stabilizing the transversal follicle axis while the microtubules seem to stabilize the longitudinal follicle axis. Thus, bioelectrical polarity is linked to axial polarity in both WT and *grk* follicles.

**Keywords:** Oogenesis, Pattern formation, Bioelectricity

PP-DB-07

**Scanning electron microscopy as a tool for studying morphogenesis in tardigrades**

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The tardigrades, also known as "water bears", are microscopic invertebrates commonly found in mosses, lichens, and all aquatic habitats. Their bodies consist of five segments: an anterior head segment followed by four trunk segments, each of which bears a pair of lobopodous walking appendages. Although the adult morphology of many tardigrade species has been fairly well characterized, their embryonic development is only beginning to be understood. Recently, work on *Hypsibius dujardini* — including the complete genome sequence, Hox gene expression data, and neural development studies — has projected this species as an emerging tardigrade model with great potential for comparative studies with the arthropods. For documenting the development of external features, such as limbs, we used scanning electron microscopy to examine embryos of the tardigrade *Hypsibius dujardini* at high resolution. In order to reveal these structures, the chorion was removed manually and the vitelline membrane was digested enzymatically. The dissected embryos were then prepared using the standard protocol for scanning electron microscopy. Using this method, we were able to visualize the development of the mouth cone, the limb buds, and in late stages, cuticular structures such as the claws and interior of the mouth from different stages throughout embryonic development. These results add a high-resolution, visual perspective to previous studies focused on internal morphology and gene expression in tardigrades.

**Keywords:** SEM, Panarthropoda, Embryogenesis

PP-DB-08

**Identification of novel genes and pathways regulating muscle development through a genome-wide RNAi screen in *Tribolium castaneum***

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**Introduction:** Embryonic muscle development in *Drosophila melanogaster* requires complex regulatory networks. Although many of the key regulators have already been identified, there are still numerous gaps in our knowledge, and additional regulatory genes and pathways need to be discovered to fully reveal the underlying developmental processes. We and others have shown that muscle development of the red flour beetle *Tribolium castaneum* shares many similarities with *Drosophila*. Thus, a genome-wide RNAi screen (iBeetle) that aims at the functional analysis of all genes in selected developmental processes may provide us with novel insights into arthropod muscle development.

**Objectives:** We aim to find genes that govern different developmental steps of the somatic musculature, ranging from early specification of muscle progenitor cells to muscle attachment and morphogenesis.

**Materials & methods:** Candidates found via iBeetle in *Tribolium castaneum* were evaluated and validated, which is followed by genetic analyses of orthologous genes in *Drosophila*.

**Results:** Since its start iBeetle uncovered more than 170 genes with an aberrant muscle pattern after knock-down in *Tribolium castaneum*, visible by thinner, missing or misshapen muscles. For further analysis, we selected the most promising candidates in terms of phenotype, penetrance and *Drosophila* orthologues. Here, we present the results on selected genes from this screen that encode proteins of classes not previously implicated in myogenesis.

**Conclusion:** The combination of existing knowledge on the cell biology and regulatory interactions in *Drosophila* together with fresh input from the iBeetle screen offers a unique opportunity to extend our insight into the process of myogenesis.

**Keywords:** iBeetle, Myogenesis, *Drosophila*

PP-DB-09

**New insights in border formation and axial patterning in *Hydra***

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One of the major challenges in developmental biology is to understand how cells become specified and organized in complex tissues, structures and organs. It is well known that cells are able to precisely sense their location within the body and to respond accordingly. In *Hydra*, a classical model for understanding developmental processes, transcriptional borders seem to play a key role in axial patterning. *Hydra*'s only three stem cell lineages are mostly restricted to the body column of the polyp whereas the completely differentiated cells are located in the head and foot. As a result of this regionalization an invisible sharp border in the interface between head/body column and body column/foot is formed. Due to this border, many genes show a strong spatial and/ or temporal controlled expression pattern, however the mechanisms controlling their expression are largely unknown. We have found that different concentrations of Trichostatin A (TSA), a histone deacetylase inhibitor, is able to either compromise or completely block the differentiation of *Hydra* stem cells, generating an extended stem cell compartment. Through transcriptome analysis using microarrays, enrichment analysis of metabolic pathways and by generating reporter transgenic lines from stem- and differentiated-cell genes, we observed that constant hyperacetylation state caused by TSA reduces or suppresses the expression of several differentiated-cell genes in the extremities of *Hydra* with a corresponding expansion of the expression of stem-cell genes towards the head and the foot. We conclude that epigenetic changes are one of the major players in formation and maintenance of the axial patterning and border in *Hydra*.

**Keywords:** Hydra, Patterning, Stem cells

PP-DB-10

**Regulatory factors controlling the functional development of the digestive system in a basal deuterostome**

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**Introduction:** Since over 100 years the sea urchin embryo has been used as a model organism for understanding the early developmental biology, gene regulatory network and cell specification of deuterostomes. In contrast to most vertebrates, the stomach of sea urchin larvae is highly alkaline, reaching a pH of 9.5. Although the mechanism of gastric alkalization were recently proposed, the regulatory factors for cell specification and maintaining gastric alkalization remain unexplored.

**Objectives:** Identification of regulatory pathways necessary for the activation and maintenance of gastric alkalization in sea urchin larvae.

**Materials & methods:** The pH microelectrodes were used to measure the gastric pH of control and morpholino injected embryos. Transcripts of markers for gastric pH regulation and upstream regulatory genes were localized by *in situ* hybridization, and the expression quantity was determined by semi-quantitative PCR and real-time PCR.

**Results:** The gene *lox* is important for the formation of the functional gut indicated by a lower alkalization capacity in *lox* morphants compared to control larvae. Furthermore, knockdown of *foxd*, a *lox* downstream candidate gene, also impaired gastric pH regulation. Feeding stimulated gastric alkalization, and also affected the gene expression pattern of regulatory factors might involved in the differentiation of stomach cells.

**Conclusion:** The gene *foxd* is downstream target of *lox*, affecting the regulation of gastric alkalization and controlling the specification of stomach cells. These findings provide first insights into the regulatory mechanisms leading to the functional development of the digestive system in a basal deuterostome.

**Keywords:** sea urchin, ion regulation, gastric alkalization

PP-DB-11

**Expression of the NK homeobox gene *clawless* in embryos of the velvet worm *Euperipatoides rowelli* (Onychophora: Peripatopsidae)**

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The NK genes belong to the ANTP class of homeobox genes, which encode various transcription factors involved in the embryonic development of animals. The expression of the NK gene *clawless* has been examined in several animal species, including both vertebrates and invertebrates. In insects, such as *Drosophila melanogaster* and *Tribolium castaneum*, *clawless* is involved in the development of the distal-most regions of the developing legs. Additionally, a single study on the onychophoran *Euperipatoides kanangrensis* showed that *clawless* is similarly expressed in the distal region of each developing appendage except in the anlagen of the antennae, where expression is lacking entirely. Nevertheless, data from onychophorans — a member of the Panarthropoda (Arthropoda + Tardigrada + Onychophora) — remain scarce. Therefore, we investigated the expression of *clawless* in several embryonic stages of another onychophoran species, *Euperipatoides rowelli*, using whole-mount *in situ* hybridization. In contrast to *E. kanangrensis*, we found *clawless* to be expressed in all developing appendages and the proctodeum. Furthermore, expression in the distal part of the walking legs of both onychophorans and arthropods suggests that *clawless* may play a similar role in the development of these structures in these two groups. Finally, data from tardigrades would help to reconstruct the ancestral condition for the Panarthropoda.

**Keywords:** EvoDevo, mesoderm development, limb musculature

PP-DB-12

**Electrochemical signals are involved in regulating epithelial cell polarity, cytoskeletal organization and tissue architecture during *Drosophila* oogenesis**

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*Drosophila* ovarian follicles provide a suitable model system for studying the potential role of electrochemical cues in controlling cytoskeletal organization and dynamics. During the course of oogenesis, ovarian follicles undergo significant changes in their bioelectric properties caused by the varying activity of asymmetrically distributed ion-transport mechanisms. Moreover, the cytoskeletal organization in the follicle-cell epithelium alters dynamically during follicle development. Since microfilaments and microtubules are known to respond to bioelectric signals we investigated whether changes of bioelectric properties, like intracellular pH (pH<sub>i</sub>) and membrane potential (V<sub>mem</sub>), correlate with alterations of the basal microfilament (bMF) pattern and the microtubule (MT) organization within the follicle-cell epithelium. Intracellular as well as transcellular patterns and gradients of pH<sub>i</sub> and V<sub>mem</sub> were analyzed using the fluorescent pH-indicator 5-CFDA,AM and the potentiometric dye DiBAC<sub>4</sub>(3). We found that changes of pH<sub>i</sub> and V<sub>mem</sub> correlate spatially and temporally with structural modifications of bMF and MT in follicle cells. These alterations were accompanied by cell migrations, cell rearrangements and cell-shape changes, like e.g. cell flattening. Using inhibitors of several ion-transport mechanisms we modified pH<sub>i</sub> and V<sub>mem</sub> and affected the bMF pattern as well as the MT organization in a way similar to changes occurring naturally in parallel with pH<sub>i</sub> and V<sub>mem</sub> alterations during oogenesis. Therefore, we suspect that electrochemical signals play a key role in the regulation of cell and tissue architecture by influencing cell polarity as well as organizing cytoskeletal elements in the follicle-cell epithelium.

**Keywords:** oogenesis, bioelectricity, pattern formation

PP-DB-13

**Reproduction before metamorphosis: Ctenophores and their secret sex life**

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**Question:** The lobate ctenophore *Mnemiopsis leidyi* successfully invaded northern and southern Europe. So far animals have been shown to be able to reproduce before and after metamorphosis in their native range. This is the first detailed study concerning larval reproduction in invasive *M. leidyi* populations. In this study we wanted to investigate egg production rates during development along with information on the proportion of reproducing individuals from two successful invasive populations of the Baltic and Caspian Sea.

**Material and methods:** We measured egg production rates and growth on population and individual level for up to 35 days post hatch.

**Results:** We found reproducing larvae from a size > 2 mm oral - aboral length without a so far described pause in reproduction during metamorphosis. The fraction of reproducing larvae between both populations differed and was 3.3 % and 25.5 % for Baltic and Caspian Sea populations, respectively.

**Conclusion:** Our results suggest that larval reproduction is a common trait for *M. leidyi* which might have played a key role in the great invasion success. Larvae are a potent vector for *M. leidyi* to disperse. Their chance of surviving the transport in ships' ballast water is high due to the species' high stress tolerance for salinity, temperature and oxygen.

**Keywords:** *Mnemiopsis leidyi*, Ctenophores, Larval reproduction

PP-DB-14

**An integrated view into epithelial homeostasis and host-microbiome crosstalk: insights from *Hydra***

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Maintaining epithelial integrity and a well-orchestrated host-microbiome crosstalk is essential for organismal health and life span all throughout the animal kingdom. Dysregulation of this complex interplay is associated with e.g. chronic inflammatory diseases of epithelia including inflammatory bowel diseases and asthma in humans. Based on recent findings, we hypothesize that the conserved transcription factor FoxO plays a central role in maintaining epithelial homeostasis and in shaping the microbiome in animals from *Hydra* to man. Moreover, its activity thereby contributes to longevity. In *Hydra* FoxO controls both stem cell maintenance and components of the innate immune system such as antimicrobial peptides (AMPs). Moreover, *Hydra* is one of the very few animals which shows no sign of aging and harbors a relatively simple microbiome of less than 10 major colonizers. Here we address the link between tissue homeostasis, innate immunity and composition of a stable host-associated microbiota in *Hydra* using multiple "-omics" approaches. Microbiome and RNA-Seq analysis of wildtype and FoxO-deficient animals shows a shift in bacterial colonization, uncovers new FoxO target genes and supports FoxO's role as a key regulator in maintaining tissue homeostasis and health.

**Keywords:** FoxO, tissue homeostasis, host-microbiome crosstalk

**PP-DB-15**

**Body size regulation in animals: lessons from Hydra.**

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Hydra is a non-senescent freshwater polyp with extraordinary regeneration capacity and virtually unlimited clonal growth, both enabled by continuous stem cell activity. In spite of intensive tissue dynamics (cell proliferation, differentiation, migration, displacement, and apoptosis) the size of the polyps in a particular Hydra species or strain remains remarkably stable. This implies tight genetic control of body size in this organism. At the same time, the size of a polyp is prone to variation depending on environmental conditions, displaying Hydras phenotypic plasticity. We investigated the developmental processes and the underlying molecular mechanisms which control size and growth of Hydra by varying environmental conditions and modifying the genetic background. Here we present the initial characterization of the putative insulin like peptide receptor (INSR) knockdown mutant and the influence of the temperature on the development and fitness of Hydra.

**PP-DB-16**

**A new way of making a maxilliped - UBX expression in the maxilliped of the mystacocarid crustacean *Derocheilocaris remanei***

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In terms of morphology, crustacean maxillipeds are hybrid appendages. They arise in anterior thoracic segments and display characteristics of both locomotory (thoracic) and feeding (gnathal) appendages. Maxillipeds are functionally integrated with the anterior gnathal appendages.

Hox gene expression patterns and immunolabeling with the FP6.87 antibody, which detects conserved epitopes of UBX and ABD-A proteins, reveals that maxillipeds are consistently associated with a shift in the expression of the homeotic gene *Ubx*. *Ubx* transcription products or proteins only appear in thoracic segments with a typical locomotory thoracopod, and are consistently absent in the maxilliped. This pattern is found in various crustaceans: the copepod *Mesocyclops*, the mysid *Mysidium*, the decapods *Homarus* and *Periclimenes*, the isopod *Porcellio* and the amphipod *Parhyale*. In *Parhyale*, which possesses maxillipeds on the first thoracic segment, gene manipulation experiments have shown that a leg-like thoracic appendage can be recovered by mis-expressing *Ubx* in that segment.

This paper focuses on the expression of UBX/ABD-A, studied using the FP6.87 antibody, in the mystacocarid crustacean *Derocheilocaris remanei*. Mystacocarids inhabit the intertidal meiofauna zone of sandy beaches and possess one pair of maxillipeds on the first thoracic segment. Strong UBX/ABD-A expression in the single maxilliped makes *Derocheilocaris* unique among crustaceans. The difference between this species and the copepod maxillipeds is of particular interest because correspondences between the feeding apparatus - including the maxilliped - in mystacocarids and copepods have been suggested as being of phylogenetic significance.

## Ecology – invited talks

### **The control of songbird migration: A complex interplay of intrinsic and extrinsic factors**

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Migratory birds react to the seasonal change of their food availability by travelling between their breeding areas and wintering grounds twice a year. The vast majority of our bird migrants are songbirds of which most migrate exclusively during the night. These nocturnally migrating songbirds rely entirely on their endogenously controlled migration program to reach their migratory destinations, because they are not guided by adults or conspecifics. Hence, an innate migration strategy guides birds through space and time. Environmental variation further modulates individual behavior within a genetically determined frame. To understand bird migration and to be able to predict the causes of climate change on migratory birds we consequently need to jointly study intrinsic and extrinsic factors and mechanisms controlling migration. For that an integrated individual-based approach is required that combines field and laboratory studies in a single species. Here, I here detail the significance of the innate migration program on birds' spatial-temporal organization of migration by cage experiments. Further I investigate the variation in the realized migration under natural free-flight conditions. The reviewed studies show that among others the endogenous time programme is involved in the regulation of departure from stopover. Furthermore, the behavioral plasticity to environmental conditions differs in relation to the remaining migration distance in free-flying birds. Hence, foreseeing how climate change will affect our bird migrants requires detailed knowledge about how both the intrinsic and extrinsic factors control species' movement ecology during periods of stopover and flight periods along their entire migratory routes.

### **Chemical signals in ants: Ecology, evolution and their effect on species interactions**

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Ants are a highly successful taxon as measured by their global biomass and number of individuals. Their success is at least partly due to their sophisticated chemical communication – ants use chemical signals to organise colony life, but also to interact with other insects.

Chemical compounds involved in interactions comprise (1) nutrients and other rewards, (2) venoms and other repellents, and (3) semiochemicals, which transmit information, and which will be the focus of this talk. One of the main information channels in intraspecific and interspecific communication are cuticular hydrocarbons (CHC). Beside nestmate recognition, they serve as cues to recognise mutualists such as aphid trophobionts or parabiotic ants. Parabiotic ants - two ant species sharing a common nest - possess CHC profiles highly different from non-parabiotic species. They show convergent CHC changes in several taxa, indicating that the mutualism exerts selection on CHC profiles.

Chemical cues can also be indirect. When insects walk around, they leave liquid droplets on the ground. These 'chemical footprints' resemble cuticular hydrocarbons. Ants detect them, and can recognize the species and (sometimes) even the colony of the ant who walked there previously. Some ants avoid areas covered with footprints of other colonies or species. This may represent a mechanism to reduce competition, and thus an important co-existence mechanism. In other insects, indirect cues like footprints are also used to avoid predators, and can even affect community composition. Further, but less commonly used, semiochemicals in interspecific interactions include trail pheromones, which are exploited by certain ant parasites.

## Ecology – oral presentations

### OP-E-01

#### Local adaptation in *Daphnia* to cyanobacterial protease inhibitors: The role of copy number variation

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1.) Eutrophication of freshwater systems and global warming has led to an increase of frequency of toxin-producing cyanobacterial blooms. One of the most frequent cyanobacterial toxins is the group of protease inhibitors (PIs) that inhibit the digestive proteases of the aquatic keystone-species *Daphnia*.

2.) We hypothesize that *Daphnia* populations that frequently come into contact with cyanobacteria should be locally adapted to PIs. These populations should therefore show specific responses on a molecular level as the underlying mechanism of adaptation.

3.) In order to test our hypothesis, we i) measured tolerance of different *Daphnia* populations as relative growth rate reduction, ii) inhibited *Daphnia* gut proteases with PIs and calculated IC<sub>50</sub> values, iii) measured copy number variation of digestive *Daphnia* proteases with droplet digital PCR.

4.) We demonstrate that populations of *Daphnia magna* differ in tolerance to dietary PIs according to the cyanobacterial background of their lake of origin. The tolerance of the populations correlated significantly with the IC<sub>50</sub> values of *D. magna* gut proteases when inhibited with natural lake seston. One of the genes coding for the proteases that are active in *Daphnia*'s gut showed a conspicuous copy number variation between populations. This copy number variation significantly correlated with relative expression of this protease gene between populations.

5.) We conclude that local adaptation of *D. magna* populations to PIs is due to a combination of changes in protease gene expression, and probably a positive selection of more resistant protease isoforms. This study is the first using droplet digital PCR to demonstrate copy number variation of a gene with ecologically relevant function.

**Keywords:** Droplet digital PCR, *Daphnia*, Adaptation to inhibition

### OP-E-02

#### The best of two worlds: A combined approach for analyzing grazing effects on biofilm communities via NGS and traditional morphological methods

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An increasing number of studies use next generation sequencing (NGS) based approaches to analyze complex communities, but the questions remains - is the method sensitive enough when it comes to identification and quantification of species? We investigated the effect of macroinvertebrate grazing on algal diversity. The aim of the study was to compare the differences between our results depending on if NGS or microscopic counts was used to determine the algae community. We conducted a mesocosm experiment using the freshwater snail *Lymnaea stagnalis* and larvae of the mayfly *Cloeon dipterum* in order to evaluate their respective grazing impact on benthic algal communities. *Traditional morphological methods* and 454 (Roche) sequencing of the V4 region in the small ribosomal unit (18S) rRNA gene were used to investigate the change in the algal communities caused by grazing. The data from the NGS and the classical morphological method detected a shift in the algal species composition, but the two methods varied strongly in their abilities to detect and quantify algal taxa. Our results show that the methods were not able to detect all species in the algal community. We thus recommend implementing both methods when estimating algal community compositions.

**Keywords:** Biodiversity, Algae, Macroinvertebrate

OP-E-03

**Food use of benthic invertebrates across the boundary between marine and terrestrial ecosystems: functional diversity within a salt marsh**

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The Wadden Sea is known for its high secondary production and strong environmental gradients. To investigate the organismal adaptations this demanding environment requires, we focused on the macrozoobenthos as an important link between primary producers and higher trophic levels. In September 2014, we sampled a land-sea transect at the back-barrier system of the island of Spiekeroog (German North Sea) to analyze the community structure from the tidal flats to the upper salt marsh.  $\delta^{13}\text{C}$  and  $\delta^{15}\text{N}$  stable isotope signatures of the macrozoobenthos and potential food sources were measured with a mass spectrometer to detect changes in carbon use and trophic structure of the macrozoobenthic community.

Multivariate community analyses showed similarities of >40 % across the whole transect except for the upper salt marsh, which had irregular inundations and a (semi-)terrestrial community. The macrozoobenthos relied chiefly on marine resources irrespective of the locality in the intertidal zone. Soil organic matter and terrestrial resources became important only in the upper salt marsh. There were no significant changes in the overall food-web structure with increasing importance of terrestrial resources. However,  $\delta^{15}\text{N}$  values of the typical polychaete *Hediste diversicolor* increased significantly from 13.5 ‰ at the tidal flat up to 16.3 ‰ at higher intertidal stations. These values indicate an increase of one trophic position in moving toward the higher stations, possibly because of a switch in feeding mode from suspension feeding at the longer inundated tidal flats to predation on other invertebrates in the salt marsh. We conclude that changes in feeding appear to represent an important mechanism of adaptation to different Wadden Sea habitats.

**Keywords:** macrozoobenthos, stable isotopes, Wadden Sea

OP-E-04

**Predator feeding modes and the adaptive value of chemical defense: A gamasid-oribatid mite predator-prey experiment**

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Body size is a major influencing factor of the interaction strength in predator-prey networks. However, body size relationships alone do not explain everything, and predator foraging as well as prey vulnerability traits have recently been introduced to food web research. We used oribatid and predatory mites to investigate the role of some of these traits in the context of morphological and chemical defense in soil food-webs. Chemical defense has been shown to provide protection even against large predators (e.g. staphylinid beetles), but many oribatid species are also well protected against predatory mites by numerous morphological traits ("enemy-free-space hypothesis"). However, since predatory mites and staphylinid beetles have very different types of attacking and feeding (predator foraging traits), the adaptive values of chemical and morphological traits might differ accordingly. The oribatid species *Archegozetes longisetosus* and the common gamasid mite *Stratiolaelaps miles* (=syn. *Hypoaspis miles*) were used as model organisms in a predator-prey experiment. We tested for effects of chemical defense and sclerotization in an orthogonal design. Chemical defense, though highly protective against large predators, was mostly ineffective against gamasid mites. Sclerotization, on the other hand, had a strong positive effect. Hence, in a natural soil food web with diverse types of predators, the "enemy-free space" seems only achievable by combinations of chemical and morphological traits.

**Keywords:** defensive mechanisms, soil food webs, behavioral ecology

**OP-E-05**

**Impact of arbuscular mycorrhiza: modifications of host plant quality mediate variation in development and behaviour of a generalist herbivore**

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Generalist chewing-biting herbivores are regularly confronted with species-specific modifications in host plant quality, which can be induced by the symbiosis with a fungus, the arbuscular mycorrhiza (AM). While previous studies already detected AM-dependent effects on larval development of foliar-feeding insects, little is known about the impact of these host plant modifications on behavioural traits. In this study, we investigated the influence of *Rhizophagus irregularis*, a generalist arbuscular mycorrhizal fungus, on the development and various behavioural traits of larvae of the generalist *Mamestra brassicae*, and analysed changes in plant quality traits caused by AM. When larvae were kept on plants with AM, they reached a higher biomass and developed slightly faster than on plants without AM. The behaviour was unaffected by the AM treatment, but differences in behaviours were found between larvae of different age. Differences in plant chemical traits, which could be detected between plants with and without AM, or potentially in other traits can thus fine-tune different life-history traits of herbivores and influence the fitness of the individuals.

**Keywords:** arbuscular mycorrhiza, plant quality modification, plant-herbivore interactions

**OP-E-06**

**Stress tolerance in early life stages determines vulnerability to climate change**

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Anthropogenic climate change may pose substantial challenges to biodiversity conservation. Well-documented biological responses to recent climate change include phenological and range shifts as well as declines in cold-adapted but increases in warm-adapted species. The latter shows that some species will suffer while others will benefit from ongoing changes. However, the specific biological features determining whether a given species is becoming a 'winner' or 'loser' of climate change are hitherto largely unknown. Here, we test if there are differences between three related butterfly species of different vulnerability to climate change and in which life stage potential differences are most pronounced. We show that surviving stressful conditions during early development may be of key importance. In comparative laboratory assays, we found that the arguably most vulnerable species showed the strongest decline in egg hatching success under heat and desiccation stress. While a similar pattern prevailed for hatchling survival, different stress levels applied later during development had generally little effect on fitness components. Collating more data on stress tolerance in different life stages from a broader range of species will be of crucial importance for enhancing our abilities to predict the fate of particular species and populations under ongoing climate change.

**Keywords:** early developmental stages, heat stress, *Lycaena* species

OP-E-07

**Sublethal doses of a neonicotinoid pesticide impair sexual communication in a parasitic wasp**

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**Introduction:** The chemical communication of insects is omnipresent in all fields of their life. This includes sexual communication, defense or foraging and is indispensable for the surviving of a species. As a result of extensive agriculture, low doses of pesticides are present in the environment. They can accumulate and enter the body of both pest and beneficial organisms. Given that many pesticides are neurotoxins, even sublethal doses can be detrimental by influencing insect olfaction. Especially neonicotinoid insecticides are suspected to cause serious problems in ecological key species such as pollinators. However, for a comprehensive risk evaluation also the effects of neonicotinoids on parasitic wasps and other natural enemies need to be investigated.

**Objectives:** We aimed to investigate if sublethal doses of the neonicotinoid imidacloprid impair the pheromone mediated sexual communication in the model organism *Nasonia vitripennis*.

**Materials & methods:** We compared the pheromone response and courtship behavior of wasps treated with sublethal doses of imidacloprid and control wasps in standard behavioral bioassays.

**Results:** Sublethal doses of imidacloprid significantly impaired the response of *N. vitripennis* females to the male sex pheromone and receptivity signaling towards courting males. Treated males were less successful in mate recognition and courtship.

**Conclusion:** Parasitic wasps are crucial for the functioning of terrestrial ecosystems. Our data add another aspect to the controversial discussion about the use of neonicotinoids in agriculture by demonstrating that sublethal doses can have a dramatic impact on the reproductive biology of these beneficial insects.

**Keywords:** Imidacloprid, *Nasonia vitripennis*, Pheromone

OP-E-08

**Ground beetles in city forests: forest age and urbanization influence behaviour**

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Urbanization leads to vast changes in natural habitats with immense effects on wildlife, including behavioural modifications. Understanding behavioural responses to anthropogenically changes is important for identifying which species may cope with those alterations, as behaviour is often the first response, with consequences for fitness and population dynamics. Yet, effects of anthropogenical changes on invertebrate behaviour are largely unknown. In a field study we tested >2000 individuals of 4 forest-dwelling carabid species, from 8 within-city forests that differed in urbanization and age (fully crossed design), for their risk-taking and exploratory behaviour. In line with prediction, individuals were more exploratory in highly urbanized forests (3 species); as well as more exploratory (2 species) and more risk-prone (1 species) in recent than in ancient forests. One species took less, another species more risks in highly urbanized areas. We discuss potential consequences of such behavioural differences in anthropogenically changed habitats for future population dynamics.

**Keywords:** anthropogenic change, exploration, carabid

OP-E-09

**Highly plastic lifespan in a semelparous, annual reptile, Labord's chameleon (*Furcifer labordi*)**

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Within tetrapods the current record holder in the category short lifespan is a small Malagasy chameleon, Labord's chameleon, *Furcifer labordi*. These chameleons from the arid south-west of Madagascar have an assumed post-hatching life span of approximately 4 - 5 month (November - March) and exhibit simultaneous mortality in both sexes at the end of the rainy season. Consequently, they spend the majority of their lifetime as a developing embryo, probably as an adaptation to a harsh dry season. This semelparous, annual life history is unique among tetrapods. So far only one population of *F. labordi* situated in the southernmost distribution range has been studied. We investigated the plasticity of the lifespan of *F. labordi* in a population in Kirindy Forest (western Madagascar), using a combination of observational and experimental methods. Specifically, we controlled extrinsic factors of mortality, such as predation and fighting, by keeping some individuals separately in outdoor aviaries.

While in the southern population no adults were found after March, in Kirindy the disappearance of adults was shifted several months forward. These differences might be due to the higher annual precipitation levels at Kirindy compared to the southern habitat. Our data also suggests an intriguing difference in sex-specific mortality, suggesting that females might have a longevity advantage. Furthermore, we found that single females were capable of surviving until next breeding season depending on the previous rainy season. Keeping *F. labordi* in captivity demonstrated that males and females can survive until the next active season and that single males can even stay alive until the next mating season. Our findings reveal considerable plasticity in the life history of *F. labordi* which might be linked to small-scale variation in ecological factors.

**Keywords:** semelparity, life history, Labord's chameleon

OP-E-10

**THE IMPACT OF THE OXYGEN MINIMUM ZONE ON THE VERTICAL DISTRIBUTION AND ABUNDANCE OF GELATINOUS MACROZOOPLANKTON IN THE EASTERN TROPICAL ATLANTIC**

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Mesopelagic oxygen minimum zones (OMZs) occur naturally in all oceans, but the consequences of their recent expansion for the pelagic fauna remain largely unknown. While OMZ expansion may result in habitat reduction of oxygen demanding species, it may result in habitat expansion for species capable to tolerate low oxygen levels. Gelatinous organisms typically have low metabolic rates and their potential resilience towards low oxygen levels may enable them to live in OMZs. To test this hypothesis, abundance and distribution of representative members of the gelatinous community of the eastern tropical Atlantic (Cape Verde Area) were correlated with oxygen concentrations.

We performed pelagic video surveys in the eastern tropical Atlantic at stations with an OMZ of different intensity. The surveys were carried out using a newly developed towed, optical observation instrument (PELAGIOS) which collects videos of pelagic organisms and measures temperature, depth and oxygen. Video transects were made at 20, 50, and 100 m depth followed by a stepwise recording every 100 m down to a maximum depth of 1000 m.

The surveyed stations had the OMZ core between 300 and 500 m depth. The measured oxygen concentrations ranged from almost saturated levels in surface waters down to a minimum of 30  $\mu\text{mol/kg}$  within the OMZ. Our video surveys provided one of the first *in situ* video observations of the large pelagic fauna in the eastern tropical Atlantic and revealed a diverse gelatinous community. The analysis of our data showed a strong vertical zonation with a shift of species composition with changing oxygen concentrations, depth, daytime and sampling location. These relations will be discussed in the context of a future ocean scenario with expanded mesopelagic OMZs.

**Keywords:** Oxygen minimum zone, Gelatinous zooplankton, Video Observation

## Ecology – posters

### PP-E-01

#### Mind the gape - dietary quality determines the strength of anti-predator defence

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Predation is a major force driving adaptation in prey. Ample evidence indicates that fluctuating predation risks have led to the evolution of inducible defenses in prey. Such defenses may e.g. involve the deployment of defensive morphologies that reduce prey mortality under size-selective (gape-limited) predation. However, if animals acquire dietary resources of inferior quality, their growth and development are retarded. This would lead to an increased time spent in the vulnerable body size range of predators with a preference for small prey. Here we hypothesize that it would be adaptive to alleviate this potentially increased risk of predation through an increased deployment of morphological defenses. We use the particularly well-studied morphological defence of the model system *Daphnia pulex* and its response to the predatory phantom midge larva *Chaoborus* to test how different quality of algal food for *Daphnia* affects the strength of defensive neckteeth induction in *Daphnia*. We crossed three clones of *D. pulex* with three different algal food and found that low food quality extended *Daphnia*'s time in the vulnerable body size range by up to 53 %. This elongation of the prey's time in the vulnerable size range resulted in an up to fourfold stronger neck-teeth induction, which was a purely maternal effect and did not depend on the diet of the offspring. The unprecedented observation of an enhancing effect of low food quality on inducible morphological defenses indicates that food quality can have strong, but yet unstudied effects on the evolution of inducible morphological defenses.

**Keywords:** inducible defense, *Daphnia*, chemical ecology

### PP-E-02

#### Comparison of techniques for the assessment of plankton community composition

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In aquatic ecosystems, phytoplankton community composition plays an important role for zooplankton (primary consumers). Resource diversity of the phytoplankton communities determines the food quality of the phytoplankton, which is one of the factors that control the zooplankton productivity. In recent years, the number of techniques for quantification and discrimination of different phytoplankton groups in water samples from field studies has increased. Frequently, phytoplankton community composition is assessed indirectly via CHEMTAX, a matrix factorization program, which calculates the contribution of different phytoplankton taxonomic groups to the total chlorophyll a using pigment concentrations derived from HPLC. Numerous other methods have been used to determine the phytoplankton community composition, the total phytoplankton biomass and its light use efficiency. Here, we evaluate the usage of CHEMTAX and three other techniques based on spectrometry, pulse amplitude modulated fluorometry and algal fluorescence. We show that usage of these methods allows a simplified assessment of the phytoplankton community composition and light use efficiency. Furthermore, we show that the phytoplankton community composition is relevant for trophic interactions with crustacean zooplankton.

**Keywords:** zooplankton, phytoplankton, community composition

PP-E-03

**Compound-specific  $\delta^{15}\text{N}$  of amino acids as a tool to understand invasions in complex freshwater food webs**

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The analysis of bulk stable isotopes has proven to be an extremely valuable tool for the elucidation of food web structure in various ecosystems. However, in complex food webs and in particular with abundant omnivores, the resolution of the food web structure via the classical bulk stable isotope analysis is strongly limited. To gain a higher resolution in both basal resource and trophic level estimates, the advanced technique of compound-specific stable isotope ( $\delta^{15}\text{N}$ ) analysis from amino acids is increasingly utilized in marine ecology, but has yet rarely been applied in freshwater ecosystems. Here, we apply this emerging method in a complex freshwater food web in order to understand the trophic position and food web interconnections of the invasive mysid crustacean *Limnomysis benedeni* and invasive gobiid fishes. Analysis of amino-acid specific  $\delta^{15}\text{N}$  allowed very precise trophic level estimates for the whole food web, which were generally consistent with those from bulk  $\delta^{15}\text{N}$  analyses. Our data demonstrate that the complex food web of the investigated gravel pit lake is mainly driven by the import of allochthonous production, rather than autochthonous production within the system. Amino-acid specific  $\delta^{15}\text{N}$  clearly indicate an omnivorous/detritivorous feeding behaviour of *L. benedeni*, which is different from previous classifications of this invasive species as a benthic herbivore or planktivore based on bulk isotope data. This case study highlights the immense potential of compound-specific stable isotope analysis from amino acid  $\delta^{15}\text{N}$  to elucidate trophic levels and general food web structure not only in marine, but also in complex freshwater ecosystems.

**Keywords:** stable isotope analysis, ecosystem ecology, invasive species

PP-E-04

**What makes good food? The impact of essential polyunsaturated fatty acids on fitness and gene expression of *Daphnia*.**

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**Introduction:** Freshwater zooplankton of the genus *Daphnia* are considered as key species in lake food webs since they form the crucial link between primary producers and consumers. This link between trophic levels depends not only on food availability, but also on food quality. In this context, an important nutritional compound of the primary producers (algae and cyanobacteria) is the availability of essential polyunsaturated fatty acids (PUFAs). To date, PUFAs are known to positively influence somatic growth, which could in turn boost population growth, since Daphnids reproduce very fast in exponential numbers through their parthenogenetic reproduction mode under favourable conditions.

**Objectives:** Since little is known about gene networks of fatty acid metabolism under different food regimes, we aimed to track transcriptomic changes in *Daphnia magna* in correlation to physiological effects under defined food sources, i.e. different algal and cyanobacterial diets differing in their PUFA composition.

**Methods:** We monitored somatic growth rates of different diet treatments and analysed transcriptomic changes in the same cohort of animals. Respective sample material was used for an explorative Illumina sequencing and transcriptome data were analysed to uncover expression patterns that become effective under certain food conditions.

**Results and Conclusions:** An enhanced growth performance correlated with the availability of essential PUFAs. The respective transcriptomic data indicate that characteristic gene networks become effective under specific dietary conditions, which allow a deeper understanding of the regulatory mechanisms that become effective under distinct dietary constraints.

**Keywords:** transcriptome, PUFAs, lipid metabolism

**PP-E-05**

**The effects of nutrients on the defensive potential of cyanobacteria against herbivores**

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Herbivory is a strong selective factor for the development of defenses in primary producers. Defensive secondary metabolites (e.g. protease inhibitors) are commonplace in primary producers to reduce herbivory. Such defenses come with costs for the prey, especially under resource limitation. According to the Carbon-Nutrient Balance Model (CNBM) the production of secondary metabolites depends rather on the availability of carbon and nutrients than on the actual threat of herbivory. In this study we used a strain of the cyanobacterium *Microcystis aeruginosa*, which produces protease inhibitors as a defense against the freshwater herbivore *Daphnia*, to investigate if the CNBM is valid. We conducted batch culture growth experiments on a gradient of nutrients (nitrogen, phosphorous) and light and quantified the content of different protease inhibitors in the cyanobacterium using high resolution liquid chromatography - mass spectrometry (LCMS). The results show that the concentrations of protease inhibitors normalized to the biomass depend on the availability of nutrients and are also related to the growth rate of the cyanobacterium. Therefore, it can be concluded that nutrients alter the potential of cyanobacteria to produce defensive secondary metabolites against its major herbivore *Daphnia* and that nutrient limitation of primary producers has to be considered in further studies investigating the interaction of a cyanobacteria and *Daphnia*.

**Keywords:** secondary metabolites, anti-herbivore defense, carbon-nutrient balance model

**PP-E-06**

**Adult leaf beetles compensate for poor larval host plant conditions**

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The life of herbivores is greatly affected by the consumed host plant quality. However, it is hardly known whether larval or adult host plant conditions are more decisive in the process of shaping the adult phenotype. This is particularly the case for holometabolous insects in which both larvae and adults feed on the same plant material. We reared larvae and adults of the mustard leaf beetle (*Phaedon cochleariae*) constantly on its natural host watercress or on the nutritious crop cabbage, or as larva on one of the hosts and after metamorphosis on the other host plant. Watercress leaves contained higher glucosinolate concentrations, whereas cabbage had a higher nitrogen and water content. Growth parameters, various reproductive output traits and the feeding preferences were determined several times throughout the lifetime of the beetles. Next to a faster development of larvae fed on cabbage, adults reared on that nutritious crop had a higher reproductive success. When larvae were kept on watercress, adults were able to compensate for poor larval food conditions when switched to cabbage. A feeding preference of larvae and adults was only expressed for the more nutritious plant (cabbage). Thereby, the adult preference was shaped by the current host condition, regardless of the larval host experience. In summary, nutritious crop plants may be more readily exploited by herbivores that show a high plasticity in reproduction and feeding preferences.

**Keywords:** Feeding preferences, Plant quality traits, Reproductive output

PP-E-07

**Trophic ecology of the orangeback flying squid *Sthenoteuthis pteropus* (Steenstrup, 1855) (Cephalopoda: Ommastrephidae) in the eastern tropical Atlantic**

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**Introduction:** In the eastern tropical Atlantic, the orangeback flying squid *Sthenoteuthis pteropus* is an opportunistic short living carnivore and among the fastest growing squids. This species is one of the dominant members of the epipelagic nekton community. So far our understanding of their trophic ecology is limited. Our study attempted to better understand its role in the pelagic food web of the eastern tropical Atlantic by investigating its feeding habits.

**Methods:** We examined 110 specimens of the orangeback flying squid *Sthenoteuthis pteropus*, ranging from 155 to 475 mm (dorsal mantle length), that were caught by hand jigging in the eastern tropical Atlantic in 2015. Besides body mass and size, factors such as sex, maturity stages and stomach fullness were determined. Stomach contents of all individuals were analyzed as well. To estimate the current trophic position of the squid in the food web, stable isotopes ( $\delta^{13}\text{C}$ ;  $\delta^{15}\text{N}$ ) were measured from mantle tissue samples of 30 squids. We also analyzed stable isotopes of gladius samples taken at 10 and 20 mm increments to track possible ontogenetic changes in the squid's diet (n=5).

**Results and Conclusion:** Preliminary results on the trophic ecology of *Sthenoteuthis pteropus* are in line with the feeding habits that have been shown for many other oceanic squids. *S. pteropus* feeds on abundant members of the oceanic micronekton such as myctophid fishes (e.g. *Electrona risso*, *Ceratoscopelus warmingii* and *Hygophum hygomii*) and flying fishes (*Exocoetus obtusirostris*). Exoskeletons of amphipods, decapods and other crustaceans were also found in smaller squid specimens and this is likely part of an ontogenetic transition from crustacean prey to fish and cephalopod prey. This transition will be studied using the results of the stable isotope analysis, which are still in progress.

**Keywords:** Cephalopods, Trophic Ecology, stable isotope analysis

PP-E-08

**Genetic diversity of widespread moss-dwelling nematode species in German beech forests**

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Molecular studies suggest that the number of microscopic animal species, especially regarding the meiofauna, has been underestimated due to a high level of cryptic diversity. A large number of species have remained undetected while using traditional light microscopy for species identification. Focussing on nematodes, many aquatic morphospecies with an assumed widespread distribution may instead comprise cryptic species complexes. In terrestrial moss habitats, the diversity of nematode communities has not been evaluated in molecular surveys so far. Thus, the aim of this study was to assess the potential for cryptic diversity among three dominant moss-dwelling nematode species (*Plectus parietinus*, *Plectus cirratus*, and *Chiloplectus andrassyi*) sampled at five locations within four German beech forests. Analyses of the molecular variation in one mitochondrial (COI) gene and in two ribosomal (LSU and SSU) subunit genes were complemented by morphological identification of specimens. The morphological-based plectid species delineation was supported by the COI gene topology, but less by the analyses of the LSU nuclear marker gene and not at all based on the SSU gene. Furthermore, the results revealed a high level of high genetic diversity in terms of number of mitochondrial haplotypes detected overall for the three investigated morphospecies at the five locations, with no evidence of cryptic diversity. However, the large number of haplotypes only to be found at a single sampling location suggested a restricted level of gene flow even over short geographic distances (6 km). Further studies of moss cushions should broaden the sampling area as well as the number of sampled individuals.

**Keywords:** nematodes, molecular diversity, cryptic diversity

PP-E-09

**Host-range assessment in *Lariophagus distinguendus* (Förster)**

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The parasitoid wasp *Lariophagus distinguendus* (Förster) (Hymenoptera: Pteromalidae) is reported to be an ectoparasitoid of several beetle species that develop internally e.g. in seeds or enclosed in cocoons. Recent findings by König et al. (2015) suggest that the species *L. distinguendus* in fact consists of two cryptic species. One (*L.d. gw*) is mostly found on the granary weevil *Sitophilus granarius* (Coleoptera: Dryoptheridea), a common pest in granaries, but is hypothesized to be a generalist with several hosts. The second species (*L.d. db*) is found on the drugstore beetle *Stegobium paniceum* (Coleoptera: Ptinidae), a common household-pest in pantries. This is considered a specialist on *St. paniceum*. To further investigate the host-range of the two *L. distinguendus* types no-choice host-recognition experiments were conducted. As expected *L. distinguendus gw* showed no significant differences in host-recognition between the hosts offered. In contrast, *L. distinguendus db* showed a significant preference for *St. paniceum* when compared with *S. granarius*. Surprisingly there was no significant difference in host-recognition behaviour between *St. paniceum* and *Gibbium psyllodes*, another household-pest. The host-range of the two *L. distinguendus* types seems to be more complex than expected. Whereas *L. distinguendus gw* can be considered a generalist, the host-range of *L. distinguendus db*, a supposed specialist of *St. paniceum*, might be larger than expected. It seems to comprise hosts being associated with households but not host that are associated with granaries.

**Keywords:** *Lariophagus distinguendus*, host recognition, host range

PP-E-10

**Viral diversity in ant communities**

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Viruses are important infectious pathogens, regularly causing epidemics in societies, whether human or social insect. While research has made considerable progress in understanding viral infections in vertebrate societies, our knowledge in social insects is limited and almost exclusive to viral infections in honey bees. In this study we explore the natural viral component communities, different virus species populating a single host species, of three host ant species across various sampling sites within Europe. Next generation sequencing allows us to catch the whole viral diversity within the sampled host populations and to disentangle real infective viruses from non-infective viruses. We will highlight the relevant viral families within the sampled ants and conserved viral community patterns within single host species across our sampling sites. The powerful sequencing techniques at hand offer valuable insights into and a first step towards a basic understanding of complex ecological communities like the so far understudied multi-host multi-pathogen systems.

**Keywords:** social insects, pathogens, viruses

**PP-E-11**

**Interference competition - Insect's detoxification mechanisms as target for filamentous fungi?**

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1. Competition is a ubiquitous phenomenon that can be observed wherever resources are limited. It can take different forms, means, and engage organisms with similar and entirely different habitus.

2. We aim to analyse interference competition of an insect-mould interaction involving mycotoxins. We characterised the insect responses to the noxious substances produced by filamentous fungi.

3. We mimicked co-infestation of *Drosophila melanogaster* breeding sites with filamentous fungi, *Aspergillus nidulans*. With use of both a wild-type strain and a toxin-impaired mutant strain of *A. nidulans* we disentangle the insect's responses to the different facets of fungi's actions; that is, alteration of pH-level, nutrients availability, fungal tissue and waste-metabolites from the responses to mycotoxins. We observed larval behaviour and conducted a time-series of transcriptome sequencing of larvae that were confronted with breeding substrate inoculated with either of fungal strains, the mycotoxin sterigmatocystin, or with mould- and toxin-free breeding substrate.

4. We did not find escape or avoidance behaviour of larvae, although *A. nidulans* had devastating impact on larval development. RNA-seq analysis of larvae during confrontation revealed several hundreds of genes with changed expression in the four conditions. A set of genes in first and second line detoxification mechanisms that were induced during mycotoxin confrontation were down-regulated in confrontations with both fungal strains.

5. An impairment of insect's detoxification mechanisms will lead to metabolic dysfunctions and cell-component-damage, and thus, to deficient development or even death; yet, it may avail the fungi to reduce negative impacts of the larvae.

**Keywords:** interference competition, detoxification mechanisms, transcriptome

**PP-E-12**

**Insects versus fungi: *Drosophila melanogaster* behaviour and performance is affected by complex fungal metabolic dynamics**

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Insect-fungus interactions are widespread and fungal chemicals can affect insects in many ways. However, the enormous fungal chemical diversity observed has rarely been considered to be driven also by the opposite mode of action: a response to insect attack. We hypothesized that larval attack of *Drosophila melanogaster* induces chemical changes in the mould *Penicillium expansum*, which in turn affect the insects' foraging and fitness phenotype. Unchallenged and insect-induced fungal strains were analyzed by metabolic profiling (HPLC-MS) and extracts obtained for this purpose were subsequently tested as to their impact on larval feeding behavior and survival, as well as adult feeding performance. Furthermore, we tested whether fungal excretions negatively affect microorganisms that otherwise promote development of the flies. We identified strong insect-induced changes in the fungal metabolic profile, which are in part strain-specific but with a distinct similarity across strains. An overall negative effect on insect survival and feeding behaviour was observed in excretions from induced strains; these were, however, strain and also concentration dependent. *Drosophila* associated yeasts were partially or totally suppressed in growth indicating that insect-induced fungal excretions can affect the whole habitat with influence on other trophic levels and symbiotic communities. Our results indicate that fungal metabolic dynamics is a general phenomenon underlying induced insect resistance and hence substantiate the explanatory power of the concept of inducible resistance in fungivore-fungus interactions.

**Keywords:** chemical ecology, induced defence, insect-fungus interactions

**PP-E-13**

**Springtail foraging responses to fungal volatiles**

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Soil arthropods display selective feeding on fungi and thereby influence decomposer food-web processes. The mechanisms underlying the foraging decisions of soil arthropods, however, are a largely underexplored aspect of ecological research. We hypothesize that volatiles of different fungal origin are important infochemicals affecting the foraging behaviour of mycophagous springtails (Hexapoda, Collembola). GC-MS analysis showed that fungal species, developmental stage, genotype and tissue wounding contribute significantly to the volatiles released. Video-tracking of individual springtails showed that some fungi and their volatiles mediate long-distance attraction, whereas others, in particular fungal-specific and wound-activated eight-carbon volatiles (e.g. 3-octanone), did not function as attractants in otherwise odourless fungi. However, we found eight-carbon volatiles (analogous to six-carbon green leaf volatiles in plants) to stimulate feeding behaviour. Therefore, variation in the release of volatiles by fungi may play a central role in regulating spatial foraging behaviour and food selection in mycophagous arthropods.

**Keywords:** chemical ecology, foraging, fungivore-fungus interactions

**PP-E-14**

***C. elegans* natural ecology: Hitch-hiking with slugs, woodlice, and chilopods**

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The abilities of very small animals to migrate over long distances are often limited. However, if these animals prefer ephemeral habitats such as decomposing fruits or other rotting plant materials the ability to migrate between locations is essential. The free-living nematodes *Caenorhabditis elegans* and congeneric taxa can be found in these short-lived environments. Animal vectors are likely to be involved in their dispersal, yet this assumption is based on a limited number of studies. Consequently, we asked which invertebrate taxonomic groups represent vectors of *Caenorhabditis* nematodes.

We conducted three comprehensive field surveys on potential invertebrate vectors in North German locations containing populations of *C. elegans* and two related species, especially *C. remanei*. *Caenorhabditis* nematodes were commonly found in slugs, isopods, and chilopods, whereas the other examined taxonomic groups did not harbor any *Caenorhabditis* species. Interestingly, slugs contained nematodes in their intestine even if the slug sampling site did not represent suitable substrates for *Caenorhabditis* proliferation. As this observation suggested the ability of *Caenorhabditis* to enter the slug intestine and persist for a certain time period we performed an experimental analysis of worm persistence in slug intestines. Under laboratory conditions *C. elegans* was able to invade slug intestines and was excreted alive with the slug feces.

We conclude that slugs, isopods, and chilopods represent potential vectors of *Caenorhabditis* nematodes. The adaptations allowing the nematodes to enter and persist in the unfavorable environment of slug intestines may indicate a first step towards the evolution of a parasitic life-style.

**Keywords:** *Caenorhabditis elegans*, Arion, vector-mediated migration

**PP-E-16**

**The invasive freshwater jellyfish *Craspedacusta sowerbii* - what's going on with occult polyps?**

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The increasing introduction of non-native species into new ecosystems is a consequence of growing mobility. The freshwater jellyfish *Craspedacusta sowerbii* is one example of a recently globally distributed species, which originated from China. Since 1905, it is known to be present in German lakes. Meanwhile, reports on jellyfish blooms in limnic systems are common worldwide, but consequences of the jellyfish's introduction are still unknown. Ecological data are missing for all life history stages, for the conspicuous free-swimming medusae as well as the tiny sessile polyps. In this presentation, we focus on the polyp stage and provide a preliminary map of its abundance and distribution in Southern Germany. We tested for differences in the food web position of *Craspedacusta* polyps in relation to polyps of the resident Cnidarian species, the brown *Hydra*, using stable isotope analyses. We also provide first results of functional response assays allowing for a more detailed characterization of the polyp's niche. The importance of persistent polyps impacting invaded food webs is one part of the scenario. To figure out the trophic position of the short-lived medusae is the next step we will approach.

**Keywords:** *Craspedacusta sowerbii*, invasive species, polyp

**PP-E-17**

**The noise-egg: A simple device that produces low-frequency noise to experimentally test the effects of aquatic noise on fish and other small aquatic animals**

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The effects of noise on animal behaviour and physiology is a field of growing scientific interest. Noise is internationally seen as major environmental concern, but knowledge on the response of animals to aquatic noise and its ecological and evolutionary consequences is disparate. Even though fish and invertebrates form the majority of aquatic taxa, little is known about the effects of aquatic noise on these taxa. While experimental studies on this subject are thus greatly needed, the expense of the equipment can be a main factor limiting data generation. Speakers that produce low-frequency sounds under water are currently either too large or too expensive to allow for sufficient replication in many research set-ups.

Here, we describe the noise egg: a device that can produce low-frequency noise, both in aquaria and the field, is completely self-contained and costs around 10 euros per noise source. The noise produced by the egg consists of frequency bands (harmonics), which has the advantage that broad-band and pulsed sounds, such as sounds produced by fish and crustaceans, are easily detected in noise treatments. Because the noise from the egg attenuates quickly, it can be used in aquaria and in the field to specifically target certain study species or individuals. We have developed the device to study the effect of noise on communication and behaviour in small aquatic animals, however it could be used for other purposes, such as testing the effects of noise on species diversity in small scale habitats such as rock-pools or the propagation of certain frequencies in shallow water habitats.

We hope the described method will facilitate the generation of experimental data on the effect of noise on aquatic animals in a wide variety of study systems and study areas.

**Keywords:** aquatic noise, experimental studies, application

PP-E-18

**Adhesion of the capture threads of cribellate spiders**

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Many spiders build webs to capture their prey. Such capture threads are often covered with droplets of glue. Some spiders, the cribellate spiders, produce dry adhesive capture threads instead. Two large core fibres are surrounded by a capture wool of nanofibres, wherein prey gets entangled. Furthermore, van der Waals-forces and in some species also hygroscopic forces support the adhesiveness of these threads.

Although it is known, that prey somehow gets entangled in the nanofibres of the cribellate thread, most previous experimental setups were performed with artificial surfaces. Thus interactions between the cribellate fibres and the cuticular features of insect prey is not represented in these studies. We therefore re-examined the adhesive mechanism of capture threads of several distantly related cribellate spider species including possible interactions of cribellate nanofibres with cuticular surface features of prey insects. The adhesion area itself was characterized using SEM, TEM and light microscopic techniques. Furthermore, the adhesive force between cribellate capture threads and the cuticle of insects was measured. We found this force much larger than those measured in previous studies for artificial surfaces. When modifying the cuticle of the insects, the adhesion force could be reduced, thus proving the surface of prey has an impact on the adhesion force as well.

**Keywords:** cribellate capture threads, adhesion, cuticle

PP-E-19

**Movement patterns and habitat preferences of red foxes (*Vulpes vulpes*) and raccoons (*Procyon lotor*) in the Havelland, Germany**

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Over recent decades, a general decline in ground-breeding birds has been recorded all over Europe and this trend is mainly a result of agricultural intensification. However, increasing predation pressure might also play an important role in this context. Previous studies show that red fox populations (*Vulpes vulpes*) have increased rapidly since the 1980s. Moreover, there are growing populations of invasive raccoons (*Procyon lotor*) and raccoon dogs (*Nyctereutes procyonoides*) that additionally increase predation pressure. The main objective of the present study is to investigate the impact of different mammalian predators on ground-breeding birds in the southern part of the Havelland, Brandenburg. Thus, home-range data and movement patterns of predators are compared with local occurrences of ground-breeding birds. Since October 2015, we captured four adult foxes and six adult raccoons with box traps and collared them with GPS-tags near the research station Linde. Preliminary results suggest that foxes are more likely to hunt in open grassland than raccoons, which show a clear preference for water bodies. For this reason, raccoons especially seem to have an impact on birds breeding in reed beds. Furthermore, the studied foxes show a preference for human settlements during the night hours, while at daytime, most of them stay close to open areas in the forest. Movement data also suggest that female foxes are more likely to change their territories during mating season, while male foxes show less migratory activity. Data collection and trapping activities are still ongoing in order to increase sample size and to get a more precise picture of seasonal variations. This will help to get a better understanding of the complex interrelations between ground-breeding birds and mammalian carnivores in the study area in order to derive management recommendations for sustainable land use strategies in the future.

**Keywords:** predators, ground breeding birds, movement patterns

PP-E-20

**Data on the ecology of Nigerian-Cameroonian Chimpanzee (*Pan troglodytes ellioti*) and Cross-River Gorillas (*Gorilla gorilla diehli*)**

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In the Lebialem Highlands of West Cameroon there is a population of Nigeria-Cameroon chimpanzees (*Pan troglodytes ellioti*) and Cross-River Gorillas (*Gorilla gorilla diehli*). The present study was conducted in the Lebialem-Mone Forest (size: 80 km<sup>2</sup>), the Tofala Reserve, in the southwest of Cameroon. The "Tofala" population of Cross River Gorillas we studied was discovered by an expedition of ornithologists in 2004. It is very special because it marks the most southeastern occurrence of Cross River Gorillas. Out of a total of eleven subpopulations, the Tofala population is the only one about which no scientific data has been available. The anthropogenic pressure exerted upon the chimpanzees and the gorillas living in the examined area is very high because there are ten villages adjacent to the area.

Our findings show, for example, that both species living in the examined area prefer to build the nests they sleep in on steep hillsides instead of building them, as they usually do otherwise, close to food resources. Cross River Gorillas generally looked for herbivorous food on farms that had been illegally built in the forest. By contrast, chimpanzees mainly had a frugivorous diet. Only because of their different eating habits is the sympatric occurrence of these two primate species possible in such a small range.

**Keywords:** Ecology, Behaviour, Apes

## Evolutionary Biology – invited talks

### Determinants of male reproductive success – why does it need so many proteins?

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In internally fertilizing organisms males often transfer a large number of proteins together with sperm in their ejaculates. These seminal fluid proteins are produced in a specialized organ in the male reproductive tract and fulfill functions key to male reproductive success. Surprisingly some of these proteins are known to show high rates of evolutionary change. It is hypothesized that sexually antagonistic coevolution between the sexes drives these high rates of change. Sexually antagonistic coevolution can arise when opposing selection pressures act on males versus females. By using the power provided by genetic manipulations we can separate the fitness effects of ejaculatory protein transfer respective receipt for males and females. I here present data for one of those proteins – the sex peptide, which is hypothesized to mediate sexual conflict between the sexes and for which we have a good understanding of the economics of mating for the two sexes. In our past work we showed that the ecological setting can alter selection dynamics between the sexes and can turn conflict into cooperation, while our current work investigates age-dependent effects for males and females separately. Together this work gives insight into the conditions under which sexually antagonistic coevolution might be operating and the fitness outcomes of male-female interactions under those conditions.

### Evolutionary genetics and genomics of the adaptive immune system

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The adaptive immune system in vertebrates has evolved to fight novel and coevolving parasites and pathogens. However, the most optimal immune response requires a delicate balance of maximizing recognition and inhibition of invading pathogens while minimizing damage to own tissue by the activated immune machinery. The major histocompatibility complex (MHC) plays a key role in this process. MHC molecules present non-self as well as self antigenic peptides to immune effector cells and can thus trigger either pathogen resistance or autoimmunity. This balance is reflected at the genetic level; while MHC genes exhibit excessive polymorphism at the population level, each individual carries only a small subset of this diversity. Here I first discuss the mechanisms of MHC-based pathogen resistance, with a special focus on functional divergence among MHC variants, and present empirical support for these mechanisms from various vertebrates, ranging from fish to humans. I then show human data from several common autoimmune diseases that indicate contrasting selection through elevated autoimmune disease risk for more diverse MHC genotypes. This supports theoretical models of antagonistic selective pressures and reveals a possible mechanism selecting for intermediate genetic diversity in the MHC. Eventually, I discuss evidence suggesting that the optimal level of individual MHC diversity may be dynamic, responding to changes in the relative strength of pathogen-mediated selection in time and space. A better understanding of these dynamics is crucial in the face of climatic changes, likely affecting pathogen communities, but also in the context of the increasing prevalence of many autoimmune diseases in human populations.

## Evolutionary Biology – oral presentations

### OP-EB-01

#### **Experimental evolution of immune priming, a form of immune memory in the red flour beetle *Tribolium castaneum***

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**Introduction:** Insect immune systems show forms of immune memory, denoted as immune priming that can be specific for types of pathogen.

**Objectives:** We addressed the question whether the specificity of the immune system of the red flour beetle *Tribolium castaneum* evolves when confronted with different re-infection scenarios.

**Methods:** We experimentally selected *T. castaneum* for its ability to survive a bacterial infection after matching vs. mismatching priming-challenge combinations. Selection regimes consisted of immune priming (heat-killed bacteria) followed by septic challenge (alive bacteria). The bacterial species an individual was confronted with for priming and challenge were either similar or different, thus creating situations where specific or unspecific (i.e. broad spectrum) immunity would be beneficial. We also added a regime where the same bacterial species was used across generations, thus selecting for genetic specificity in resistance to the respective bacteria, rather than phenotypically plastic immunity.

**Results:** We found that after 14 generations, the selection lines differed in their resistance after priming, with a trend for higher resistance in the lines selected for genetic specificity and specific immunity. However, specificity of priming was not generally higher in the lines selected for specific immunity. Responses to selection differed depending on the bacterial species that were used for challenge.

**Conclusion:** We conclude that in this host-pathogen system, short-term resistance evolution seems more strongly affected by genetically hard-wired rather than acquired defence components. Furthermore, priming ability and its evolvability seem to depend on the bacterial species encountered.

**Keywords:** Experimental Evolution, Insect Immune Specificity, *Tribolium*

### OP-EB-02

#### **Effects of environmental temperature on interactions of the cestode *Schistocephalus solidus* with its specific host, the three-spined stickleback (*Gasterosteus aculeatus*)**

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**Introduction:** It is widely accepted that environmental variation influences host parasite interactions and their coevolution, but experimental evidence to this end is scarce. We hypothesised that environmental temperature is a strong modulator of host parasite interactions in ectothermic systems. We suspect that rising temperatures, as predicted by climate change models, will accelerate parasite reproduction rates.

**Objectives:** We wanted to test, (1) if host parasite pairs reproduced from populations along a North-South climate gradient (Iceland, Norway, Germany, Spain) differ in their susceptibility to temperature variation and (2) if rising temperature benefits parasite development.

**Materials & methods:** Parental stickleback - *S. solidus* pairs, were collected from a warm and a cold site of lake Myvatn on Iceland, a lake in Western Norway, a brook in central Germany and a lake in Northern Spain. Laboratory F1 offspring was used for infection experiments in sympatric and allopatric combinations and exposed to temperatures ranging from 9-24°C.

**Results:** Distinct patterns of local temperature adaptations were not detected. However, fitness correlates of the parasites were highest at intermediate to high temperature. Immune parameters and fitness correlates of the host were highest at relatively low temperature and reduced at intermediate to high temperature.

**Conclusion:** Sticklebacks and their *S. solidus* parasites have different temperature optima. At low to intermediate temperature sticklebacks are able to restrict parasite growth and maintain relatively high fitness, whereas the parasite is able to exploit its stickleback host more thoroughly at rising temperature and thereby likely accelerates its reproductive rates.

**Keywords:** host-parasite-coevolution, temperature, stickleback

OP-EB-03

### **Patterns of MHC-dependent mate selection in humans and non-human primates: a meta-analysis**

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Genes of the major histocompatibility complex (MHC) in vertebrates are integral for effective adaptive immune response and are associated with sexual selection. Evidence from a range of vertebrates supports MHC-based preference for diverse and dissimilar mating partners, but evidence from human mate choice studies has been disparate and controversial. Wide discrepancies in results among human populations may be real or artifact due to the specific sampling and methodology applied to humans. To better understand what processes may affect MHC-mediated mate choice in humans and non-human primates we performed phylogenetically controlled meta-analyses using 58 effect sizes from 30 studies across 7 primate species. Primates showed a general trend favoring more MHC-diverse mates, which was statistically significant for humans. In contrast, there was no tendency for MHC-dissimilar mate choice, and for humans, we observed effect sizes selecting both MHC-dissimilar and MHC-similar mates. Considering the magnitude of effect size separately from direction showed that MHC similar and dissimilar preferences were significantly stronger in relatively isolated and homogeneous human populations, consistent with the MHC-optimality hypothesis. We also found that couples, as opposed to males and females tested separately, primarily showed preferences for MHC similar mates. This might reflect that human socio-cultural assortative mating biases that would affect the entire genome may be responsible for some patterns of MHC-associated mate choice. Overall, our results demonstrate that preference for more MHC diverse mates is significant for humans and likely conserved across primates, and suggest that MHC-based mate choice may be stronger for direct than indirect benefits.

**Keywords:** inbreeding avoidance, sexual selection, mating preference

OP-EB-04

### **When the audience is fooled - costs of using public information**

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Animals use public information in different contexts of life by observing individuals during sexual interactions to assess the quality of others as prospective mates. However, when observing individuals are recognized by observed individuals, the latter individuals often change their mate-choice decision. We therefore asked, whether the audience will copy the pretended mate choice in Atlantic mollies (*Poecilia mexicana*) in the lab. We found that males and females changed mate choice decision when a same sex audience was present. The audience males and female, which experienced this pretended mate choice copied that "wrong" mate choice. The audience was fooled and might make wrong decisions. Our controls could not support alternative explanations to copying this mate choice. Thus, the audience effect is an adaptive strategy to lead a competitor away from the preferred mate in both sexes. It also bears cost of using public information in mate choice for the audience.

**Keywords:** public information, audience effect, mate choice copying

OP-EB-05

**Impacts of mate quality and subadult experience on male mate choice in a sexually cannibalistic spider**

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Mating decisions often underlie decision rules that are flexibly adjusted to prevailing conditions. In mating systems in which males have few mating chances, mate choice decisions are of considerable relevance for fitness. In *Argiope bruennichi*, the mating system is marked by male sacrifice and by mutilation of the paired genital organs. Thus, mating rates are strongly limited, and males can either invest in one (monogyny) or maximally two females (bigyny). We predicted that males use mating tactics depending on female quality and social cues received early during the mating season. Additionally, we expected to find differences in populations from (N)orthern and (S)outhern Europe that vary in mate quality and seasonality. We used two experimental set-ups to test for differences in the frequency of mating tactics. First, we used experimental choice arenas in which males could choose between three N or S-females of different body sizes. Second, subadult males did either receive cues in the form of female silk or not. In no-choice mating tests, adult males had the chance to either monopolize a female or to leave her after one copulation (bigyny). In both experiments, frequencies of the two mating tactics were the same. While in both populations social cues had no effect on mating tactics, we found that in N-males, the probability of monogyny increased with female size independent of the female's geographical origin. This is adaptive because female fecundity increases with female size. S-males used the monogynous tactic independent of female size why we assume that the reproductive success of S-males is affected by other factors. Moreover, we assume that in both populations, social cues are irrelevant before mate search.

**Keywords:** male mate choice, phenotypic plasticity, female quality

OP-EB-06

**Sexual conflict and population divergence in *Drosophila melanogaster***

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Sexual conflict describes the genetic conflict that arises between males and female when their reproductive interests are not aligned. This conflict has the potential to generate sexually antagonistic coevolution between the sexes which can cause rapid evolutionary changes. As the traits involved in sexual conflict directly impact reproductive success, it has been hypothesised that sexual conflict and the resulting sexually antagonistic coevolution may act as important drivers for divergence between allopatric populations that could ultimately result in reproductive isolation. *Drosophila melanogaster* males produce more than 100 seminal fluid proteins that are transferred together with the sperm to the female at mating. As these proteins are important mediators of male reproductive success and manipulate female behaviour and physiology, they have been proposed to mediate sexual conflict in this species. In an experimental evolution experiment using *D. melanogaster* I established replicated populations experiencing different levels of sexual conflict through enforcing monogamy or allowing for promiscuity to test the hypothesis that sexual conflict drives divergence between populations. After more than 50 generations of implementing this selection regime I started testing for phenotypes associated with male seminal fluid proteins including population fitness, sperm competition and cost of mating. Here, I present these results and discuss their implications for the hypothesis that sexual conflict is a driver of population divergence.

**Keywords:** sexual conflict, experimental evolution, *Drosophila melanogaster*

OP-EB-07

**A new perspective on the twofold cost of sex - testing the basic assumption of equal reproductive investment**

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Sex is the 'queen of problems in evolutionary biology' (G. Bell), and it seems hard to explain why not all species reproduce asexually (=parthenogenetically). Asexuality has a twofold numerical advantage over sex because all offspring are females, while in sexual populations half of the offspring are males. Traditionally, the number of offspring is thought to be identical for both reproductive modes: 'The number of eggs laid by a female will not normally depend on whether she is parthenogenetic or not ...' (J. Maynard Smith). Hence, the numerical twofold cost of sex becomes a rather long-term effect of population dynamics. Numerous counteracting short-term advantages of sex have been discussed, mostly focusing on DNA repair, parasite resistance or resource allocation (e.g., red queen, tangled bank).

Oribatid mites are soil-dwelling micro-arthropods with an exceptionally high proportion of asexual species (many of them being ancient), and both reproductive modes coexist in stable community assemblages and abundances. We counted the number of eggs in more than 6.000 females from 50 oribatid mite species (including 15 asexuals), collected from different geographic regions, microhabitats and seasons. While the relative individual egg size did not differ between reproductive modes, sexuals produced double the number of eggs.

Hence, for oribatid mites, the twofold cost of sex is covered by an immediate twofold investment in the production of offspring, thereby moving the numerical difference in population growth from an exponential to a linear dynamic. These findings support the importance of sexual reproduction for resource allocation, underlining the significance of the tangled bank and related models.

**Keywords:** Sex, Parthenogenesis, Reproduction

OP-EB-08

**The consequences of predator-induced phenotypic plasticity during intrasexual selection**

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Phenotypic plasticity allows individuals to adjust their phenotype in order to optimally respond to the environment, for example, to predation. However, plastic modifications are supposed to be costly and little is known about the long-term consequences of a plastic response. Intrasexual competition has been suggested to be a selective factor favoring a phenotype different from the optimal antipredator phenotype. Consequently, costs of predator-induced plasticity are likely to arise during intrasexual competition but this topic has been neglected thus far. Here, we study this question in *Pelvicachromis taeniatus*, a West African river cichlid fish with mutual mate choice and strong intrasexual competition in both sexes. Predator presence was simulated by exposing fish to conspecific alarm cues. In aquatic animals, chemical alarm cues are passively released by injured individuals during a predation event and thus reliably signal predation risk to conspecifics. In *P. taeniatus*, the presence of conspecific alarm cues is known to induce adaptive antipredator plasticity. We applied a split-clutch rearing design and exposed fish continuously since fry stage to either conspecific alarm cues or control treatments for a time period of 3 years. Afterwards, in both sexes we assessed the competitive ability of individuals. For this purpose, we evaluated the course and the outcome of staged contests between size-matched siblings of the same sex that originate from different treatments. Our results may allow inferences about how predator-induced plasticity may lead to altered patterns of intrasexual selection.

**Keywords:** phenotypic plasticity, intrasexual selection, predation

**OP-EB-09**

**Partitioning fitness consequences of developmental conditions over age: a method and case study with sibling rank in a long-lived seabird**

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The conditions under which individuals are reared vary because of parental decisions and quality as well as differences in the natal environment. When conditions are sub-optimal, individuals are predicted to trade their long-term somatic maintenance for their immediate survival (i.e. to allow for disposable soma). Long-term fitness consequences of various natal conditions have therefore received considerable empirical attention, but results are equivocal. We suggest that the relative strength of selection in early and late life may affect the expression of individual heterogeneity over life. We therefore develop a framework to partition fitness consequences of developmental conditions over age, and present a case study in which we investigate how sibling rank, a trait predictive of developmental conditions among siblings, translates to individual heterogeneity in life-history trajectories. Making use of a 20-year longitudinal dataset on common terns *Sterna hirundo*, we find that 74% of fitness costs of low rank occur during development, while late-life costs are small. We suggest that while natural selection may favour deferred fitness costs of poor developmental conditions in individual offspring, it can be counteracted by kin selection favouring rapid reduction in offspring numbers when resources are limiting.

**Keywords:** disposable soma, individual heterogeneity, life history theory

**OP-EB-10**

**Evolutionary Biodemography of Hydra - Life in the absence of senescence**

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To understand the mechanisms that favor the evolution of extended lifespan and the biological causes of aging, the study of organisms that do not show senescence might be beneficial. Hydra has a particular life-history that may allow us to gain a better fundamental understanding of the process of senescence. We aim to study this in more detail:

First we draw on comprehensive large-scale experiments with a total of 3.9 million days of observations (2.256 individuals over an 8-year period) to revisit the notion of non-senescence in mortality and fertility schedules. Our data show that hydra does display extremely low and constant rates of mortality and a constant rate of fertility with increasing age.

A second set of experiments investigated how trade-offs between reproduction and maintenance are modified under environmental stresses. The results of the study show that asexual reproduction and maintenance of Hydra depends on fluctuation in environmental conditions and can increase simultaneously in both components of fitness, asexual reproduction and maintenance. We propose that this trade-off effect is related to a hormetic stress response, resulting in an increase in organism efficiency.

Third, we conduct a series of experiments aimed to identify ways in which Hydra prevent damage and mutation accumulation to achieve non-senescence. Our first results suggest that there might exist a mechanism for the evasion of aging in Hydra that is based on the asymmetric segregation of damaged cells between parental and offspring generations.

**Keywords:** life history, aging, evolution

OP-EB-11

**Intracolony genotypic diversity in corals: a potential mechanism for climate change adaptation?**

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The current El Niño event has once again proven that climate change is a severe and imminent threat to marine sessile organisms. In corals, recently, a potential mechanism to compensate these environmental challenges has been described: intracolony genotypic diversity – the presence of more than one genotype in a coral colony. Genotypic variability within a coral colony could provide the colony with enhanced levels of allelic variation and thereby improve the immediate reaction flexibility as well as increase the adaptive potential by transferring genetic variability into the next generation. So far, however, intracolony genotypic diversity was described mainly on the basis of neutral genetic markers (microsatellites) while its adaptive potential remained unclear. To understand if intracolony genetic diversity might also increase a coral colony's phenotypic (protein) diversity, we used a genomic (ddRAD) approach to identify and map inter- and intra-colonially variable and potentially translated gene regions. 42 samples of 14 different *Acropora hyacinthus* colonies were used for the analyses. We found a large number of highly variable loci and colony specific SNPs as well as allelic diversity within the same colony could be detected. Our results indicate that genomic variability in corals is much larger than expected and might influence a colonies' adaptive potential.

**Keywords:** mosaicism, ddRAD, *Acropora hyacinthus*

OP-EB-12

**Understanding the mechanisms underlying thermal acclimation in a butterfly: an RNAseq approach**

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Phenotypic plasticity is a pervasive property of all organisms and considered to be of key importance for dealing with environmental variation. Plastic responses to temperature, which is one of the most important ecological factors, have received much attention over recent decades. A recurrent pattern of temperature-induced adaptive plasticity includes increased heat tolerance after exposure to warmer temperatures and *vice versa*. However, the mechanisms underlying these plastic responses and phenotypic plasticity in general are hitherto largely unknown. Using a RNAseq approach, we here show that several antioxidant markers (e.g. *peroxidase* and *cytochrome P450*) were up-regulated at a higher compared with a lower temperature in the tropical butterfly *Bicyclus anynana*, which may play an important role in the plastic responses subsequently providing increased heat tolerance. Furthermore, several metabolic pathways were up-regulated at the higher temperature, likely reflecting increased metabolic rates. Although the important role of antioxidant defence mechanisms in alleviating detrimental effects of oxidative stress is firmly established, we believe that its potentially important role in mediating heat tolerance and survival under stress has been underestimated thus far and deserves more attention. We additionally report sexual differences in expression patterns, providing some evidence for a trade-off between reproduction and general maintenance as some genes involved in the innate immune response were down-regulated in females.

**Keywords:** transcriptome, gene expression, heat tolerance

### OP-EB-13

#### Genetic modularity of mate recognition behaviours and their warning pattern cues in mimetic butterflies

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(1) The genetic architecture of traits that contribute to reproductive isolation can profoundly influence speciation in the face of gene flow. *Heliconius* butterflies are well known for brightly coloured mimetic warning patterns. Because wing colour patterns are also used as mating cues, mimetic shifts can cause both pre- and post-mating isolation. (2) However, shifts in colour pattern cannot drive reproductive isolation alone: they must be accompanied by corresponding mate preferences. (3) We performed a genome-wide QTL analysis of mate recognition behaviours in *Heliconius* butterflies. (4) Our results suggest that at least three QTL of major effect influence mating decisions that contribute to reproductive isolation between the sympatric species *Heliconius cydno* and *H. melpomene*. Of these, one appears to influence attraction to the white wing patterns of *H. cydno*, whilst the other two are associated with attraction to the red patterns of *H. melpomene*. (5) These new results are important for three reasons: First, they represent the only behavioural study in *Heliconius* to consider effects across the entire genome. Second, it is striking that just three loci explain >50% of the difference between the parental species. Finally, because different loci influence the degree of attraction to white females, and others the attraction to red females, these results suggest a modularity underlying visual mate recognition, paralleled by that underlying the corresponding wing pattern cues.

**Keywords:** Speciation, Mate choice, Genetics

### OP-EB-14

#### Birth of a new gene: the problem of self-tolerance versus autoimmune reaction

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In vertebrates, the adaptive Immune system has an extraordinary potential for generating receptors that sense and neutralize any foreign antigens entering the body. Efficient recognition of the foreign antigens through self and non-self separation depends on the regulation in Thymus tissue where T cells are selected positively and negatively. Any failure in the regulation of sense and non-sense separation in Thymus results in autoimmunity.

*De novo* evolved genes usually bring novel expression pattern with newly evolved genetic content to specific tissues and therefore, new protein products within certain cell types. These novel protein products or peptides, which are expressed within the cells and presented by the major histocompatibility complex on the cell surface, have to be introduced to the immune system to avoid autoimmune reaction. Otherwise any tissue having a newly emerged peptide, which is represented on their cell surface, will be considered as foreign antigen and tissue/cells that are having such peptide will be attacked and destroyed by the immune system. Therefore, we propose that *de novo* evolved protein-coding genes should also be expressed within the thymus tissues to generate self-tolerance.

Based on the analysis from Thymus RNA seq data along with 9 other tissues within the phylogeny of *Mus* genus, we provide evidence that Thymus plays a very critical role in the evolution of metazoan by controlling birth of a new gene in a specific tissue. Our results indicate a primary role for the Thymus controlling expression of all protein coding genes within both annotated Genic and Non Genic regions. The mechanisms may also be relevant for hybrid incompatibility effects between species and sub-species and thus also of relevance for speciation processes.

**Keywords:** De Novo Gene Evolution, Thymus in Evolution, Hybrid incompatibility

OP-EB-15

**How do structural changes in genome lead to evolution of brain and novel behavior?**

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Throughout evolutionary history, organisms have evolved a variety of sophisticated novel traits for survival and reproduction. One of these novel traits that recently have been known is house mouse mate choice preference that strongly influenced according to their father origin; however, the molecular mechanism of this complex trait remains unknown so far. Analysis brain transcriptome sequencing data of ten different mouse populations revealed that an imprinted cluster in chromosome 7 and also Peg13 on chromosome 15 which are orthologous to the region involved in the Angelman /Prader-Willi syndromes (PWS) in humans has been highly differentiated between mouse populations. These regions have important role in mammal cognition and here for the first time we showed how Structural variation in genome could lead to a novel trait during evolution of mammals. Data from transcriptome assembly showed different number of paternal new genes in every population in PWS region in chr7 which only express in brain and all of them were classified as long non coding RNA. Interestingly we also detected two repeated clusters in PWS region in chr7 which compared to other mammals is two-five times more expanded in mouse. Our small RNA sequencing data revealed that these repeated clusters are host for two paternal snoRNA families which highly duplicated in mouse and interestingly rate of snoRNA duplication for both families is different from one population to another. The other interesting point from small RNA analysis is that although in human these snoRNA have expression in different tissues, in mouse their expression has been limited in brain. As conclusion, we assume that some specific paternal structural variations in PWS region in mouse could be responsible for their paternal mate choice preference and subsequently their fast evolution.

**Keywords:** genome, brain, behavior

OP-EB-16

**Assembly of a novel gene network in a conserved developmental field yields an evolutionary novelty**

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How novel morphological traits arise in organisms has long been a major question in evolutionary biology. Most of the studies about the evolutionary novelty are based on candidate genes known from *Drosophila melanogaster*, leading to a bias against towards conserved genes. Gin-traps are physical defensive organs found at the lateral margin of the abdomen of pupae among many Coleoptera and some Lepidoptera species.

Gin-traps are considered as an evolutionary novelty for the following reasons. Firstly, they are only present in some holometabolous insect taxa. Secondly, they are only present in the pupal stage which emerged during the evolution of holometabolous insects. Therefore, gin traps are an excellent study case in order to answer the question on how evolutionary novelties arise.

Gin-traps were reported to be wing serial homolog because they required the function of two wing selector genes, *vestigial* and *scalloped*. We wanted to know to which extent they share the common gene regulatory network. Therefore, we used the candidate approach to detect the involvement of *Tribolium castaneum* wing genes in the gin-trap development. Among the 22 wing genes, 10 were involved in both wing and gin-trap formation while 7 were wing-specific.

In order to identify novel genes integrated to the network, we selected all the gin-trap phenotypes from the iBeetle-Base which contains phenotypic data of 4480 genes knocked down at larval stages. Three signaling pathways, EGFR, Notch and Bursicon, were involved in the gin-trap development. We also found several gin-trap specific genes, *empty spiracles*, *highwire*, *Abd-A* and *caspar*.

Taken together we found that the evolution of gin-traps was based on the re-deployment of a large part of the wing patterning network at the same segmental position. However, some genes were lost from the network while a similar number of other factors were newly integrated into the network.

**Keywords:** Evolutionary novelty, RNAi, gin-trap

## Evolutionary Biology – posters

### PP-EB-01

#### Accumulation of structural mutations in an invasive fish of hybrid origin

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Mixing of genetic material from previously separated gene pools may cause evolutionary change and hybrid speciation. This has been mostly explained through interactions of existing genetic traits. In contrast, evolutionary novelty through new mutations after admixture is less explored. Herein, we tested the hypothesis that structural mutations accumulate in invasive *Cottus*, an evolutionary young fish of hybrid origin, relative to both parental species *Cottus rhenanus* and *Cottus perifretum*. Among 10,979 genes screened for CNVs using comparative hybridization arrays, 25 genes showed significant changes in copy number in a natural population of invasive *Cottus*. Three genes with the most pronounced increase in copy number were previously found to be upregulated in invasive *Cottus*, suggesting potentially adaptive gene dosage effects. Transposable element copy number was estimated by mapping whole-genome sequencing reads against a de novo genome assembly of transposable elements. We found a significant copy number increase in 20.7% of all putative transposable elements in invasive *Cottus*, compared to a very rare decrease (0.01%) of TE copies relative to the parent species. The possibility of rapid evolution of de novo copy number variants was tested in laboratory crosses between the parental species. F2 individuals of two families (*C. rhenanus* x *C. perifretum*) were screened for de novo copy number changes of three candidate genes and two transposons using digital droplet PCR. Although our results do not support high rates new structural mutations they nonetheless show that structural mutations accumulate after admixture and that copy number increases of protein coding genes can manifest phenotypically in an evolutionary young hybrid species. This supports the idea that structural variants contribute to rapid evolution of admixed lineages.

**Keywords:** structural mutations, hybrid speciation, copy number variation

### PP-EB-02

#### Using *Drosophila* as a model to better understand the role of microbes in metazoan evolution

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All metazoans are associated with microbes. Pathogenic microbes exert strong selection pressures on their hosts. On the other hand, microbes can have beneficial effects and participate in host adaptive processes. Therefore, microbes play a prominent role in metazoan evolution. Nonetheless, many studies that aim at understanding the evolution of an organism ignore its associated microbial communities. Here, we leverage the powerful *Drosophila melanogaster* model system to better understand the role of microbes in the evolution of metazoans. A first step towards understanding the role microbes play in the evolution of *Drosophila* is a comprehensive assessment of the natural microbial communities associated with *Drosophila*. We will present a survey of these communities based on metagenomic shot gun sequencing and 16S rRNA gene sequencing of more than 50 samples from over 30 locations spanning Europe. We will furthermore present experimental data on the fitness effects of a bacterial family that is ubiquitously associated with *D. melanogaster* in nature, acetic acid bacteria, and relate differences in fitness effect to genomic differences between more than 10 fully sequenced bacterial strains from this family.

**Keywords:** metagenomics, microbial communities, *Drosophila*

PP-EB-03

**Variations of a theme: sex determination in East African cichlid fishes**

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Establishing two sexes within the same species and hence from one genome, is a complex developmental process. It came therefore as a surprise that the mechanisms and genes driving this process show little conservation across taxa, sometimes being different even between sister species. In the animal kingdom, the diversity and turnover in primary sex-determining signals, including genetic and environmental factors, is particularly high in teleost fish. The exceptionally diverse assemblages of cichlid fishes in the East African Great Lakes represent perhaps the most astonishing cases of ongoing adaptive radiations with a great variety in morphology, ecology and behavior. How sex is determined and if different sex-determining mechanisms contribute to speciation is still unknown for almost all of the over 1,500 cichlid species of the Great Lakes. Here, we present first data on a particular species of Lake Tanganyika, *Astatotilapia burtoni*, a member of the most species-rich cichlid lineage, the so-called haplochromines. We identify different sex chromosomes in different populations of *A. burtoni*. In our laboratory population, we show that a fused chromosome (LG5) is the sex chromosome. This chromosome has also independently been recruited as a sex chromosome in cichlids from Lakes Malawi and Victoria. We investigate this chromosome for its sequence evolution and gene content in more detail.

**Keywords:** sex determination, cichlid fish, sex chromosome

PP-EB-04

**Pre- and postmating isolation in the parasitoid wasp species (*Lariophagus distinguendus* Förster) (Hymenoptera: Pteromalidae)**

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To understand the process of speciation, it is essential to understand the evolution and the order of appearance of pre- and postmating isolation barriers, which prevent gene flow between populations. The aim of this study is to identify barriers, which occur early during separation as well as those barriers, which are associated with the completion of the speciation process in two species as well as between different populations hidden in the parasitic wasp species *Lariophagus distinguendus* Förster (Chalcidoidea: Pteromalidae).

We studied sexual isolation, occurrence and number of female F<sub>1</sub> and F<sub>3</sub> offspring, and the number of F<sub>2</sub>-male offspring and calculated Isolation indices of the different barriers.

The study revealed a strong premating barrier by sexual isolation and strong postmating, postzygotic barriers, mostly by sterility of F<sub>2</sub> hybrid males between the two species. Between populations within each species, postmating, postzygotic barriers affecting hybrid males were found between all conspecific populations. Premating sexual isolation within the same species occurred only between two populations of one species, which were also characterized by the highest postzygotic isolation.

We propose a hypothetical scenario of speciation in *L. distinguendus*, starting with postzygotic isolation due to reduced viability and fertility of hybrid males and followed by sexual isolation due to female mate choice. Isolating barriers completing the speciation process are a reduction in the offspring number from hybrid couples, a reduced fertility of F<sub>1</sub> females, and separation into different ecological niches.

**Keywords:** Speciation, Isolating barriers, Parasitic wasps

PP-EB-05

**The genetics of migration - insights from Scandinavian willow warblers**

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Migratory birds possess an inherent time schedule and at least an inherited initial migratory direction to cope with the challenge of migration. But the exact identity of genes controlling migration remains largely unknown, making it difficult to obtain an accurate understanding of this fascinating behaviour on the molecular level. Our knowledge about the genetics of migration today is still mainly based on crossbreeding and displacement experiments, and even though a heritable basis of migratory traits is well accepted, virtually nothing is known about the genes shaping these traits. Using genomics approaches we are currently evolving the field of bird migration from phenotypic to molecular approaches. I will focus on the willow warbler, a small migratory songbird that form a migratory divide, i.e. a narrow area where neighbouring populations exhibit strikingly different migratory strategies, in central Scandinavia. We have capitalised on this variation in migratory strategy to narrow in on the genes that regulate migratory traits. Specifically, we have employed state-of-the-art next generation sequencing techniques to assemble a draft reference genome, resequenced individuals with different migratory strategies, developed a SNP chip to genotype >1000 individuals throughout its breeding range, and identify genomic differences between populations with different migratory strategies. We also use gene ontology analyses and evidence of directional selection to identify new genes that may be involved in migratory strategy. Our results relate not only to which genes control migratory traits but also how this might translate into differences in behaviour, with important implications for understanding the ecology and evolution of seasonal migration.

**Keywords:** bird migration, orientation, behavioural adaptation

PP-EB-06

**Fitness consequences of polymorphic inversions in the zebra finch genome**

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**Introduction & Objectives:** Inversion polymorphisms constitute an evolutionary puzzle: they should increase embryo mortality in heterokaryotypic individuals, but still they are widespread in some taxa. Some insect species have evolved mechanisms to reduce the cost of embryo mortality, but humans have not. In birds, a detailed analysis is missing although intraspecific inversion polymorphisms are regarded as common. In Australian zebra finches (*Taeniopygia guttata*), two polymorphic inversions are known cytogenetically and we set out to detect these two and additional inversions using genomic tools and study their effects on embryo mortality and other fitness and morphological traits.

**Methods & Results:** Using whole-genome SNP data, we screened 939 wild zebra finches for polymorphic inversions and describe four large (12-63 Mb) intraspecific inversion polymorphisms with an allele frequency close to 50%. Using additional data from more than 5,000 birds and almost 10,000 eggs from wild and captive zebra finch populations, we show that only the largest inversions increase embryo mortality in heterokaryotypic males, with surprisingly small effect sizes. We test for a heterozygote advantage on other fitness components, but find no evidence for heterosis for any of the inversions. Yet, we find strong additive effects on several morphological traits.

**Conclusions:** The mechanism that has carried the derived inversion-haplotypes to such high allele frequencies remains elusive. It appears that selection has effectively minimized the costs associated with inversions in zebra finches. The highly skewed distribution of recombination events towards the chromosome ends in zebra finches and other Estrildid species may function to minimize crossovers in the inverted regions.

**Keywords:** structural variant, overdominance, miscarriage

PP-EB-07

**Tracing signatures of adaptive evolution of *de novo* genes in natural populations of the house mouse (*Mus musculus*)**

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The house mouse (*Mus musculus*) is not only an excellent model for biomedical research, but also for evolutionary studies, with many sub-species and species, as well as recent population expansions across the world. We have established genomic resources for such wild type populations of *Mus musculus* and its close relative *Mus spretus* which includes whole-genome sequence variation and transcriptome data for ten tissues (Harr et al. 2016). Structural variation like large insertions and deletions as well as copy number variations contribute to the evolutionary divergence of these populations. Here we are especially interested to disentangle the linkage of signals for adaptive evolution and *de novo* gene emergence among wild mouse populations using the “common genome”, so to say the shared chromosomal regions found in all analyzed taxa. Deep analysis of transcriptome data has already proven that any part of the non-coding genome can potentially become subject to evolutionary functionalization via *de novo* gene evolution (Neme and Tautz 2016). Our results will contribute to detect possible selection effects in the context of the emergence of new genes, comparing so far un-annotated transcribed regions as compared to known genomic features like protein coding genes and non-coding RNAs. This will provide deeper insights into the processes of *de novo* evolution of genes, as well as generate candidate genes for further functional studies.

Neme R, Tautz D (2016). Fast turnover of genome transcription across evolutionary time exposes entire non-coding DNA to *de novo* gene emergence. *eLife* 5: e09977.

Harr B et al. (2016). Genomic resources for wild populations of the house mouse, *Mus musculus*, and its close relative *Mus spretus*. *Scientific Data* (in revision)

**Keywords:** *Mus musculus*, *de novo* genes, population genetics

PP-EB-08

**Analysis of the evolution of Polyneoptera (Insecta) by using precursor sequences of neuropeptides**

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Neuropeptides are key players in information transfer and act as important regulators of development, growth, metabolism, and reproduction within multi-cellular animal organisms (Metazoa). These short protein-like substances show a high degree of structural variability and are recognized as the most diverse group of messenger molecules. We use transcriptome sequences from the 1KITE (1K Insect Transcriptome Evolution) project to search for neuropeptide coding sequences in more than 100 species of polyneopteran insects.

Polyneoptera is a lineage within Pterygota that rapidly evolved in the Carboniferous and radiated into a variety of morphologically and biologically diverse orders (e.g. locusts, cockroaches, stick insects). Due to their fast succession of branching events, the inner phylogeny of this group remains partially cryptic despite recent molecular and morphological attempts to solve internal relationships. We examined transcriptome assemblies for neuropeptide precursor sequences; resulting alignments served as basis for phylogenetic analyses. In this context, the evolution of FXPRLamides (pyrokinins/PBANs, CAPA) was studied in more detail. Genes coding for these neuropeptides are characterized by a number of evolutionary changes occurring with the origin of Hexapoda; including new receptor ligands, internal gene duplications and gene duplications with differentiation of cellular expression patterns in the nervous system of hexapods. Here, we give a first overview regarding the evolution of these precursors; these data will be used for a complementary approach to resolve internal phylogenetic relationships within polyneopteran insects.

**Keywords:** Neuropeptides, Polyneoptera, transcriptome analysis

**PP-EB-09**

**An unexpected diversity of myoglobins in the lungfish**

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The lungfish is of high evolutionary interest because it is considered as the closest living relative of terrestrial vertebrates. Recent studies on the transcriptomes suggest that the African lungfish *Protopterus annectens* has at least seven distinct myoglobin genes while other vertebrates usually have only a single myoglobin gene. Myoglobin is a respiratory protein and one of the best-studied proteins in biological science. It is well known for its function in oxygen (O<sub>2</sub>) transport and storage. Given its role in O<sub>2</sub> supply and the diversity of myoglobins in *Protopterus annectens*, it provides a perfect starting point to study the evolution of respiratory proteins in the transition from water to land and is an ideal model to study gene subfunctionalization and neofunctionalization. We found that the myoglobins are differently expressed in the various tissues, suggesting distinct functions. We further identified at least six myoglobin genes in the spotted African lungfish *Protopterus dolloi*. This shows that lungfish myoglobins diverged early in evolution. In addition, they revealed enhanced evolutionary rates, supporting the adaptive evolution of the genes.

**Keywords:** myoglobin, lungfish, evolution

**PP-EB-10**

**Check-up for virtual lovers to study mate-choice in sailfin mollies, *Poecilia latipinna***

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The use of computer animation is a state of the art method for the presentation of artificial stimuli to study animal behavior, especially in the field of visual perception and communication. The use of computer animated stimuli has numerous advantages compared to the use of live stimuli. Computer animated stimuli are highly variable in both morphology and behavior, leaving all other parameters constant. Moreover, the use of computer animation bears the potential of 'replacing' and 'reducing' test animals as well as 'refining' experimental setups which is in line with the 3Rs. The validation of this new technique, however, is often missing.

To test the relevance of quality and quantity of visual information in mate choice, we take advantage of computer animated fish. We designed custom made simulation software for freely steerable animated 3D sailfin mollies (*Poecilia latipinna*) which were presented on LCD screens to live test fish in binary choice tests. To validate the usage of animated fish stimuli, we measured association time as the validating parameter and analyzed how it was affected across different stimulus types.

Live females responded similar to animated males as to a video or even a live male. Movement of the animation was important but live females responded stronger to the animated swimming fish than to a 'swimming' box. Live test males discriminated between animated males and animated females based on sex specific characteristics.

We conclude that our software is a useful tool for the study of mate choice in sailfin mollies. Furthermore, we here present a new approach of a closed-loop simulation in which the 'virtual lover' responds to the live fish in real-time, which opens new horizons for studying fish behavior in future research.

**Keywords:** computer animation, fish behavior, mate choice

PP-EB-11

**Identification and functional studies of *Mus*-specific *de novo* genes**

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**Introduction:** *De novo* genes are molecular entities which originated recently in evolutionary history of a given lineage from non-genic ancestral sequences. They can quickly acquire functions, probably through recruitment of downstream interactors and by reshaping global gene networks. These aspects have not been extensively addressed in previous studies.

**Objectives:** We want to identify *de novo* genes originating in *Mus* genus, and understand their functions and how they reshape global gene networks.

**Materials & methods:** We used genome sequences and gene annotations of all organisms to identify *Mus*-specific *de novo* genes, and further used genome sequencing data of different populations and species of *Mus* genus to fine date their origination time. The transcriptional expression of *de novo* genes was supported with the evidence from RNA-Seq data across individuals, developmental stages, and tissues, and their translational expression was supported with the evidence from proteomics and ribosome profiling data. We performed gene knock-out experiments of three *de novo* genes in mice. We will obtain RNA-Seq data from knock-out and wild-type mice, and analyze the differentially expressed genes. We will further investigate gene networks by integrating data retrieved from manually curated pathway databases, protein-protein interactions, co-expression networks, and regulatory networks.

**Results:** We identified 298 *Mus*-specific *de novo* protein-coding genes with high-throughput translational expression evidence. We generated knock-out mice of three *de novo* genes. The knock-out mice of one gene showed abnormal clinical blood chemistry levels and abnormal auditory brain stem response.

Conclusion

*De novo* genes largely exist, and they have important functions.

**Keywords:** *de novo* gene, gene origination, knock-out mice

PP-EB-12

**Functional characterization of evolutionarily advantageous sequence divergence between MHC alleles**

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The highly polymorphic genes of the major histocompatibility complex (MHC) encode for cell-surface glycoproteins with a key role in adaptive immunity. Divergent allele advantage, a mechanism of balancing selection, has been proposed to maintain the exceptional sequence divergence and ancient allelic lineages at these genes. Heterozygous individuals with more divergent MHC allele combinations (i.e. larger sequence difference along the antigen-binding domains) are thought to express glycoproteins presenting a wider array of antigens to immune effector cells, conferring an advantage against pathogen infections. However, the exact association between sequence divergence and the corresponding peptide binding properties has not been studied systematically across the different MHC genes. Here, we investigated the allele-specific repertoire of bound peptides for all common alleles at the five key classical human MHC genes (HLA-A, -B, -C, -DRB1 and -DQB1) using established computational binding prediction of 115,752 pathogen-derived peptides. For all five MHC genes, the genetic distance between two alleles of a heterozygous genotype showed a significant positive correlation with the combined number of bound peptides. A significant correlation between an allele's population frequency and its average pairwise sequence divergence was also observed for four of the investigated MHC genes, suggesting still ongoing selection for divergent MHC genotypes in modern human populations. Overall, our results support the divergent allele advantage hypothesis as a plausible scenario, contributing to the exceptional genetic diversity in classical MHC genes.

**Keywords:** MHC genes, allele divergence, balancing selection

PP-EB-13

**Genomic organization and standing structural variation of the Major Histocompatibility Complex of the three-spined stickleback**

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Parasites are known as a major driver for the evolution of host genetic diversity, but less is known about their effect on structural variation in the host genome. The Major Histocompatibility Complex (MHC) is a genomic region that plays a key role in adaptive immunity and mate choice of vertebrates. As such, this region has many characteristics that make its study both interesting and complex, such as allelic variability and, sequence divergence, but also potentially adaptive copy number variation of functional loci. So far little is known about the evolutionary factors that drive this structural variation. In this context, the three-spined stickleback (*Gasterosteus aculeatus*) is an excellent model to investigate parasite-mediated selection for potentially adaptive structural variation in the MHC. Populations of sticklebacks are exposed to different parasite communities and are known to exhibit locally adapted MHC genotypes. Furthermore, substantial population differences in the number of MHC IIB alleles per individual suggest potentially adaptive variability in the number of MHC loci. The aim of this project is to unravel the genomic organization of the MHC region in the stickleback using state-of-the-art genomic tools, including BAC library construction and next generation sequencing. The MHC region of several distinct haplotypes will be assembled and annotated, creating a reference map for the characterization of the haplotypic diversity found in natural populations. This work will improve our understanding of how the dynamics of host-parasite coevolution can affect the structural organization of complex genomic regions and highlight the potential role of such genomic variation in the context of ecological speciation.

**Keywords:** Genomic Organization, MHC, Three-spined stickleback

PP-EB-14

**Polyandry is independent of genitalia complexity in bushcrickets**

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**Introduction:** Animal genitalia are believed to evolve rapidly under sexual selection. In some bushcricket families, males possess sclerotised copulatory organs. Like other genitalic structures, these bushcricket titillators show considerable variation across species. Bushcrickets also vary widely in mating traits like polyandry and refractory period.

**Objectives:** We tested the hypothesis derived from sexual selection theory that genitalia complexity should increase with mating numbers, especially polyandry (Simmons 2014, *AustralEntomol* 53: 1-17).

**Material and methods:** Data on the mean polyandry ('lifetime number of matings for females'), and male and female refractory periodswere obtained for 45 species of tettigoniid bushcrickets.

For titillators we developed a ranked classification system to reflect complexity.

We fitted models for the parameters using titillator complexity as a predictor variable using phylogenetic generalized least squares models.

**Results:** There was a high variation in polyandry in females, ranging from 1.5 up to 28 matings during lifetime. Polyandry was unrelated to titillator complexity. The male refractory period was highly labile among species; titillator complexity reliably predicted neither male refractory period nor differences in refractory periods between females and males.

**Conclusion:** Our result does not support the hypothesis of postcopulatory sexual selection being a driver for male bushcricket genitalia evolution.

**Keywords:** Genitalia, Titillator, Polyandry

## PP-EB-15

### Morphological Evolution in Neotropical Ariidae

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Ariidae (sea catfishes) from the Neotropics are studied here to address a lineage with a deep divergence in the Cenozoic, and with a growing Neogene fossil record. Most commonly studied clades of fishes are of much younger origin than the Ariidae. The evolutionary history of Ariidae is special in the sense that some marine ariid lineages evolved into secondarily adapted freshwater species within the clade of Ariidae.

In this context, we investigate the radiation of the Ariidae, examining the effects of macrohabitat (fresh, brackish, and salt water) and phylogeny on shape changes.

We first established a time-calibrated phylogenetic framework for 21 recognised ariid species belonging to the genera *Sciades*, *Ariopsis*, *Bagre*, *Notarius*, and *Cathorops*. 1000 polymorphic markers, derived from RAD-seq and ariid fossils for internal node calibration, were used. The resulting phylogeny represents the most marker-rich phylogenetic hypothesis for Ariidae to date. The analysis of morphological shape changes was based on the neurocranium. We applied 3D geometric morphometrics followed by multivariate statistics to investigate habitat and phylogenetic signals.

We first identified a cryptic species within *B. pinnimaculatus*. Further, we provide the first genetic proof that *C. wayuu* and *C. nuchalis* from the Maracaibo region are separated, and that this separation dates back to approx. 70.000 years. Two populations of *S. herzbergii* were found to be separated genetically, possibly due to vicariance. Finally, we found that neurocranial shape is strongly constrained by phylogeny.

In summary, molecular analyses revealed cryptic species in arid catfish, and supported the distinction of one species otherwise only recognised on morphological level.

**Keywords:** macrohabitat, morphometrics, adaptation

## PP-EB-16

### Mate-copying in *Drosophila melanogaster* males

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Using social information constitutes a potential strategy to assess potential mates' quality by observing sexually interacting conspecifics. Mate-copying is such a socially determined mate-choice strategy. During mate-copying an individual witnesses sexual interactions between two heterosexual conspecifics, which influence the future mate choice of the observing individual. Up to now, most studies focused on mate-copying in females as it is usually assumed that females are the choosier sex and much less is known about male mate-copying. As mate-copying was demonstrated in female *Drosophila melanogaster*, we tested whether males can also mate-copy in that species. We created two artificial female phenotypes by dusting females with green or pink powder, and naïve observer males were given the opportunity to see a demonstrator male choosing between a pink and a green

female. Afterwards, these observer males were given the choice between two new females, one of each color. We found that males mate-copied in that they developed a preference for the females of the color they saw being selected during the demonstration. In a control experiment, males having no opportunity to see an ongoing demonstration, chose randomly between pink and green females. Thus, *D. melanogaster* males can perform mate-copying based on a single observation. The importance of such mate-copying abilities in the field, and their potential impact on *Drosophila*'s evolution, need to be further evaluated.

**Keywords:** *Drosophila melanogaster*, social learning, mate-copying

#### PP-EB-17

##### **Mi(gh)ty Vectors - Bumble bees, their mites and the potential for virus transmission**

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Pollinator decline is one of the great ecological and economic threats of our time. Newly emerging pathogens have been identified as one of the main drivers of this decline. This, so far, mostly applied to honey bees. However, several recent studies have shown that honey bee diseases may also infect wild bees, with horizontal transmission between managed and wild bees being associated with contaminated flowers. Between different species of bumble bees, a different route may play a role for interspecific transmission, phoretic mites living commensally in bumble bee nests. However, the specialization and diversity of phoretic mites on bumble bees is largely unexplored. Hence, we used DNA barcoding to identify bumble bees and delimit molecular taxonomic units of their phoretic mites and constructed a preliminary co-phylogeny of both to test for the degree of specialization of mites. We screened both groups for viruses and mapped these on the phylogeny to explore potential patterns of transmission. We found that bumble bees carry multiple strains of strongly divergent mites; mites appear not to be species specific to single bumble bees. Finally, mites carry bee viruses suggesting that they may play a role as vector.

**Keywords:** Pollinator decline, DNA barcoding, Co-Phylogeny

#### PP-EB-18

##### **The evolution of chemical communication in the genus *Leptopilina***

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Studying evolution can be a challenging issue, especially when it comes to chemical ecology. Although being considered the oldest and most wide-spread form of communication, the origin and evolution of pheromones remain often puzzling. The precursor hypothesis predicts that semiochemicals used for intra- and interspecific communication can evolve from already used non-communicative chemical compounds. A rare example for this hypothesis and thus an optimal system for reconstructing the evolution of pheromone communication offers the parasitic wasp genus *Leptopilina* (Hymenoptera: Figitidae). Females of *Leptopilina heterotoma* use their defensive compound (-)-iridomyrmecin also as major component of their sex-pheromone.

Here we present data on the chemical profile and the female sex pheromone of eight species of *Leptopilina*. All species produce iridomyrmecin, although some different stereoisomers thereof, and several other iridoid compounds, resulting in species-specific chemical profiles. However, *L. heterotoma* and *L. boulardi* are the only species of those eight that followed the evolutionary route of the precursor hypothesis and have made the iridoid compounds an essential part of their sex-pheromone, while all other species solely use cuticular hydrocarbons (CHCs) as female sex-pheromone. Also the parthenogenetic *L. tsushimaensis*, which lacks a sex pheromone, produces both iridoid compounds and CHCs. The phylogenetic relationship of the species cannot explain this diversity. Therefore, other factors, like the mating system might have shaped the composition of the female sex-pheromone in *Leptopilina*.

**Keywords:** *Leptopilina* wasps, evolution, sex-pheromone

PP-EB-19

**Specificity of oral immune priming in *Tribolium castaneum***

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**Introduction:** In many invertebrate species, enhanced survival of infection has been observed after prior exposure to the same pathogen ('immune priming'). In insects, oral infection is assumed to be the natural route of infection with the spore-forming bacterium *Bacillus thuringiensis*. The major virulence factors of *B. thuringiensis* are the plasmid-encoded Cry toxins that are toxic upon ingestion and characterised by high insecticidal specificity.

**Objectives:** While priming via septic wounding in the red flour beetle *Tribolium castaneum* shows a high level of specificity, it is unclear whether the same phenomenon can also be observed via oral immune priming. Thus, we investigated in our study whether *T. castaneum* is able to mount an immune priming response to three different strains of *B. thuringiensis* that are known for their entomopathogenic activity.

**Materials and Methods:** We conducted a full factorial experiment by using our well-established high throughput method for oral infections of individualised larvae.

**Results:** We demonstrate that immune priming can be triggered by oral uptake of the spore supernatant in two of the three bacterial strains. Furthermore, the results point to a certain level of specificity towards two of the strains.

**Conclusions:** We are currently exploring whether the priming response to the third strain might be dependent on the spore dose. However, our results suggest that specificity towards *B. thuringiensis* is also present in oral priming.

**Keywords:** Immune memory, *Bacillus thuringiensis*, *Tribolium castaneum*

PP-EB-20

**Host Specificity in the Honeybee Parasitic Mite, *Varroa* spp. in *Apis mellifera* and *Apis cerana***

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The ectoparasitic mite *Varroa destructor* is a major global threat to the Western honeybee *Apis mellifera*. This mite was originally a parasite of *A. cerana* in Asia but managed to spill over into colonies of *A. mellifera* which had been introduced to this continent for honey production. To date, only two almost clonal types of *V. destructor* from Korea and Japan have been detected in *A. mellifera* colonies. However, since both *A. mellifera* and *A. cerana* colonies are kept in close proximity throughout Asia, not only new spill overs but also spill backs of highly virulent types may be possible, with unpredictable consequences for both honeybee species. We studied the dispersal and hybridisation potential of *Varroa* from sympatric colonies of the two hosts in Northern Vietnam and the Philippines using mitochondrial and microsatellite DNA markers. We found a very distinct mtDNA haplotype equally invading both *A. mellifera* and *A. cerana* in the Philippines. In contrast, we observed a complete reproductive isolation of various Vietnamese *Varroa* populations in *A. mellifera* and *A. cerana* colonies even if kept in the same apiaries. In light of this variance in host specificity, the adaptation of the mite to its hosts seems to have generated much more genetic diversity than previously recognised and the *Varroa* species complex may include substantial cryptic speciation.

**Keywords:** Host-Parasite coevolution, Population genetics, Honeybees

PP-EB-21

**Evaluating the evidence for parapatric evolution via the distribution and behaviour of genetic clines across a population transition zone**

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Ecological based speciation models assume adaptational processes that restrict gene flow between populations living within life-time dispersal distances. In these so-called speciation-with-gene-flow models, sympatric speciation has received much attention whereas parapatry, the exchange of genes, but not freely, in a continuous landscape along an ecological gradient, is hardly examined in natural populations. The tephritid fly *Urophora cardui* exhibits an allozyme and mtDNA genetic pattern adhering to predictions for parapatry. Originally studied in 2001, I resampled the transition zone in 2014 with the aim of gaining genome-wide representations to address the stability, distribution and behaviour of genetic clines to distinguish between parapatric (*in situ*) vs. vicariant origin of the transition zone. I used original and new markers (microsatellite, genotyping-by-sequencing (GBS)) and compared the markers for their information contents. The genetic data was combined with data of population dynamics and of putative selective agents. The genetic results show that the transition zone is stable and involves not just two but probably three population groups arranged in a linear geographic distribution. Although the intermediate group does not show primary genetic admixture it nevertheless seems to be a transition group between the northern and southern groups, i.e. divergence seems fixed. While the genomic distribution of clines contradicts predictions for parapatry, outgroup analysis has so far (GBS not completed) failed to locate a vicariant origin. Genetic analysis suggests that sex chromosomes (rearrangements) may play a decisive role in *in situ* diversification. Supported by DFG JO-325/5-1.

**Keywords:** Parapatry, genetic clines, genotyping-by-sequencing

PP-EB-22

**Gene duplication as an escape from evolutionary constraint: a study of the Na,K-ATPase function in milkweed bugs**

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Using targeted gene knockdowns, we investigated the role of triplicate copies of the Na,K-ATP $\alpha$  subunit coding gene in providing resistance to toxic plant secondary compounds, namely cardiac glycosides. Cardiac glycosides are anti-herbivory compounds that bind to the Na, K-ATPase, a protein subject to high levels of evolutionary constraint. Several insect species, including the milkweed bug *O. fasciatus*, contain multiple copies of the Na, K-ATP $\alpha$  subunit coding gene (*O. fasciatus* has three copies: A, B and C) which are differentially resistant to cardiac glycosides.

We knocked down the A, B and C copies using a 540 base pair segment from each of the three copies, located at the 3' end of the Na, K-ATP $\alpha$  subunit. The probes were injected with a Hamilton injector into the haemolymph of adult bugs. Alterations in transcript levels were monitored using qPCR for the target gene copies as well as a set of reference genes.

We found that all three copies are in fact expressed in adult bugs, but that the C copy is expressed at much lower levels than the A and B copies. Tissue-specific expression revealed that the A and B copies are expressed in the Malpighian tubules, whereas the C copy is predominantly expressed in the nervous tissue. RNAi knock-down bugs for the A and B copies were healthy, whereas C-copy knockdowns proved lethal. However, the A and B knockdowns became lethal when challenged with cardiac glycosides.

These results show that the various Na, K-ATP $\alpha$  gene-copies have taken on diverse functions and that these functions have facilitated the bugs ability to feed on a highly toxic host plant. The C copy appears to perform the ancestral, constrained ion-pumping function of the Na, K-ATP $\alpha$ , while the A and B copies appear specialized to handle cardiac glycosides.

**Keywords:** resistance evolution, genotype phenotype, RNA interference

**PP-EB-23**

**Recombination in the eggs and sperm in a simultaneously hermaphroditic vertebrate**

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When there is no recombination in one sex, it is in the heterogametic one. This observation is so consistent that it constitutes one of the few patterns in biology that may be regarded as a 'rule' or 'law', and Haldane proposed that it may be driven by selection against recombination in the sex chromosomes. Yet differences in recombination rates between the sexes have also been reported in hermaphroditic species that lack sex chromosomes, and alternative hypotheses are required to explain this phenomenon. In non-selfing hermaphroditic angiosperms, recombination rates tend to be higher in the female gametes, which has been proposed to be driven by selection at the haploid stage. Things may be different in animals though, since they usually lack a haploid phase in females. Yet few data are available for hermaphroditic animals, and even fewer for hermaphroditic vertebrates. Here, we leverage reciprocal crosses between two black hamlets (*Hypoplectrus nigricans*, Serranidae), simultaneously hermaphroditic reef fishes from the wider Caribbean, to generate egg- and sperm-specific linkage maps for each parent. A total of 2697 informative RAD markers genotyped in the two parents and 95 larvae identified 24 linkage groups (LGs), with recombination patterns typical of acrocentric or telomeric chromosomes. We observe higher recombination rates in the eggs than in the sperm in both parents, and this difference is particularly pronounced at one extremity of the LGs. We hypothesize that this extremity corresponds to the centromere, and that higher recombination rates in the eggs in this region is due to female meiotic drive. We also identify what appears to be a large non-recombining region on linkage group VIII in the two parents and in both sexes.

**Keywords:** Recombination, Meiosis, Adaptation

**PP-EB-24**

**Adaptations of the brain to hypoxia induced by diving in marine mammals**

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One of the greatest challenges encountered in the evolution of diving mammals is the cessation of breathing and with it of oxygen supply during dives. The brain is one of the tissues most vulnerable to hypoxia, and yet, whales and some seals exhibit remarkable diving durations without suffering from neuronal damage. While the majority of the research focused on adaptations of the whole body, little is known about mechanisms in the brain to prevent neuronal damage induced by diving. Focusing on the hooded seal (*Cystophora cristata*), we aim to understand the adaptations of the brain to a low availability of oxygen. We built upon previous work by our group that identified candidate genes by comparative expression analysis in the visual cortex of the hooded seal and the ferret and determined the cellular localization of proteins expressed by candidate genes using immunofluorescence. Further, the candidate genes were tested for positive selection in a range of deep diving seals and whales.

A major study target was clusterin, known to be involved in the response to neuronal oxidative stress. Clusterin is the most highly expressed gene in the visual cortex of the hooded seal, and four times higher expressed than in the visual cortex of the ferret. Clusterin was found to be positively selected in seals and whales. Preliminary immunofluorescence results indicated that clusterin is expressed in the same cortex cell types in the hooded seal and the mouse. Taken together, our results suggest a possible neuroprotective role of clusterin in diving mammals that might be brought about by a change in clusterin abundance and possibly in its function. We will present ongoing work on further candidate loci and discuss potential roles in the 'brainy response' to hypoxia.

**Keywords:** hypoxia, brain, diving mammals

PP-EB-25

**Genomic Footprints of Positive Selection in the Heterogeneous Differentiation Landscapes of *Ficedula* flycatchers**

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Identifying genome regions that are subject to adaptive differentiation related to local adaptation or species evolution is paramount to understand the trajectories along which biodiversity unfolds. Several recent studies have identified abundant genome regions of accentuated differentiation ('differentiation islands') in diverse taxa. However, differentiation islands frequently appear to evolve as a consequence of purifying selection at linked sites (background selection, BGS). Therefore, the interpretation of differentiation islands as candidate regions involved in adaptive differentiation remains contentious. Here, we tested predictions of a model of long-term linked selection to infer genome regions in *Ficedula* flycatchers that evolved under positive selection and are likely involved in adaptive divergence of present-day species and populations. We show that there is no clear role for positive selection in the evolution of differentiation islands shared among closely related species ('shared islands'). Although shared islands display haplotype structures and site frequency spectra (SFS) indicative of positive selection, simulations reveal that qualitatively similar footprints can arise from BGS. Using the distributions of haplotype structure and SFS statistics of shared islands as a conservative null distribution, we then show that differentiation islands specific to single species or to a subset of species ('species-specific islands'), and differentiation islands in populations within species ('intraspecific islands') exhibit significantly stronger footprints of positive selection than the remainder of the genome, and are enriched for candidates likely involved in adaptive differentiation.

**Keywords:** Adaptation, Linked selection, Population genomics

PP-EB-26

**With whom to mate? Effects of multiple paternity in the wild boar (*Sus scrofa*).**

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Heavier, adult female wild boars (*Sus scrofa*) have been shown to produce more variable litters compared to lighter, younger females concerning offspring body mass. The mechanism facilitating this size diversification, however, is unknown. We investigated whether multiple mating and thus multiple paternity provides a mechanism for the diversification of juvenile body mass within litters in the wild boar. Besides investigating paternal and maternal effects on juvenile body mass of female wild boars, we also evaluated parental effects on their reproductive success. Our results show (i) a high frequency of multiple paternity in the wild boar under semi-natural conditions with ~ 70% of litters consisting of more than one offspring being fathered by multiple boars and a maximum of 4 males fathering one litter (litter size = 5); (ii) that paternal half-siblings and full-siblings were more similar in terms of juvenile body mass (at ~ 8 month) compared with maternal half-siblings and unrelated animals, indicating strong paternal effects; (iii) that the litter size (first litter at 2 years of age) was also affected by a dam's father, again resulting in a lower diversity among paternal half-siblings compared with unrelated females. In contrast, (iv) similarity in juvenile body mass and reproductive success was low in maternal half-siblings and did not differ from that found in unrelated females. These strong paternal effects and the high degree of multiple paternity show that multiple mating is an important mechanism for offspring diversification in the wild boar.

**Keywords:** paternal effects, offspring diversification, bet-hedging

**PP-EB-27**

**Patterns of trait integration across multiple predator environments.**

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Predation is known to be heterogeneous in space and time and prey often experience threats by multiple predator species rather than a single predator. Current theory suggests that to avoid and repel predators, prey apply sets of integrated antipredator traits by altering morphology, behaviour and life history simultaneously. Predator species differ qualitatively in their foraging characteristics suggesting that the magnitude and direction - the integration - of trait changes will be predator specific. Here, we studied the integration of antipredator traits among genotypes of the waterflea *Daphnia pulex* facing antagonistic selection regimes by predatory fish (*Gasterosteus aculeatus*; stickleback) and an insect predator (*Chaoborus spec.*; phantom midge larvae). These two predators select for opposite pattern in size and age at maturity, in morphology and in behavioural antipredator traits. By studying the covariance of antipredator traits along a gradient of both predators, we show that anti-predator responses are sensitive to specific predators, but that the integration of traits is a graded multivariate response governed by levels of risk

**Keywords:** phenotypic intergration, phenotypic plasticity, predation

**PP-EB-28**

**Investigating the role of tRNA methyltransferase (*Dnmt2*) in the red flour beetle *Tribolium castaneum***

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**Introduction:** Epigenetic regulation enables rapid phenotypic adaptation to environmental change. Cytosine methylation of small RNAs is an important epigenetic mechanism, generated by an evolutionarily conserved enzyme, tRNA methyltransferase (*Dnmt2*). For a long time *Dnmt2* was thought to be involved in DNA methylation, because of its sequence similarities to the two other known DNA methyltransferases (*Dnmt1* and *3*). But, recent studies have shown that *Dnmt2* is responsible for methylating RNAs, especially tRNA.

**Objectives:** The genome of the red flour beetle *Tribolium castaneum*, encodes for *Dnmt1* and *2* but lacks a copy for *Dnmt3*. Additionally, there is an ongoing debate, whether the beetle exhibits functional cytosine DNA methylation. We therefore investigated the status of *Dnmt2*, to determine whether it could contribute to the phenotypic plasticity observed in the beetles.

**Materials & methods:** We analyzed the gene expression of *Dnmt2* across all life history stages and in the reproductive tissues. We also applied parental RNAi to male and female pupae and monitored the effect of the knockdown in the treated and offspring generation.

**Results:** *Dnmt2* is expressed across all stages and in the gonads. Furthermore, RNAi treatment led to a significant systemic downregulation. However, development and fitness were unaffected by the downregulation of *Dnmt2*.

**Conclusion:** Although *Dnmt2* is expressed during the entire life of the beetle and in the germline, its expression does not seem essential for the survival of the beetle under *ad libitum* conditions. In the future, we plan to investigate the status of tRNA methylation in *T. castaneum* and the effect a knockdown of *Dnmt2* has on phenotypic plastic traits, e.g. trans-generational immune priming.

**Keywords:** tRNA methyltransferase, phenotypic plasticity, RNA interference

PP-EB-29

**Insights in signaling pathways contributing to the outgrowth of the elongated jaws in halfbeaks and needlefish**

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Evolutionary novelty can drive rapid lineage diversification, e.g. by allowing a lineage to occupy new ecological niches. The order of *Beloniformes* contains two sister families, the *Adrianichthyidae* (ricefishes) and the *Belonoidei* (halfbeaks, flying fishes, sauries and needlefishes) with about 20 and 200 species, respectively. While the ricefishes only have little variation in their mouth morphology, their sister family displays pronounced interspecific variation in the elongation of the upper and lower jaws. In spite of their iconic jaws, only little is known about the molecular and developmental bases of jaw outgrowth in the halfbeaks and needlefish. We examined major signaling pathways for their contribution to *Belonoidei* jaw elongation during larval development using a halfbeak and a needlefish representative, as well as their outgroup Medaka (a ricefish). By treating larvae of these three species with agonists or antagonists of major morphogenic signaling molecules, such as RA, BMP, WNT, FGF during jaw outgrowth, insights in the specific pathways' effects on the timing and shape of the outgrowing jaws were gained. We find that particularly signaling pathways affecting ossification rates have significant influence on the timing and length of jaw outgrowth. We propose that an altered ossification pattern in the head of the common ancestor of the *Beloniformes*, which may still be observable in Medaka, may have allowed the *Belonoidei* to evolve their unique elongated jaws.

**Keywords:** Evolutionary novelty, Signaling pathways, Jaw elongation

PP-EB-30

**Early reproductive success and competitiveness in *Drosophila melanogaster* males is dependent on maturity of the accessory gland**

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Sexual maturity is often defined as the point when mature gametes are produced or as mating success. We study the process of sexual maturation in males and could show that this is a much more complex process where several traits, including post-copulatory traits, need to mature before full reproductive competence is reached. Our study organism the fruit fly *Drosophila melanogaster* belongs to the insect taxa Diptera, where sexual maturity is not directly attained at adult eclosion. Quite unusually, in *Drosophila* males mature even later than females.

Using a suit of behavioral assays we document the order in which pre- and post-mating traits mature and how they affect male reproductive success. Additionally, we monitored the development of the male accessory gland, since in a number of taxa mating success is tightly linked with size of the accessory gland, the production site of a complex cocktail of proteins important for male reproductive success.

Our results show that young *D. melanogaster* males shortly after eclosion up to the age of six days are less likely to persuade a female into mating and show significantly less courtship behavior. Young males that managed to obtain a mating however were inferior in many post-copulatory traits like sperm competitiveness and effectiveness in suppressing female remating. Also the accessory gland in *Drosophila* males is significantly increasing in size over the first 6 days after adult eclosion.

We argue that prolonged sexual maturation is associated with the immaturity of the accessory gland and that the observed inferiority of young males for several reproductive traits is most likely caused by the incomplete growth of the accessory gland at eclosion.

**Keywords:** *Drosophila melanogaster*, Accessory Gland, sex peptide (SP)

PP-EB-32

**Beyond doubly uniparental inheritance of mitochondria: complex population-, sex- and tissue-specific patterns in the long-lived bivalve *Arctica islandica***

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Mitochondria are normally maternally inherited whilst the paternal mitochondria are eliminated. In some bivalves, these paternal mitochondria are retained in the male gonads whereas all other tissues only contain maternal mitochondria (Doubly Uniparental Inheritance or DUI).

We studied the mitochondrial lineages of *Arctica islandica*, a marine bivalve known for its extreme longevity, across its palaeartic distribution and analyzed patterns in the a) presence, b) expression and c) physiological characteristics of the two mitochondrial alleles and their products.

We found a dominant mitochondrial lineage in all seven tested populations with little geographic structure. A divergent (male) sequence type (8-10% p-distance) was found in several types of somatic tissue of 15-20% of the tested individuals from Norway, Iceland and the USA.

The temperate European populations of *Arctica* showed a DUI-like pattern in that the divergent sequence type was confined to male gonads. Contrary to the expectation, in Arctic populations the divergent sequence type was also present in somatic tissues of males and females, replacing the maternal mitochondrial lineage. Both mitochondrial alleles are expressed in both sexes, mitochondria are measurably distinct in their maximum capacities of some enzymes composing the mitochondrial respiratory chain of either lineage.

Our findings challenge the DUI concept because the coexistence of mitochondrial lineages within a single species does not require one type to be confined to male gonads only and shed light on the question how this coexistence can be stable over evolutionary times despite being exposed to natural selection.

**Keywords:** mitochondrion, natural selection, doubly uniparental inheritance

PP-EB-33

**Side matters: Integration of genital asymmetry and behavioral lateralization**

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Asymmetry in the external morphology is known to be a possible cause of behavioral lateralization. If asymmetry affects genital structures, a lateralization of mating behavior due to structural restraints is likely. Yet, it is unclear if genital asymmetry is correlated with behavioral laterality and/or morphological asymmetry of traits not directly related to mating. Fish of the genus *Jenynsia* are livebearers that exhibit internal fertilization. The male intromittent organ (gonopodium) shows pronounced asymmetry, based on which males can be assigned to either a right or a left morph. We determined if genital asymmetry is correlated with lateralization in mating behavior, as well as with other behaviors not directly related to mating (inspection behavior), and with asymmetry in sensory organs (eyes and lateral line system), which are likely to be involved in mating. We found mating behavior to be highly lateralized in all males with a positive correlation to the respective genital morphology. A detour test indicated that lateralization of other behaviors strongly depends on the presented stimulus and can evoke lateralization on either individual or population level, but is in general not correlated to genital asymmetry. Finally, variation in eye size asymmetry and asymmetry in the number of neuromasts in the caudal peduncle region were related to the variation in genital asymmetry, suggesting the integration of several morphological asymmetries and lateralization of male mating behavior.

**Keywords:** Asymmetry, Lateralization, Livebearing fish

**PP-EB-34**

**A refined species-tree estimate for Lake Tanganyika cichlids - incorporating introgression and incomplete lineage sorting**

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Phylogenetic inference of species from an adaptive radiation is hindered by rapid lineage formation and occasionally occurring gene flow. In this study, we present a novel approach for species-tree estimation in rapidly diversifying lineages, where introgression is known to occur. We apply it to a dataset encompassing 40 phylogenetic markers from up to 16 individuals per species for a set of 45 species. Using age distributions of most recent common ancestors in individual gene trees, we identify lineages in our dataset that show strong signatures of past introgression - leading to the formulation of hypotheses of introgression between different lineages. These hypotheses were then tested with a likelihood function from the PhyloNet package. Next, we inferred the species-tree of Lake Tanganyika cichlids applying the multispecies coalescent model, but excluding the lineages involved in introgression events (as this violates the requirements of the multispecies coalescent model). This resulted in a novel highly supported species-tree estimate for Lake Tanganyika cichlids.

**Keywords:** species tree, cichlids, introgression

**PP-EB-35**

**Phylogeography and genetic structure of the ascidian *Cnemidocarpa verrucosa* along the Antarctic Peninsula.**

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The Southern Ocean is one of the most physical and thermally isolated marine ecosystems characterized by high levels of endemism. The ascidians are an important group in the benthic community and locally very abundant in the Antarctic Peninsula. Here, we study the genetic variation within *Cnemidocarpa verrucosa*, one of the most widely distributed ascidians in Antarctica. Using the mitochondrial gen cytochrome oxidase, I (COI), the nuclear gen 18S and restriction site associated DNA (RAD) markers, we studied the phylogeography and demography of ten different populations of *C. verrucosa*, distributed along the Antarctic Peninsula. The bimodal distribution of genetic distances in COI (two mitochondrial lineage separated by 39 substitutions) suggests the existence of an as yet undescribed cryptic species within nominal *C. verrucosa*.

**Keywords:** Phylogeography, Cryptic species, *Cnemidocarpa verrucosa*

PP-EB-36

**High levels of realized dispersal and phenotypic plasticity in the polymorphic squat lobster *M. gregaria* (Decapoda: Anomura: Munididae)**

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The marine shallow-water squat lobster *Munida gregaria* (Decapoda: Munididae) is a coastal species that has an amphi-Pacific disjunct distribution off southeastern New Zealand as well as Pacific and Atlantic waters of Patagonia. Within *M. gregaria* sensu lato there are two different ecotypes, *gregaria* sensu stricto and *subrugosa*, that are characterized by differences in morphology, ecology and behavior.

Here we test if the morphological differences among the *M. gregaria* ecotypes are reflected in underlying genetic differences.

A total number of 297 *M. gregaria* s.l. adults and juveniles from 28 locations of its global distribution were included in this study. We applied nine species-specific nuclear microsatellites and mitochondrial COI marker to conduct genetic clustering and reconstruction of evolutionary history. We also tested if the more complete geographic sampling continues to support discrete morphological clusters.

Morphological analyses of South American specimens showed two discrete groups representing the existing two ecotypes and a third discrete group comprising *gregaria* s. str. from northern Chilean Patagonia. Genetic analyses on this subset sample confirmed a high level of realized dispersal indicated by a lack of genetic differentiation among the two ecotypes in Patagonia. The only detectable genetic structure is a differentiation across the Pacific but many shared alleles as well as testing in a Bayesian framework confirm gene flow at different timescales across an open water barrier spanning more than 7000km.

We conclude that the sharply distinct ecotypes in this transoceanic squat lobster *M. gregaria* s. l. are the result of phenotypic plasticity rather than underlying genetic differentiation.

**Keywords:** phenotypic plasticity, gene flow, microsatellites

PP-EB-37

**Causes of telomere length variation in wild jackdaw nestlings: Genetic, parental and other environmental influences**

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Telomeres, evolutionary conserved DNA sequence repeats, located at the ends of chromosomes present a candidate biomarker of ageing and phenotypic quality. Short telomeres relate to reduced life expectancy and poor health in several mammal and bird species. Already at the start of life telomere length differs substantially between individuals. Our aim was to identify and distinguish potential influences on early-life telomere length. We used a large multi-generation dataset of wild jackdaws (*Corvus monedula*) with various degrees of relatedness whose telomere length at age 4 days has been measured. It allowed us to investigate genetic, parental (e.g. age) and other environmental (e.g. cohort, nest, egg size, brood size) influences and their relative importance determining early-life telomere length. To be able to disentangle genetic and early life effects, chicks were cross-fostered prior to hatching. Telomere length was measured performing telomere restriction fragment analysis including terminal telomere sequences only that are subject to age-related shortening. Heritability was estimated using animal models. First results indicate a stronger resemblance in early-life telomere length between mother and offspring than father and offspring. While the effect of nest of origin seems negligible, additive genetic effects are present. We will quantify and discuss the contribution of genetics vs. environment on telomere length as it will determine the response to selection.

**Keywords:** telomeres, ageing, heritability

PP-EB-38

**RAD-seq vs whole genome re-sequencing - how well can we infer demographic history?**

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**Introduction:** The pied flycatcher (*Ficedula hypoleuca*) is part of a relatively young (1.5-2 my) species complex that also includes the collared flycatcher (*F. albicollis*), the Atlas flycatcher (*F. speculigera*) and the semicollared flycatcher (*F. semitorquata*). Over the past few years the *Ficedula* flycatchers, and in particular the pied flycatcher - collared flycatcher species pair, have emerged as an important avian system in speciation research. It has long been assumed that the historical demography of these two species has been very similar; however, recent comparative genomics studies (e.g., Nadachowska-Brzyska et al. 2016, Mol Ecol) suggest otherwise. Understanding how demographic processes have influenced the distribution of genetic variation across the genome forms an important first step in evolutionary genetics studies by providing a baseline against which the action of selection can then be studied.

**Objective:** Here we investigate the evolutionary history of pied flycatchers. In particular, we are interested in testing the long-standing hypothesis whereby all European populations of this species derive from a refugial population in the Iberian Peninsula.

**Methods:** We use next-generation sequencing data and demographic inference methods to test alternative demographic scenarios that are obtained with the aid of ecological niche modelling.

**Results:** Ecological niche modelling suggests that pied flycatcher habitat declined during Pleistocene cold stages and expanded during warm stages; however, so far there is no indication that the Iberian Peninsula played a major role as a glacial refugium for this species. Instead, the species seems to have been able to maintain its presence in Central Europe. We present results of model testing and parameter estimation

**Keywords:** Ficedula, Evolutionary History, Ecological niche modelling

PP-EB-39

**Evolution of DNA methylation in molluscs**

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DNA methylation is an epigenetic mechanism influencing gene expression. It involves a chemical modification of the genomic DNA by which a methyl group is added to a nucleotide - usually a cytosine followed by a guanine (CpG) - by specific DNA methyltransferases (DNMTs). While the mechanism itself is evolutionarily ancient, the distribution and function of DNA methylation may vary considerably both within and among phylogenetic groups. One taxonomic group that has been heavily neglected from epigenetic investigations is the phylum Mollusca. Studies on *Mytilus edulis*, *Donax trunculus*, *Crassostrea gigas* and *Octopus vulgaris*, however, suggest that DNA methylation in molluscs has important gene regulatory functions. In the present study we used transcriptome data to indirectly infer the DNA methylation status of various molluscan species by identifying DNMTs and calculating the observed-to-expected CpG ratio distribution. The subsequent comparison of DNA methylation patterns among different taxa of molluscs is intended to increase our knowledge about the evolution of DNA methylation in this fascinating phylum.

**PP-EB-40**

**Predator exposure affects development of male ornamentation and female mate choice in three-spined stickleback**

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Predator-induced phenotypic plasticity is a wide-spread phenomenon in prey animals. Here, we examined whether and how predator exposure during development and acute predator presence affect male secondary sexual traits and female mate choice in the three-spined stickleback, *Gasterosteus aculeatus*, a fish with conspicuous male ornamentation. Males that were reared in the presence of predators developed a less intense red colouration, but showed higher activity during mate choice than non-predator-exposed males. Blue eye colouration and body size of males were not affected by long-term predator exposure. Acute predator presence during mate choice did not influence any male behavioural or ornamental trait. Predatory developmental environment did not affect female choice behaviour, but acute predator presence did. In the presence of a predator, females preferred less active males, whereas the opposite was true without predator presence suggesting an adaptive switch in preferences. Generally, male ornaments that were not affected by long-term predator presence (male body size, eye colouration) influenced female choice. Males having more intense coloured blue eyes and larger body size were preferred. In contrast, traits that were responsive to predator exposure (redness) had no impact on female mate choice. Our results demonstrate that the interplay between predator-induced plasticity in male ornamental traits and flexible female mate choice leads to highly dynamic processes which can alter the strength and even the direction of sexual selection.

## Morphology – invited talks

### Of nerve cords and glial cells – an annelid perspective

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Bilaterian animals usually possess a centralized nervous system composed of different types of neurons and additional supportive cells - the glial cells. In the epithelial central nervous system of the Deuterostomes a particular bipolar glial cell type with secretory function and stem cell capability is described and is called radial glial cell. Notably, the presence of such radial glial cells has never been reported in protostomian nervous systems. The latter fact has caused various discussions of whether glial cells in general represent a homologous bilaterian characteristic or whether they - and therefore the centralized nervous systems - evolved convergently in Deutero- and Protostomia.

With focus on the presence of radial glial cells, different taxa representing the bilaterian main clades were examined using a combined morphological and molecular approach including histology, transmission electron microscopy, immunolabeling and gene expression studies. The comparative investigations support the presence of radial glia-like cells in annelids as well as in other members of the Protostomia, and indicate homology to the glial cells reported for deuterostomes. Furthermore, the antibody stainings and gene expression studies suggest that the secretory character of radial glial cells is maintained throughout their various evolutionary adaptations. This implies an early evolution of radial glial cells in the last bilaterian ancestor and an intraepidermal nervous system as being the plesiomorphic bilaterian condition.

### Reconstructing the locomotion of fossils: where do we stand, where are we going? The case of a stem amniote

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In many cases the goal of morpho-functional analyses of vertebrate fossils is to reconstruct the locomotion, because it may provide insight into diverse aspects of the biology of the extinct taxon. To achieve this, often fragmentary and distorted skeletal remnants need to be linked to the function of the musculoskeletal system. The talk will present a case study of one possible research approach. At the center of the study is a roughly 300 million year old early tetrapod fossil, *Orobates pabsti*—a diadectid from the Lower Permian. This fossil not only is exceptionally well preserved, but also fossil trackways have been assigned to this species as the trackmaker. This combination thus presents an ideal case for the attempt to reconstruct the locomotion. In the project expertise from zoologists, biomechanists, palaeontologists, professional animators and engineers is recruited to understand the locomotion of *Orobates* and its evolutionary implications.

## Morphology – oral presentations

### OP-MO-01

#### Life-long production of neural cells in the CNS of sea spiders (Pycnogonida) - evidence for an ancestral system of adult neurogenesis in Arthropoda?

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**Introduction:** In the vertebrate brain, neurogenesis continues throughout adult life in specialized neurogenic niches. In many invertebrates, however, this phenomenon has not been adequately investigated. This is certainly true for arthropods, in which only few tetraconate species have been studied while data on myriapods or chelicerates are still lacking.

**Objectives:** We aimed to elucidate whether specialized systems of adult neurogenesis can be traced back to the arthropod ancestor. Therefore, we studied sea spiders (Pycnogonida), the descendants of one of the oldest chelicerate lineages that diverged in the Cambrian.

**Material and methods:** We conducted pulse-chase experiments using two *in-vivo* cell proliferation markers (BrdU, EdU) in four different pycnogonid species. This allowed us (1) to assess if and where adult neurogenesis occurs in the CNS, (2) to reveal migration routes of newly born cells and (3) to gain first insights into cell production rates.

**Results:** Neurogenesis persists in all ganglia of the adult CNS. BrdU+ and EdU+ cells are found in the so-called 'ventral organs' and along migratory streams that extend into the soma cortex and towards the central ganglionic neuropil. Variations in cell numbers between ganglia within specimens suggest a highly dynamic regulation of this process. Interestingly, pycnogonids are the only known arthropods with neurogenesis continuing in *all* body segments, which we suggest to be the plesiomorphic condition within arthropods.

**Conclusions:** For the first time, we demonstrate production of neural cells in adults of a non-tetraconate arthropod. Similarities between the adult neurogenic systems of pycnogonids and some crustaceans may indicate a common origin in the arthropod ancestor.

**Keywords:** adult neurogenesis, arthropod evolution, neurophylogeny

### OP-MO-02

#### There is much more than lobsters and crabs - Adult neurogenesis in the central olfactory pathway of shrimps and prawns

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It is known for a long time that neurogenesis, the generation and maturation of new neurons, persists during adulthood in the olfactory system of mammals. However, within the last two decades adult neurogenesis could be shown in the central olfactory pathway of many reptant crustaceans ("ground-dwelling decapods" like lobsters and crabs), too. Today, numerous studies are available which focus on the mechanisms as well as the factors that regulate the rate of the generation of new neurons in the adult crustacean brain. All investigations have been restricted to representatives of reptant decapods. Nevertheless, similarities to the mammalian neurogenic system have been suggested.

Now, we are interested in the question how widespread adult neurogenesis occurs across malacostracan crustaceans and if there are any variations of its morphological appearances. To this end, we investigated the brains of adult *Penaeus vannamei* (Dendrobranchiata) and *Crangon crangon* (Caridea) as "shrimp-like" decapods. With the assistance of the thymidine analogon Bromodeoxyuridine (BrdU) that incorporates DNA of dividing cells we are able to detect evidence for persistent proliferation of neurons by using immunohistochemical stainings combined with confocal laser-scanning microscopy. Both scanned taxa exhibit proliferation zones with newly generated cells within brain structures that process olfactory input (lateral cluster of deutocerebral-chemosensory lobes and hemiellipsoid body cluster). However, next to these comparable appearances our results also suggest that differences may exist in the neurogenic system of adult shrimps versus that of reptant decapods like lobsters and crabs. This study is funded by the DFG HA 2540/16-1.

**Keywords:** Crustacea, olfactory system, adult neurogenesis

OP-MO-03

**A mity brain in time and space - development and morphology of the synganglion of *Archezogetes longisetosus***

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Synchrotron X-ray micro tomography (SR $\mu$ CT) has proven to be a valuable method for the investigation of millimeter-sized arthropods. Most research, however, is focusing on exoskeletal and muscular characteristics only. Softer tissue is often neglected and in 'mites' there are only a few studies dealing with for example the reproductive or digestive system. In this study we investigated the development and morphology of the synganglion, a highly condensed central nervous system characterized by the loss of the ancestral metameric organization, as well as the organization of the nervous system in the oribatid mite *Archezogetes longisetosus* (Trhypochthoniidae). As found in other 'mites' and ticks, the synganglion is one solid fused mass and shows the classic subdivision into sub- and supraesophageal region, both consisting of cortex and neuropil tissue. Within the synganglion, however, we found structures resembling the ancestral metameric organization. During development the synganglion volume increases linearly with body size. But cortex and neuropil volume, respectively, do not increase in the same way. After the deutonymphal stage, the volume of the neuropil increases at a faster rate. The bifurcating nature of the nerves projecting into walking legs 2 - 4 is not based on a functional division into a motor and a sensory ramus, but both rami contain motor and sensory neurites.

**Keywords:** Synganglion, Nervous system, Oribatida

OP-MO-04

**State of the heart - an evolutionary investigation of arthropod cardiac structures**

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Arthropods are not only the most species-rich taxon within Metazoa but do also show a remarkable disparity concerning body organization. From the beginning of zoomorphology and especially in recent years, the circulatory system of arthropods has been investigated in great detail and has been shown a model organ system for evolutionary morphology. The heart as the central organ of the circulatory system has gone through major evolutionary changes: while some arthropods show very powerful hearts and complex vascular systems, other arthropods do not have any vascular system or heart at all. And although a great body of works exists, a comprehensive study investigating the structure of arthropods hearts using a defined set of methods has never been undertaken. We therefore investigated hearts of more than 30 species of all major arthropods groups using various imaging techniques (cLSM, micro-CT, SEM, histology) and described the hearts by addressing e.g. the structure of the myocard, composition of ostia or structure of arterial valves. Additionally, the descriptions were used to refine the respective concepts of the Ontology of Arthropod Circulatory Systems (OARCS). Complemented with data from the literature, we in a next step conceptualized characters and character states related to heart structure and elaborated the differences between characters and ontological concepts. We then mapped the characters onto prevailing phylogenetic hypotheses to reconstruct putative evolutionary transformations of the arthropod hearts under these different hypothetical scenarios of arthropod phylogenesis.

**Keywords:** heart, morphology, evolution

OP-MO-05

**Comparative study of serotonin-like immunoreactivity in the branchial basket, digestive tract, and nervous system in tunicates**

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As one of the three major chordate taxa the highly diverse taxon Tunicata has always played a key role in considerations of evolutionary origins of vertebrates. Molecular phylogenetic studies of the relationships within Tunicata are highly contradictory and cladistic analyses of morphological characters for Tunicata remained limited. In order to come to a better understanding of chordate evolution, we comparatively investigated nine different tunicate species belonging to the five different higher tunicate taxa: Phlebobranchiata, Aplousobranchiata, Stolidobranchiata, Thaliacea, and Appendicularia using immunofluorescence labeling with antibodies against serotonin in conjunction with confocal laser scanning microscopy. We found that adult ascidians are comparable in regards to their respective patterns of serotonin-like immunoreactive (serotonin-lir) cells, whereas the planktonic tunicates differ in several aspects. The distribution patterns of serotonin-lir cells in tunicates suggest that serotonin-like immunoreactivity can behave as an independent character during evolution. While the distribution pattern of serotonin-lir cells agrees well with classical taxonomic groupings, phylogenetic interpretation remains inconclusive, as ad hoc hypotheses are always necessary to explain contradictory character distribution. Based on light-microscopically observed morphology, we could distinguish three different types of serotonin-lir cells, most probably functionally distinctive. These were approximately spherical serotonin-lir cells, possibly involved in the control of ciliary beating and mucus secretion, elongated serotonin-lir cells potentially involved in hormonal regulation of feeding, and serotonin-lir neurons that might be implicated in the initiation of locomotory behavior.

**Keywords:** 5-HT, evolution, Chordata

OP-MO-06

**Making heads or tails of *Xenoturbella bocki***

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*Xenoturbella bocki* is a marine worm found at the bottom of a Swedish fjord. It is a representative of the Xenacoelomorpha (Xenoturbellida and Acoelomorpha). Where it fits in the animal kingdom is highly controversial and has been argued about since its discovery in 1915. Its evolution remains a mystery - ranging from ancient ancestor to simplified close relative of chordates.

Until recently, *X. bocki* and *X. westbladi* have been the only two nominal species described within the Xenoturbellida but the recent discovery of four new *Xenoturbella* species from the deep waters of the eastern Pacific Ocean has brought up the potential for new investigations. Taking into account that most of our knowledge is based on "older" studies it is about time for a revised view of *X. bocki*.

We are comparing its morphology in close detail using techniques ranging from traditional histology over scanning electron microscopy (SEM) to more recent techniques like Micro Computed Tomography ( $\mu$ CT). Our revised perspective also comprises molecular biological features and we are presenting insights into the first gene expression studies in *X. bocki*. Similar experiments are performed in an acoel and hemichordate representative in order to discuss the gathered data of *X. bocki* in a broader context.

This combined approach of morphological and gene expression studies will hopefully help us to better understand the evolution of this controversial animal.

**Keywords:** Xenoturbella, Morphology, Evolution

OP-MO-07

***Scutigera coleoptrata* (Chilopoda) - past, present and future as model species in arthropod neuroanatomical research**

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Myriapods are chronically understudied with respect to their anatomy and morphology. This is, however, astonishing as their phylogenetic position within arthropods has been controversially discussed and a consensus is still in debate. For instance, on one hand they display conspicuous novelties of their body plan that require developmental explanations and on the other hand many characters are considered plesiomorphic for mandibulatan arthropods. Thus, myriapods in general have much to offer and for the last 10 years the centipede *Scutigera coleoptrata* became an intensive studied species in terms of its nervous system and sensory organs.

Here, focused analyses always revealed results that had an impact on general arthropod anatomy and phylogenetic implications. Indeed, characteristics of the nervous systems when compared to other arthropod taxa were promising to construct or support hypotheses about phylogenetic relationships as well as character transformation. As an example, the organization of single ommatidia or deutocerebral processing neuropils strongly gave support to the Mandibulata hypotheses and a sistergroup relationship to Tetraconata. However, the organization of visual neuropils contradicts previous transformation scenarios and roots evolutionary morphology of the visual system in mandibulatan arthropods. This talk will focus on recent investigations using myriapods as model-species and light up new questions to be answered in future research projects.

**Keywords:** Myriapoda, nervous system, evolution

OP-MO-08

**The shaft organ of *Scutigera coleoptrata* (Linné, 1758) (Chilopoda): tracing scolopidia back to ground pattern of Mandibulata?**

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In Myriapoda, many cuticular sensilla or even complex sense organs are still unknown. One example of the latter is the shaft organ at the antennal base of scutigermorphcentipedes. There wasn't a single study since its first discovery by Heinrich Fuhrmann (in 1922) who noticed minute sensory cones inside a cuticularized cavity on the scape of *Scutigera coleoptrata*. We provide a comprehensive description of the shaft organ. SEM and TEM revealed that the 10-15 sensory cones sitting in the cuticular cavity are surprisingly complex. Each sensory cone bears a huge terminal pore and includes three biciliated receptor cells and three sheath cells. The cilia emitted by receptor cells are different in length and possibly transduce mechanical stimuli via different mechanisms. Two receptor cells extend long cilia that project into the sensory cone where they adhere to a presumably expandable secretion pin plugging the terminal pore. This pattern is reminiscent of hygroreceptors found in various insects. The cilia of the third receptor cell are much shorter and terminate within depressions of the thickened dendritic sheath deeply below sensory cone. The dendritic sheath is connected to a scolopale-like structure built by the third sheath cell which strongly resembles scolopale cells in hexapod/crustacean scolopidia, except for the absence of an internal cuticular cap. For the first time, sensilla with scolopidial elements are recorded in Myriapoda. This finding may allow to add bimodal cone-/peg-like sensilla with scolopidial elements to mandibulate ground pattern, whereas unimodal, internalized, cap-enforced scolopidia remain a synapomorphic character state of Tetraconata.

**Keywords:** Sense organs, Evolution, sensilla

OP-MO-09

**Neck mobility in barn owls - analyzing adaptations underlying head rotations of more than 270°.**

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**Introduction:** Barn owls are well known for their high effectiveness in catching prey. Adaptations underlying this effectiveness are tubular-shaped eyes that allow good night sight and the heart-shaped ruff that functions as a sound amplifier. Both lead to a high frontal sensitivity as often seen in predators. Owls evolved an extraordinary head rotation capability allowing them to focus prey also in the periphery. Head rotations of more than 270° are possible.

**Objectives:** In earlier work we have described the shape of cervical vertebrae involved in head rotation (Krings et al. PlosOne 0091653, 2014). Here we use these data and knowledge about the joints between the vertebrae to examine mechanisms enabling the large head rotations.

**Material and methods:** Based on biplanar, high-speed X-ray films, micro-CT-scans and computer reconstructions of the vertebrae we used scientific rotoscoping to analyze movements. Furthermore, we manipulated forced rotations in an anaesthetized specimen and carcasses.

**Results:** Rotation capabilities were high in the upper and lower cervical joints while the flexibility of the middle region was limited. In the horizontal lower region of the cervical spine the rotation is by lateral bending (rolling). This causes a sidewise translation of the head. In the upper region the rotation was characterized by longitudinal axis rotation (yawing). The middle cervical joints contributed marginally to large head rotations.

**Conclusion:** These rotational movements can explain the large head rotations observed in owls. Furthermore, the movements in the individual joints are consistent with the anatomically based regionalization of the cervical spine of the barn owl.

**Keywords:** cervical joints, spine, CT-reconstructions

OP-MO-10

**Functional properties of microstructures on vertebrate skin**

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Vertebrates have conquered a wide range of climate zones and habitats. This process required concerted adaptations of the whole body. The skin, which constitutes the interface between the organism and the surrounding medium, plays a key role in the organisms adaptation to their environment. It protects the animals against chemical and mechanical influences, contributes to thermal control and locomotion, and determines the optical appearance fostering camouflage and signaling. The range of the available skin material is, however, genetically determined and therefore limited.

Here, adapted surface structures and materials in reptiles, teleost fishes, and mammals for camouflage and locomotion are presented.

Fish scales are well known for their protective functions and their optimizations to reduce drag. Here, scale adaptations of benthic fishes are presented optimizing the friction properties for burying. The skin of reptiles is a multifunctional material. Studies on its hierarchical system of scale, micro- and nanostructures revealed specific adaptation to climbing and limbless locomotion, optical and thermal requirements. A further topic are the mechanical properties of human skin.

**Keywords:** Scales, Fish, Reptiles

**OP-MO-11**

**Processing of nanofibres by cribellate spiders**

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Spider silk has been intensively investigated during the last decades, especially with respect to its mechanical properties, which are of high interest for technical applications. However, not only the mechanical properties of spider silk are amazing: Cribellate spiders' capture threads are a complex arrangement of three different types of silk. Within the production, the spiders produce, process and handle up to 40.000 nanofibres, surrounding two stabilizing and larger axial fibres in the final thread. Both are connected to each other by the third type of silk, thus building a stable complex. The complete process is nearly unstudied, mainly due to the small scale of the involved fibres, its complex arrangement and the occurring difficulties studying nocturnal and small animals. The importance of resolving the mechanism behind the production has however not only been emphasised by the biological side, but is also interesting for a technical reproduction.

We found a coordinated movement of the spinnerets involved in the assembly of the fibres. To process and handle the nanofibres, the spider employs a special structure on their fourth legs: the calamistrum, a row of specialized setae forming a comb. Although the calamistrum morphology can differ remarkably among different species, contact seems to occur always at a similar structured area. Those finding enabled us to pin down, how the calamistrum is processing and handling the cribellate nanofibres. With the help of a 3D-Model generated by FIB tomography we could visualize the process and provide a detailed insight in this nanoscale world.

**Keywords:** cribellate spider, nanofibres, 3D-Model

**OP-MO-12**

**How do leaf beetles generate propulsion of a hyper-elongated penis that is as long as their body length during copulation?**

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The occurrence of males having a hyper-elongated penis with a length of several times their body length is widespread in the animal kingdom, especially in insects. This phenomenon helps males to increase their probability of paternity by being chosen by females. Despite of this advantage, male insects with such a hyper-elongated penis are challenged by a length-related mechanical problem: the penis' insertion into the female genitalia requires precise propulsion control. To examine how males generate propulsion of their hyper-elongated penis into female genitalia, we examined the reproductive system of *Cassida* beetles by using different approaches including microscopy, computer tomography and computer simulations. The results show that muscles surrounding the penis are responsible for generating the propulsion force of the penis. A bending test and a material composition analysis using autofluorescences revealed a stiffness gradient along the penis, with the tip being softer than the rest. We performed a numerical simulation of this beetle system and demonstrated that a penis with such a stiffness gradient is inserted into female genitalia considerably faster than penises featuring other hypothetical stiffness conditions. It is likely that the stiffness gradient helps the penis to adapt to the complicated female genital shapes. In conclusion, the propulsion of the hyper-elongated penis is based on the contraction of the muscles being arranged along the penis, and the mechanism is reinforced by the stiffness gradient of the penis.

**Keywords:** Genitalia, Beetles, Biomechanics

## Morphology – posters

### PP-MO-01

#### Investigating the architecture of the brain in the Pacific White Shrimp *Penaeus vannamei* (Boone, 1931): evidence for corresponding brain structure and sensory input

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*Penaeus vannamei* (Dendrobranchiata, Decapoda) is best known as “Pacific White Shrimp” and currently the most important crustacean in commercial aquaculture worldwide. Although the neuroanatomy of crustaceans is well examined in representatives of reptant decapods (“ground-dwelling decapods”), there are just few studies focussing on shrimps and prawns. Hence, in order to obtain insights into the architecture of the brain of the shrimp *P. vannamei* we have used neuroanatomical methods including X-ray micro-computed tomography, 3D reconstruction, immunohistochemical staining combined with confocal laser-scanning microscopy and serial sectioning.

The brain of *P. vannamei* exhibits all prominent neuropils and tracts which characterize the ground pattern of decapod crustaceans. However, the size of some neuropils is salient: first of all, the huge lateral protocerebrum which comprises the visual neuropils as well as the hemiellipsoid body and medulla terminalis is remarkable. This observation corresponds with the large size of the compound eyes of *P. vannamei* and suggests that visual input is one of the major sensory modalities which this brain processes. In contrast, the remaining median part of the brain is relatively small. It is dominated by the paired antenna 2 neuropils, while the deutocerebral-chemosensory lobes play a minor part. The combination of a large visual system and pronounced mechanosensory input from the second antenna seems to adequately satisfy the requirement which a pelagic mode of life demands from these shrimps.

This study was supported by the DFG project HA 2540/16-1.

**Keywords:** Crustacea, neuroanatomy, sensory pathway

### PP-MO-02

#### Ultrastructure of tip-pore sensilla in *Argiope bruennichi* (Araneae, Araneidae)

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Chemical communication through volatile or contact pheromones is an important means to attract and find mating partners and assess their reproductive status. For spiders, behavioural studies demonstrated that their primary sensory mode is chemical sensing. Spiders are considered to use s-shaped sensilla with terminal pores as receiving structures. The only electrophysiological study available tested for contact chemoreception. We explore whether these sensilla are also used for olfaction and if similar sensilla on different body parts differ in internal structure and consequently in function.

In the wasp spider *Argiope bruennichi* males are attracted by a volatile sex pheromone emitted by virgin females. Tip-pore sensilla are found on all body appendages of males. We first explored the ultrastructure of tip-pore sensilla on tarsi of *A. bruennichi* males. The sensilla possess a thick cuticular sensillum shaft, a double-lumen divided in three canals and dendrites surrounded by a dendritic sheath. These ultrastructural features are comparable to gustatory tip-pore sensilla described for insects. However, the sensillum shaft shows breakthroughs on the innermost cuticular sheath suggesting that molecules can be transported through the cuticle and not only through the tip-pore. Thus, an olfactory function of tip-pore sensilla or a combined olfactory and gustatory function seems possible. As the next step we investigate the ultrastructure of leg podomers with and without contact to the substrate. This comparison may allow detecting morphological differences that might be related to functional differences. Furthermore, we conduct electrophysiological recordings on the sensilla to further clarify their function and specificity.

**Keywords:** chemical communication, tip-pore sensilla, Araneidae

**PP-MO-03**

**3D-Morphology of Inducible Morphological Defences in *Daphnia***

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Quantitative analysis of shape and form is critical in many biological disciplines as alterations reflect a visible result of e.g. changes in gene expression and physiology. Published 3D-shape capture and render methods produce models with arbitrarily numbered mesh points, preventing a direct comparison of individual point positions derived from different morphotypes. We here introduce a strategy that allows the generation of comparable 3D models, which can also be used for comparative finite element analysis. Specimens are scanned using confocal imaging or alternative strategies conserving information on the third dimension. Subsequently, surface structures are extracted for averaging, comparison and visualisation in Matlab. Via so-called 'casts', sets of statistically comparable point clouds can be acquired. After running a Procrustes-fit, calculation of displacement vectors between vertices of the defended and undefended model are conducted, enabling a coloured display of regions of interest by plotting the vectors' lengths as heat maps in Matlab. We tested our approach with different morphotypes of the pond-dwelling microcrustacean *Daphnia*, which is an excellent model for shape comparisons, since it forms various morphotypes under varying environmental conditions, e.g. predation pressure. In *Daphnia magna*, we found a significantly altered shape in reaction to *Triops*, despite this defence is quite unobtrusive. With our strategy we are now able to detect significant shape alterations in all spatial dimensions that may alter the handling and biomechanical performance in the mouthparts of respective predators.

**Keywords:** 3D-Morphology, *Daphnia*, inducible morphol. Defences

**PP-MO-04**

**Structure and distribution of different sensilla types in *Argiope bruennichi* (Araneae, Araneidae)**

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Spiders use various sensory modes to interact with their environment, to get kinesthetic information and to interact with other individuals on an inter- and intraspecific level. Accordingly, specific receiving structures such as mechano-, hygro-, thermo- or chemosensilla can be found on the spider's body.

We investigated the structure, quantity and distribution of tip-pore sensilla, trichobothria, slit sense organs and tarsal organs on all walking legs and pedipalps of *Argiope bruennichi* females by means of scanning electron microscopy. We chose *A. bruennichi* since its mating system is well explored and the pheromone involved in mate attraction is identified. We show that *A. bruennichi* females possess all sensilla types on all legs and pedipalps. Tip-pore sensilla that are suspected to be chemosensory organs do not occur on coxae and trochanters, but they are common on metatarsi and tarsi. The mechanosensitive trichobothria are distributed on the distal part of tibiae and on metatarsi. Strain detectors, so called slit sensilla, occur as lyriform organs (compound slit sensilla) next to the joints, mainly on ventral and lateral sides, or as single slit sensilla on all podomers mainly in rows. All tarsi possess a tarsal organ on the dorsal side. Apart from providing a survey of sensilla, our data pave the ground for targeted electrophysiological studies and ultrastructural analysis of sensilla and may contribute to a better understanding of the sensory ecology of spiders.

**Keywords:** sensory structures, SEM, Araneidae

PP-MO-05

**Serrations at slotted wing feathers of owls**

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**Introduction:** Owls have developed serrations at the leading edge of wing feathers that are supposed to be involved in reduction of flight noise. The serrations occur predominantly at 10<sup>th</sup> primary feathers. At some species with slotted wing tips, serrations can also be found on further primary feathers.

**Objectives:** While the serrations at 10<sup>th</sup> primaries are well investigated; serrations of further primaries are less well described. To fill this gap, we obtained morphological data of the serrations at 9<sup>th</sup> primaries of two nocturnal owl species, the long-eared owl (*Asio otus*) and the eagle owl (*Bubo bubo*).

**Materials & methods:** Ninth primaries of the two species were digitized with a scanner to estimate the emarginated feather part. Pictures from serrations at several positions of the outer vane were taken to obtain morphometric data of the serrations. A confocal laser scanning microscope was used to obtain three-dimensional reconstructions of single serrations.

**Results:** The serrations of 9<sup>th</sup> primaries from *A. otus* and *B. bubo* occur only at the emarginated feather parts that are exposed to the air flow. In general, the serrations show similarities to serrations at the distal feather part of 10<sup>th</sup> primary feathers but are less pronounced than serrations of the proximal part of 10<sup>th</sup> primaries.

**Conclusion:** The presence of serrations at 9<sup>th</sup> primaries supports the importance of serrated leading edges for the flight conditions of owls, including reduction of flight noise. The short serration length and differences in orientation are probably due to the orientation of the feather vanes or the air flow conditions at the wing tip. Further studies on the serrations at the wing tips are necessary to better understand the functionality in regard to slotted owl wings.

**Keywords:** Leading-edge serrations, owls, silent flight

PP-MO-06

**Neuroanatomy in the banded cleaner shrimp (Malacostraca, Stenopodidea) - Structure of mechanosensory neuropils in *Stenopus hispidus* (Olivier, 1811)**

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The pan-tropic decapod *Stenopus hispidus* (Stenopodidea, Malacostraca) is a cleaner shrimp. Its specific cleaning behavior, characterized by attracting and cleaning fish, as well as an exclusively monogamous life-style was investigated in a variety of behavioral studies. The most prominent head appendages of *S. hispidus* are the two very long and slender pairs of antennae (first and second antennae) which are used in attracting fish as well as for intraspecific communication. Thus, *S. hispidus* features a broad communicative repertoire which is considered to depend on superb motor skills and its underlying mechanosensory circuits in combination with sensory structures. Here, we investigated the brain of several specimens of *S. hispidus* by using histological sections, immunohistochemical labeling as well as X-ray microtomography in combination with three-dimensional reconstruction. These analyses show that especially mechanosensory neuropils associated with the first (deutocerebrum) and second (tritocerebrum) pair of antennae are markedly pronounced in relation to all other neuropils. Both neuropils share structural similarities, such as size and a characteristic striated layering to a unique extent within decapods. A striated layering of mechanosensory neuropils is known either from tritocerebral mechanosensory neuropils in a variety of crustacean species or from deutocerebral mechanosensory neuropils in myriapods and basal hexapods; but was never reported in both neuropils within one species. Hence, from an evolutionary perspective, *Stenopus* might be a good example of how functional demands shape the architecture of mechanosensory processing areas.

**Keywords:** nervous system, Crustacea,  $\mu$ CT

**PP-MO-07**

**Brain anatomy in the Japanese skeleton shrimp *Caprella mutica* (Malacostraca, Amphipoda)**

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The Japanese skeleton shrimp *Caprella mutica* Schurin, 1935, a representative of the Caprellidae (Malacostraca, Amphipoda), is an invasive species to European seas. It is natively occurring in shallow areas of the Sea of Japan, but has extended its range since its first description in 1935, to both northern and southern hemispheres within only a few decades. Although amphipods are distributed globally and can be highly abundant, neuroanatomical studies in this taxon are scarce. *Caprella mutica* features a strong sexual dimorphism regarding its external morphology which holds also true for the majority of amphipod species. We investigated the brain of male and female specimens of *C. mutica* to give an overview of the general brain anatomy by the use of immunohistochemistry and X-ray microtomography in combination with three-dimensional reconstruction. With the aid of morphometry, we aim at the identification of a putative neuroanatomical representation of this sexual dimorphism within the brain, which was previously described from deutocerebral neuropils in a few insect and other malacostracan species (e.g. in Euphasidacea, Mysidacea, and Brachyura).

**Keywords:** Crustacea, nervous system,  $\mu$ CT

**PP-MO-08**

**Phylogeny of Malacostraca reconstructed considering pleon characters**

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The phylogeny of Malacostraca is still controversially discussed, though many attempts were made for clarification using various sources of information. Remarkably, the hind-body region, the so-called pleon, was never in the focus to enlighten malacostracan evolution. Our current study concentrates, therefore, on the morphology of the pleon in order to test its capacities for a more robust reconstruction of the phylogeny for Malacostraca. Our interpretations summarized: In the stem species of Malacostraca the tagma pleon consisted of seven segments (pleomeres) and a conical telson with anus and furca. The anterior six pleomeres bore appendages (pleopods), each consisting of eight coxal sclerites and a cylindrical basipod carrying exopod and endopod. The pleon was filled with the gut, dorsal heart, and straight muscles running through pleomeres. In Eumalacostraca sensu lato (comprising Bathynellacea and Eumalacostraca sensu stricto) pleomere 6 and 7 fused, whereby pleopod 6 moved to a postero-lateral position (= uropod), contrasting the anterior pleopods, remaining in a midventral position. Other pleon conditions are plesiomorphically retained from the malacostracan ground pattern in this taxon. Bathynellacea changed some of these conditions due to their interstitial life style (reduction of pleopods, fusion of pleomere 6 and telson) but retained the plesiomorphic pleonal musculature and furca, which led us to place them in this more basal position as traditionally hypothesized. In Eumalacostraca sensu stricto (Hoplocarida + Caridoida) a tail fan occurs made of the uropods and a flattened and elongated telson. Furthermore, the pleonal muscles are drilled. Lastly, Caridoida display a twisted musculature, which is even more complex and enables the animals to execute the so-called "caridoid escape reaction", an autapomorphy of this taxon - and lacking in Bathynellida.

**Keywords:** Phylogenetic Systematics, 'Abdomen', Tail fan

PP-MO-09

**Spider attachment setae explored using nanofocus scanning X-ray diffraction**

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The hairy attachment system of hunting spiders enables them to walk vertically and upside-down on rough and smooth surfaces without the use of gluey secretions. This ability is provided by the attachment pads situated on the distal end of each walking leg comprising hundreds to thousands of specially structured setae facing the substrate. Our study was aimed to gain in-depth understanding of the working principle of the attachment process of single setae to a substrate.

We used nanofocus scanning X-ray diffraction in order to reveal structurally determined material properties of the contact elements (microtrichia with terminal spatulae) on the same individual setal tips attached and not attached to a substrate in the same experiment. The experiments on fresh single setae of the large hunting spider *Cupiennius salei* were performed at the nanobranch of beamline ID13 of ESRF (Grenoble, France). The setal tips were scanned in windows sized 20 × 20 μm<sup>2</sup> at a resolution of 200 nm. For the first time, we obtained quantitative information about both the structure and orientation of the seta (thickness 10 μm) and its contact elements (width 1 μm) and their changes upon attachment. Our results show that the functional setal tips are three times more X-ray dense than the more distal setal shaft. This can be explained by more densely packed microtrichia. The uniformity of their orientation increases upon attachment. Single spatulae change their orientation by 90° indicating a self alignment in parallel with the substrate.

Ongoing research will further elucidate the structural composition of the setae, the deformation of their cuticle microfibrils, and the orientation change of the contact elements leading to the formation of close contact with the substrate resulting in strong attractive forces crucial for the animal's attachment.

**Keywords:** Spiders, Attachment, Nanobeam X-ray diffraction

PP-MO-10

**Brain structure of the jumping spider *Marpissa muscosa* (Arachnida: Salticidae), an arthropod with extraordinary cognitive abilities**

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Jumping spiders are known for their elaborate cognitive abilities. The underlying brain structures, however, are largely unknown. We explored and described the anatomy of the central nervous system (CNS) in the jumping spider *Marpissa muscosa* by means of paraffin histology, microCT, immunohistochemistry and whole-mount immunolabelling. We focused on the neuropils as the processing and integrating centers of the brain.

In the prosoma of *M. muscosa*, the CNS is a clearly defined mass that surrounds the esophagus. The anterior part, the protocerebrum, comprises nine bilaterally paired neuropils, including the mushroom bodies (MB) and one unpaired midline neuropil, the arcuate body (AB). Further ventral, there are cheliceral neuropils (deutocerebrum) and a pair of pedipalpal neuropils (tritocerebrum). The synapsin-immunoreactivity of all neuropils is generally stronger than the allatostatin-immunoreactivity.

The most prominent neuropils, the mushroom bodies (MB) and the arcuate body (AB), are suggested to be higher integrating neuropils of the arthropod brain. Both are connected to the visual neuropils in *M. muscosa*. The MB is connected to first and second order neuropils of the lateral eyes, and the AB to the second order neuropils of the anterior median eyes through an optic tract.

The connection of the neuropils and the eyes as well as their large size corroborates the hypothesis that these neuropils play an important role in cognition and locomotion control of jumping spiders.

**Keywords:** neuroanatomy, neuropils, immunohistochemistry

**PP-MO-11**

**Human craniometry reveals express train into Polynesia**

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Several models for the human colonization of Polynesia have been proposed. For instance, the express train model is the most accepted theory, which suggests a rapid intrusion of aboriginal Taiwanese people into uninhabited Polynesia and little interaction with aboriginal neighbors. However, other surveys like craniometric analyses seem to support the theory of a slow migration tempo, and thus the admixture of those proto-Polynesians with Melanesians (slow boat model). Thus, the purpose of this study was to reanalyze published craniometric data in order to check for indications of support for the express train scenario. Therefore, means, standard deviations, and sample sizes for 24 standard cranial measures of 1719 individuals have been collected for Austronesian-speaking populations from the Pacific and pooled for samples from identical populations. For that data set of 30 unique populations a NJ tree was calculated using Euclidean distance. Additionally, mean variation coefficients have been calculated as measures of phenotypic diversities within populations. Contrary to previous findings, the analysis of this big data sets revealed a strong association between Polynesian islanders and aboriginal Taiwanese people that belong to the same phylogenetic cluster. Additionally, there is another strong relation between Taiwanese with inhabitants of Indonesia, too. On the other hand, the analysis of within-population diversities indicated three geographical spots with increased phenotypic diversity in comparison to surrounding populations which may indicate regions of potential admixture of aboriginal people and proto-Polynesian migrants. Thus, these findings support the theory of an express train migration into Polynesia.

**Keywords:** Craniometry, Polynesia, Express train

**PP-MO-12**

**The parasitic way of thinking - reconstructing the brain of *Gordius aquaticus* (Nematomorpha)**

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Horsehair worms (Nematomorpha) are related to nematodes and scaldiphorans (Priapulida, Kinorhyncha, Loricifera) that all have a particular type of brain called the cycloneuralian brain. This is ring-shaped around the pharynx and composed of a neuropil with anterior and posterior somata. Nematomorphs do not show a typical cycloneural brain architecture and available reconstructions do not show a uniform picture. Alterations in brain structure may be due to the parasitic lifestyle of nematomorphs. To clarify whether there are cycloneuralian patterns in the nematomorph brain we investigated the anterior end of *Gordius aquaticus* with histology, immunohistochemistry and  $\mu$ CT. 3D reconstructions were made from serial histological sections. The brain is composed of a central neuropil which is an anterior enlargement of the unpaired ventral nerve cord and a ring-shaped structure with somata. A pharynx/esophagus is not present. In addition to the brain, a peripheral, basiepidermal nerve plexus could be shown to be present. We interpret the structure of the brain as being a consequence of the reduction of the pharynx. The neuropil occupies a central position and the somata either fuse or are partly reduced into one massive ring-shaped structure.

**Keywords:** Nematomorpha, Nervous system, brain

**PP-MO-13**

**Ontogenetic transformation of a water to a land nose: terrestrial adaptations of the hermit crab olfactory system during larval development**

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During the evolutionary history of Crustacea, several taxa independently invaded land to establish a terrestrial life style. Terrestrial crustaceans include for example members of the hermit crabs (Anomala), such as the giant robber crab *Birgus latro* (Linnaeus, 1767). These animals depend on the ocean for reproduction but conquer the land during late larval development. However, the majority of hermit crabs, like the common hermit crab *Pagurus bernhardus* (Linnaeus, 1758) are fully marine. During ontogeny, both species go through a series of four pelagic larvae (zoëa stages) before they develop into a marine benthic megalopa, which enters an empty gastropod shell. The marine megalopa of *B. latro* finally invades the terrestrial habitat. During larval settlement and metamorphosis to the megalopa stage as well as during the transition to land, the larvae undergo drastic changes in habitat, morphology, behavior and physiology.

We are interested in the development of the olfactory pathway of anomuran larvae and its possible ontogenetic adaptation to the terrestrial habitat. Therefore, we used scanning-electron microscopy and fluorescence microscopy for the analysis of the peripheral olfactory pathway as well as X-ray micro-computed tomography, histochemical and immunohistochemical stainings combined with confocal laser scanning microscopy to analyse the olfactory brain centers. Comparing the developmental stages of *B. latro* (terrestrial as adult) and *P. bernhardus* (marine), we found shorter and stouter aesthetascs as well as fewer plumose setae on the antennae and enlarged deutocerebral chemosensory lobes in the brain of *B. latro* juveniles as possible adaptations to the terrestrial lifestyle. Supported by the DFG: Ha 2540/13-1.

**Keywords:** olfactory system, Anomura, terrestrial adaptation

**PP-MO-14**

**Re-Investigation of the visual system of Opiliones**

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Previous studies of the visual system of Opiliones have yielded inconsistent results concerning the number and morphology of its neuropils. Hence in this study we analyse the neuroanatomy of the visual system of several harvestmen species (*Platybunus pinetorum*, *Rilaena triangularis*, *Opilio canestrinii*, *Phalangium opilio*, *Leiobunum spec.*) with different neuroanatomical techniques (Cobalt backfills, Dil/DiO labelling, Wigglesworth technique, 3D-reconstruction in Amira).

We identified the following structures within the visual system of the opilionid brain: The optic nerves, which project ventrally from the two eyes to the protocerebrum, consist of several bundles of retinula axons. Distal to the optic lobe the bundles conjoin and enter the optic lobe and the visual neuropil complex.

These results allow a detailed comparison of the opilionid visual system with that of other previously studied chelicerate taxa (Pycnogonida, Xiphosura, Scorpiones, and Araneae) and contribute neurophylogenetic arguments to the lively discussion about the phylogeny of Chelicerata.

**Keywords:** Opiliones, visual system, neuroanatomy

PP-MO-15

**The ventral nerve cord and individually identifiable neurons of the centipede *Lithobius forficatus***

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The phylogenetic position of Myriapoda within arthropods has been controversially discussed for decades and a consensus is still in debate. Characteristics of nervous systems in the past have been compared between arthropod taxa and successfully used to construct or support hypothesis about phylogenetic relationships. In the ventral nerve cord of many arthropod taxa, individually identifiable neurons have been reported. Comparisons of these neurons have contributed new arguments in the discussion on arthropod phylogeny and favored the Tetraconata hypothesis. However, only a low number of species and transmitter systems (mostly serotonin) have been investigated, and only one species of centipedes has been included in such analyses (Harzsch 2004 J Morph).

Here we analyze the ventral nerve cord of the centipede *Lithobius forficatus* (Myriapoda, Chilopoda), to (1) characterize specific ganglia and (2) to illustrate individually identifiable neurons. In a multi-method approach we used classical histology, immunohistochemical experiments with different transmitter systems combined with confocal laser-scanning microscopy, backfilling with neuronal tracers, as well as X-ray micro-computed tomography to explore ventral nerve cord anatomy. The ventral nerve cord is composed of well separated ganglia with eight pairs of nerves. Within the completely fused hemiganglia, distinct neuropils are located in the ventralmost part. Serotonin-immunoreactive somata are distributed in characteristic clusters, anterior and posterior serotonin-immunoreactive neurons possess contralateral projections. Results from other transmitter systems (RFamid, allatostatin, histamine) also show characteristic patterns.

**Keywords:** nervous system, imaging, microCT

PP-MO-16

**A Hard Nut to Crack:  
Revealing Evolution Tooth by Tooth**

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**Introduction:** The paludomids of Lake Tanganyika are the most spectacular species flock among gastropods, with c. 40-60 species of highly divergent morphologies. It has been shown that they represent ancient lineages that probably originated in the adjacent river systems much earlier than the formation of the lake basin. As a consequence, most of their broad spectrum of phenotypes and their unique morphological features are not necessarily to be interpreted as adaptation in context of intralacustrine radiation within the lake.

**Objectives:** In this study we re-examine and evaluate the distinct radula morphologies of this species flock and its surrounding river systems, mapped on a revised molecular backbone phylogeny using e.g. 16S rRNA.

**Materials & methods:** Radulae from representative taxa collected during an earlier study in 1995 were visualized using SEM. Radula morphologies are characterized, evaluated in a cladistics analysis and used for an ancestral state reconstruction.

**Results:** The results of the ancestral state reconstruction allow hypotheses as to the evolution and adaptation of radula characteristics and to develop possible scenarios of their role in the evolution of this proposed adaptive radiation. The distinct radula types can not only be used for systematic-phylogenetic purpose; they also provide possible insight into ecologically divergent lineages.

**Conclusion:** It remains to be tested whether these differences hint at environmental-phenotype correlations (e.g. habitat as proxy for trophic specialization). We plan to use in an interdisciplinary approach new visualization techniques and physical technologies to further test this. We anticipate this paludomid species flock to provide an ideal model system in the search for drivers of speciation under specific ecological conditions.

**Keywords:** Radula, Morphology, Ecology

**PP-MO-17**

**Limb co-variation and fluctuating asymmetry in the *Mus musculus* hybrid zone**

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Two subspecies of the house mouse—*Mus musculus musculus* and *Mus musculus domesticus*— form a narrow hybrid zone in central Europe. Hybridization may serve as a source of genetic variation for adaptive evolution. To discern whether a genetic difference is adaptive or not, it is important to consider how it influences the resulting phenotype. Natural hybrid zones have been shown to be a suitable source for exploring the genetic basis of complex traits, including skeletal characters.

Fore- and hind limb in tetrapods are serially homologous structures that show patterns of co-variation produced by joint genes involved in limb development. Characters that co-vary due to sharing common developmental factors are explained by morphological integration.

Furthermore, phenotypic variability could be affected through reduction of developmental stability. It can result in small random differences in two sides of a bilaterally symmetrical character of an organism that are produced by the same genome (i.e. fluctuating asymmetry).

In this study, we investigate co-variation between and within fore- and hind limbs and fluctuating asymmetry in samples from the mouse hybrid zone using 3D landmarks and geometric morphometrics. Further, we are performing a genome-wide association study (GWAS) in first generation lab-bred offspring of wild-caught hybrid mice to identify loci associated with limb variation. We will report on the first results of this analysis.

**Keywords:** Morphological integration, Fluctuating asymmetry, GWAS

**PP-MO-18**

**The importance of surface wettability for permanent underwater adhesion of *Balanus improvisus***

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Each surface exposed to seawater will be overgrown by marine hard foulers like barnacles. In general, permanent underwater adhesion of marine organisms is based on glue secretions. Since strong attachment can only be achieved, if the glue is able to readily wet the surface before hardening, adhesion basically represents a wetting problem. Here, we demonstrate the importance of the wetting ability of the glue secretion of *Balanus improvisus* for strong attachment. We compared the amount of barnacles fouled on following substrates: (1) silicone rubber covered with mushroom-shaped surface microstructures (MSM), (2) silicone rubber covered with micropillars in the dimensions similar to MSMs, (3) a smooth control made of the silicone rubber and (4) a smooth control made of PMMA. The surfaces have been exposed to seawater for 17 weeks from 29 May 2014 to 25 September 2014 in a field trial in the Kiel Fjord, Germany. For both MSMs and micropillars, we observed the same number of settlement events of cyprid larvae of *B. improvisus*. After 13 weeks all barnacles were detached from MSMs. In contrast, 42% of barnacles remained attached on micropillars after 17 weeks. We hypothesize that due to the difference in surface topography, both types of microstructured surfaces have different wetting resistance. We investigated residues of barnacle cement after detachment in a scanning electron microscope and barnacles in contact with both microstructures using a  $\mu$ -CT. The latter results showed that while barnacle cement is only able to wet the terminal end structures of MSMs, micropillars are completely wetted. Barnacle cement creates a much higher contact area on micropillars than on MSMs. In conclusion, wetting resistance of microstructured surfaces is of key importance for the long-term attachment ability of marine organisms and may be exploited for anti-fouling purposes.

**Keywords:** Barnacle adhesion, wettability, re-entrant surface

**PP-MO-19**

**Influence of ambient humidity on the attachment ability of ladybird beetles *Coccinella septempunctata* (Coleoptera, Coccinellidae)**

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Many insects possess adhesive foot pads that enable them to scale smooth vertical surfaces. The function of these organs may be highly affected by environmental conditions, such as the surface topography of the substrate. Ladybird beetles (Coccinellidae) possess dense tarsal soles of tenent setae, supplemented with an adhesive fluid. We studied the attachment ability of the seven-spot ladybird (*Coccinella septempunctata*) at different humidity by horizontal traction experiments. We found that both low (15%) and high (99%) relative humidity lead to a decrease of attachment ability of this species. The significantly highest attachment forces were revealed at 60% humidity. This relationship was found both in female and male beetles, despite of a microstructural difference in the structure of adhesive setae and a significant difference in the total forces. These findings demonstrate that not only dry adhesive setae are affected by ambient humidity, but also setae that functionality is mainly based on the capillarity of an oily secretion.

**Keywords:** adhesion, humidity, sexual dimorphism

**PP-MO-20**

**When the button is gone: Pleon attachment in male and female *Carcinus maenas* (Decapoda: Brachyura: Portunidae)**

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The pleon of eubranchyuran crabs is typically folded underneath the cephalothorax and secured in this position with specialized holding structures. Most prevalent is a press-button mechanism, which is present in juveniles of both sexes and adult males. The press-button consists of a protrusion on the 5th thoracic sternite and a pit on 6th pleonal segment (Guinot & Bouchard, 1998) The aim of the study was to evaluate which part of the pleon and the sterno-abdominal cavity contributes to holding the pleon in its folded position and whether there are differences between the sexes. Adult male and female specimens of the European Green Crab *Carcinus maenas* from the Baltic and the Wadden Sea were subjected to tensile force testing. Attachment forces of the press-button mechanism in both sexes were tested in air and under water. In males, measurements with intact sternal protrusions and without them were performed. Female crabs were tested with setae on the edge of the pleon and intact pleopods as well as without both structures. In males, a wide range of maximum forces were obtained, but even the weakest performances had in common that the pleon stays firmly secured in the folded position. It was shown, that pleon attachment is possible in different environments. The pleons of adult females stay attached well in air, but not underwater. Attachment is achieved in males due to press-button structures only. In females, who lack the press-button mechanism, a suction effect can be observed in air, which results from a collective effect of residual moisture, setae on the edge of the pleon and the strongly ramified pleopods.

Guinot & Bouchard, 1998, *Zoosystema* 20(4), 613-694.

**Keywords:** Eubranchyura, pleon attachment, tensile force testing

**PP-MO-21**

**Palaeo-morphology: extracting the maximum information from extinct arthropods preserved in amber**

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Fossil remains of arthropods are an important source for investigating morphological aspects of species that lived millions of years ago. With this, they can help to reconstruct evolutionary changes in deep time. Especially fossils enclosed in amber are often preserved in nearly life-like conditions, which allows studying also very fine structures such as setae or details of eyes. However, the visualisation of these details is often challenging; limitations can arise from:

- scratches and irregularities of the surface,
- inclusions, e.g. of gases, other animals, remains of plants,
- reflexions, e.g. caused by different layering events of amber in one piece.

We present here some examples of arthropods in Baltic amber (40-50 mya) and show different methods to reduce these limitations by using micro- and macro-photography, in addition to autofluorescence microscopy as well as micro-computed-tomography ( $\mu$ CT). For micro- and macro-photographic documentation of specimens, our ambition is to establish a low-cost and transportable setup, which is especially useful for investigating specimens directly in museum collections.

Images were processed with different mainly free accessible software, such as ImageAnalyzer, CombineZM/ZP and Drishti. The combination of these methods allows us to generate high-resolution composite images in 2D and 3D for documenting as much structural information as possible. With these images, we are also able to do extensive comparisons to extant species, for reconstructing morphological changes within several millions of years, which can add important components for the reconstruction of the evolution of arthropods.

**Keywords:** Imaging, multi-method approach, fossil arthropods

**PP-MO-22**

**Fluid modeling of the fish lateral line based on 3D reconstructions**

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The lateral line of fish is a sensory organ used to detect minute water motions. The lateral line consists of up to several thousand mechanoreceptors (called neuromasts) located on the epidermis or in lateral line canals. Neuromasts are distributed across the head, trunk and tail fin. Especially the anterior part of the lateral line can exhibit a complex arrangement of canal structures including small canal pores. Moreover, a striking diversity in lateral line morphology exists among different fish species. Here we report various reconstruction techniques of the head of Ide (*Leuciscus idus*), a European cyprinid, by means of photogrammetry, 3D-Laser scanning and contrast-enhanced Micro Computer Tomography. We demonstrate the advantage of our technological approach in the context of morphological investigations and explore the complex interactions between fish and their hydrodynamic surrounding by means of Finite Element Modeling using actual three-dimensional reconstructions.

**Keywords:** Lateral Line, Finite Element Modeling, Flow

**PP-MO-23**

**Comparative study of different contrasting agents and protocols for SR $\mu$ CT imaging of soft-bodied invertebrates**

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Non-invasive imaging such as synchrotron radiation-based micro computer tomography (SR $\mu$ CT) and laboratory source based CT systems has become a widely used tool in zoological science. However, the contrasting required for an improved identification and discrimination level of soft tissues in x-ray imaging has mainly been optimized for medical applications and to some extent in "model organisms" (e.g. vertebrates), whereas the best approach for studying soft-bodied invertebrates remains unclear. Therefore, we applied different contrasting agents and protocols to assess the internal anatomy of the onychophoran *Euperipatoides rowelli* using SR $\mu$ CT. These included osmium tetroxide (OsO<sub>4</sub>), phosphotungstic acid (PTA), ruthenium red (RR), OsO<sub>4</sub> vapour, iodine, as well as a non-contrasted specimen (pures absorption) and a single grating differential phase-contrast. Grey value measurements from different tissues were used for quantitative comparisons and show that the contrast within and between different tissues varies substantially depending on the approach used. In general, OsO<sub>4</sub> provides the best overall contrasting property, followed by RR. Broader tissue differentiations are possible with PTA, although the penetration of this agent is limited. Moreover, embedding specimens in resin prior to analyses slightly reduces the tissue contrast. Quantitative analysis revealed an overlap among grey values from different tissues, irrespective of the approach used, thus preventing these tissues from being separated automatically by software tools. Nevertheless, manual segmentation and 3D rendering of organs are possible for all of our data sets. Hence, the best approach should be selected based on the target structure.

**Keywords:** Morphology, Peripatopsidae, Velvet worms

**PP-MO-24**

**Flight adaptations in peregrine falcons (*Falco peregrinus*)**

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While diving peregrine falcons (*Falco peregrinus*) reach a speed of up to 320 km h<sup>-1</sup>. During a dive and the subsequent pull-out, peregrines have to resist high forces. We investigated the bones and 15 flight muscles of the arm skeleton and the shoulder girdle of peregrine falcons. For comparison, we extended our investigations to European kestrels (*Falco tinnunculus*), sparrow hawks (*Accipiter nisus*) and pigeons (*Columba livia*), i.e. to species that differ in flight styles and do not dive with high speeds. The volumes of the muscles holding the wing to the body (*M. coracobrachialis posterior*, *M. latissimus dorsi pars cranialis* and *pars caudalis*) were biggest in *F. peregrinus*, even when normalized with respect to body mass. Moreover, the normalized bone mass of the entire arm skeleton and the shoulder girdle (coracoid, scapula, furcula) was also significantly higher in *F. peregrinus* than in the other species. The midshaft cross-section of the humerus of *F. peregrinus* had the highest specific bending stiffness per body mass and the biggest second moment of area. The mineral densities of the humerus, radius, ulna, and sternum were highest in *F. peregrinus*, indicating a larger overall stability of these bones. Both, the muscles holding the wings to the body and the bones of the arm skeleton were strongest in peregrine falcons.

**Keywords:** peregrine falcon, bird flight, flight adaptations

PP-MO-25

**Damping behaviour of primary flight feathers of the common wood pigeon (*Columba palumbus*)**

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The avian feather is mainly composed of keratin and exhibits a unique combination of outstanding mechanical properties, such as robustness and flexibility while maintaining low weight. In spite of previous extensive studies, the damping properties of the feather are still poorly studied. The aim of this study was to investigate the microstructure and the damping characteristics of primary wing feathers of the common wood pigeon *Columba palumbus*, which consist of the central rachis and the vane.

For this purpose, scanning electron microscopy (SEM) was used to obtain detailed information about the hierarchical microstructure of feathers. Laser Doppler vibrometry (LDV) was utilized to measure the damping properties of feathers (decay constants at fundamental frequencies) in the plane of the vane and perpendicularly to the vane.

The results show that there are two fundamental vibration modes in both directions, which are responsible for specific damping property of the feather. We demonstrated that the vane had relatively small influence on the decay constants in primaries. Only the vibration of mode 1 (low frequency) perpendicular to the vane plane decayed quicker in the feather with vane than in that without vane, supposed, mainly due to the air friction. The structure-function relationship of damping in feathers is discussed.

**Keywords:** feather, damping, microstructure

PP-MO-26

**Morphology of sound producing organs can be used as hint for males' attractiveness in the bushcricket *Poecilimon ampliatus*.**

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**Introduction:** Body size in many species indicates male's quality. In bushcrickets the sound generating apparatuses and thereby the acoustic signals emitted may be influenced by body size. In *Poecilimon ampliatus* (Orthoptera: Tettigoniidae), the calls are produced only by males, which rub together the forewing structures scraper and teeth. The body mass of the singers is related to the quality of the emitted song and lead therefore to different female preferences.

**Objectives:** The aim of this study was to investigate if morphological wing parameters correlate with male body dimensions and can be used as a predictive indicator of a male's attractiveness.

**Materials & methods:** The relationships between body size, body mass and morphology of sound production structures (wing area, length of the stridulatory file, number, density and length of stridulatory teeth) in adult males of *Poecilimon ampliatus* was measured. Allometric relations and stepwise multiple regression analyses were performed between body dimensions and wing parameters.

**Results:** Body weight and body size were positively correlated with wing area and length of the stridulatory file. However, the absolute number and density of stridulatory teeth were negatively correlated with body weight. Thus, heavier males possess bigger sound producing organs, which present fewer, less densely packed stridulatory teeth.

**Conclusion:** Size-dependent differences in morphology of the sound producing organs in bushcricket males lead to more or less attractive songs. A female preference towards heavy males (already shown in previous studies) is the consequence. Thus, the morphology of the song producing apparatuses is an indicative feature of a male's attractiveness.

**Keywords:** Sound structures, Allometry, Sexual selection

**PP-MO-27**

**Push or pull? The light-weight architecture of the *Daphnia pulex* carapace is adapted to withstand tension, not compression**

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*Daphnia* (Crustacea, Cladocera) are prominent for their ability to form morphological adaptations thwarting the threat of coevolved predators. In addition to spines and helmets, the carapace, encapsulating the main body, offers protection. It is an evagination of the head integument and thus a double layer of the integument. The two integumental layers are interconnected by small pillars, which were previously described as providing higher mechanical stability against compressive forces. Following this hypothesis, we analyzed the carapace structure using histochemistry in combination with light and electron microscopies. Furthermore, we measured the hemolymphatic gauge pressure, because the space between the integumental layers of the carapace is filled with hemolymph. We found the distal integument of the carapace to be significantly thicker than the proximal. The pillars appear fibrous with slim waists and broad, sometimes branched bases where they meet the integument layers. Based on these findings, we give a new hypothesis describing the functionality of these pillars. We suggest that pillars resist tensile loads rather than compressive forces.

**Keywords:** *Daphnia*, Carapace, Cuticle

**PP-MO-28**

**Feeding tools with complex micro- and nanoscale composite architectures in marine planktonic copepods**

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Copepods are among the dominant marine zooplankton taxa and play an important role in particle and energy fluxes of the marine water column. Their diets often comprise large proportions of diatoms with silicified frustules that provide mechanical protection against grazers. Despite of this protection, many copepods are able to break even the most stable frustule types. This ability requires specific feeding tools with mechanically adapted architectures, compositions and properties. Copepods use their mandibular gnathobases to grab and, if necessary, crush the food items. By applying confocal laser scanning microscopy, electron microscopy and micro-particle-induced X-ray emission, this study revealed in great detail the gnathobase morphology and material composition of copepods that mainly feed on diatoms. The gnathobases possess compact silica-containing tooth-like structures that are complex microscale composites with siliceous cap-like structures located on chitinous exoskeleton sockets. These sockets are connected with rubber-like bearings formed by structures with high proportions of the soft and elastic protein resilin. In addition, the cap-like structures exhibit a nanoscale composite architecture. They contain some amorphous silica and large proportions of the crystalline silica type  $\alpha$ -cristobalite and are pervaded by a fine chitinous fibre network that probably serves as a scaffold during the silicification. These intricate composite structures are assumed to be the result of a coevolution between the gnathobases and the frustules in an evolutionary arms race, and they very likely increase both the performance of the silica-containing tooth-like structures and their resistance to mechanical damage.

**Keywords:** Marine planktonic copepods, Mandibular gnathobases, Silica-containing composites

PP-MO-29

**To be or not to be - the issue of the *velum* in the reproductive system of spider crabs (Decapoda: Brachyura: Majoidea).**

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The reproductive system of female true crabs (Eubranchyura) is a complex system consisting of five paired structures: *ovaries*, *oviduct*, *seminal receptacle (SR)*, *vagina* and *vulva*. When the female ovulates, mature oocytes move through the oviduct that connects ovaries and SR. Within the SR sperm can be stored for extended periods after copulation. Arriving in the SR, the mature oocytes are mixed with the stored sperm and become subsequently extruded through the sternal vagina (and vulva). The reproductive system of the Majoidea (spider crabs) has been subject of various studies. For several majoid species, a division of the seminal receptacle into a secretory dorsal “storage chamber” and a cuticle ventral “fertilisation chamber” has been described. A characteristic structure separating both chambers is the *velum*, an iris-diaphragm like muscular sheet that allows females to control the amount of sperm used for fertilisation. Here we present a study on the reproductive systems of the two majoid species, *Mithraculus sculptus* and *Stenorhynchus seticornis* using morphological techniques such as  $\mu$ CT scans and 3D-reconstruction, complemented with (paraffin) histology. Our results show that no *velum* is present in any of the species studied. A comparison of our results with those of other studies, allow for the conclusion that some cuticle structures within the SR may have been misinterpreted and mistaken for a *velum* by previous authors.

Thus, the concept of a *velum* in Majoidea and the hitherto accepted division of the SR needs to be reconsidered. Our results cast a new light on majoid reproduction and demonstrate the importance of methods such as 3D-reconstruction for the spatial understanding of morphological characters.

**Keywords:** spider crabs, reproduction, velum

PP-MO-30

**Plesiomorphic or derived? - The unusual morphology of the female reproductive system of the dorippoid crabs *Medorippe lanata* and *Dorippe quadridens* (Brachyura; Crustacea; Dorippidae)**

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The male and female copulatory organs of crabs form a complex interacting system for sperm transfer and sperm storage. The female reproductive system consists of paired ovaries and sperm storage organs (seminal receptacles) which open via the vaginae onto the females ventral body side. The seminal receptacles of the Eubranchyura are connected to the ovaries and during ovulation mature oocytes are led from the ovary into the receptacle, thus fertilisation is internal. Different character states in the morphology of the sperm storage organs are represented among brachyuran subgroups but their evolutionary context is still uncertain. The Dorippoidea with several plesiomorphic characters, are discussed as one of the early diverging lineages within the Eubranchyura. Due to their role as prime candidates for the assumed plesiomorphic character states in the reproductive system of the Eubranchyura, we investigated the vaginae, seminal receptacles and ovaries of *Medorippe lanata* and *Dorippe quadridens* (Dorippidae) with histological methods. Despite the hypothetical systematic position, the female reproductive system of the Dorippidae shows a number of putatively derived character states: a concave vagina (sensu Hartnoll 1968) and a ventrally located oviduct orifice which classifies the receptacle as of the ventral-type (sensu Diesel 1989) in a wider sense. In contrast to other Eubranchyura, the oviduct does not enter the receptacle, but rather is connected to the vagina and bordered by specific valve-like cuticle structures. The female reproductive system of *Dorippe quadridens* is remarkable in further aspects because the SR is completely cuticle lined and an accessory sperm storage structure, the bursa, is present.

**Keywords:** sperm storage, seminal receptacle, histology

**PP-MO-31**

***Tagmatisation in camel spiders with a focus on the special condition of the anterior body***

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Body organisation (tagmatisation) of arthropods is still not well understood in many in-groups, especially within Euchelicerata and its in-group Arachnida. Here we describe the body organisation of solifuge “spiders”. These are ferocious-appearing arachnids with a huge first pair of raptorial appendages (chelicerae). Functional needs of these influence the shape of the anterior body part dramatically. In consequence, the main axis appears “distorted”, and it remains unclear which segments contribute to which areas of the body. We used fluorescence microscopic and computer-tomographic (CT) imaging to study the tagmatisation of especially the anterior body area, both dorsally and ventrally.

It is generally assumed that the most anterior dorsal sclerotisation, the propeltidium, is formed by the first five segments, including the fourth appendage-bearing segment. Here we question whether this segment contributes to the propeltidium, based on aspects of endoskeleton, muscles and also the morphological changes due to the huge chelicerae. Also ventrally a conjoined condition of appendage-bearing segments two and three clearly sets off the fourth appendage-bearing segment from the propeltidium.

The tagmatisation of Solifugae appears even more complex than already assumed. Further research is necessary, also including data from other arachnids, to elucidate the evolutionary history of tagmatisation within Arachnida and Euchelicerata.

**Keywords:** solifuges, tagmatisation, prosoma

**PP-MO-33**

***How to build a psammophilus insect? Adaptations of an enigmatic long horned grasshopper to the life in sand dunes***

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Insects living in ecologically extreme habitats, like the arid environment of deserts and sand dunes, show tremendous adaptations to cope with these challenging conditions. One of these insect groups is the Schizodactylidae, splay-footed or dune crickets, a species-poor lineage of longhorned grasshoppers. This relict group is represented by only two extant genera: the winged Eurasian genus *Schizodactylus* and the wingless genus *Comicus* in southern Africa. The most well known adaptation towards the life in those challenging habitats is their extremely modified tarsi, characterized by lobe-like extensions that facilitate the movement on sandy underground. The present study reveals a number of additional modifications in the morphology of Schizodactylidae that, similar to the legs, are directly related to their psammophilous way of life. These include for instance a characteristic setation of thoracic sclerites that prevent sand grain from intrusion into vulnerable membranous areas, the striking decrease in size of the thoracic spiracles reducing the respiratory water loss, and a general trend towards a fusion of sclerites in the thorax.

**Keywords:** Orthoptera, adaptations, Schizodactylidae

**PP-MO-34**

**New insights into the evolution of Brachyura: The female reproductive systems of two dorippoid crabs**

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A unique feature of the reproductive biology of eubranchyuran crabs is internal fertilization. Due to the direct connection of the ovary to the seminal receptacle, which functions as a sperm storage organ, the vitellogenic oocytes are fertilized within the seminal receptacle during ovulation. To the present day, the seminal receptacle follows a known standardized pattern. According to this pattern, it has a sac-like morphology with a dorsal mesodermal lining by glandular epithelium and an ectodermal ventral part lined by cuticle. The seminal receptacle opens through a cuticle lined vagina and a vulva on the sixth thoracic sternite. With regard to the position of the oviduct connecting the seminal receptacle and the ovary, the basal pattern can vary. Currently known are three types: the ventral-, the intermediate- and the dorsal-type of seminal receptacles.

The major objective of this study was the investigation of the morphology of the reproductive system of female *Ethusa mascarone* (Herbst, 1785) and *Dorippe sinica* Chen, 1980. Subsequently, the results are compared to other known eubranchyuran reproductive organs.

The reproductive systems of both dorippoid crabs were studied with a combination of histological sections and magnetic resonance imaging.

New results revealed a fundamentally different morphology of the reproductive organs of dorippoid crabs that does not conform to the known pattern.

The arrangement of the reproductive organs confirms the expected phylogenetically basal position of the Dorippoidea. Therefore, the morphology of the reproductive organs sheds a different light on the evolution of seminal receptacles.

Diesel, 1991, Crustacean sexual biology. Columbia University Press, New York, 145-163

McLay and López-Greco, 2011, Zoologischer Anzeiger-A Journal of Comparative Zoology, 250(4), 378-406.

**Keywords:** seminal receptacle, histology, magnetic resonance imaging

**PP-MO-35**

**Micro structures on the skin of moisture harvesting lizard modify wetting properties**

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Moisture harvesting lizards such as species of the genera *Phrynosoma* (Iguanidae) and *Moloch* (Agamidae) have remarkable adaptations for inhabiting arid regions. Special skin structures enable them to access water sources such as moist sand and dew: their skin is capable of collecting and transporting water. Even small amounts of water were observed to immediately spread over the skin. That physical ability comprises two features, a micro-structured scale surface and capillary channels in between the imbricate overlapping scales. The micro ornamentation on the scales varies in size between body side and species; their diameter is in the range of 10 to 30 µm. Nevertheless, that structure on the scales was found being able to hold a water film through which the skin can become super-wettable (a contact angle  $\leq 10^\circ$ ). We investigated morphological parameters of the micro ornamentation of seven lizard species using SEM imaging and tested their wetting behaviour. High-speed video analysis led to precise characterization of the interaction between liquid and surface structure. Investigations in view of functional morphology enabled us to not only identify the influence of structural parameters on surface wettability, but also to abstract the observed structures for fabrication of micro structured steel surfaces. We conclude that moisture harvesting lizards benefit from their skin micro ornamentation in terms of enhanced skin wettability to facilitate a faster water collection. The technical transfer shows the biomimetic potential of the skin surface structures for modification of surface wettability.

**Keywords:** wettability, micro ornamentation, *Phrynosoma*

**PP-MO-36**

**Cuticle architecture in the wing of the true bug, *Graphosoma italicum***

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Fiber-reinforced composite materials play an important role in modern engineering, especially in surface elements in architecture, as they provide a lightweight but durable basis for movable constructions incorporated in modern building. Especially the foldable hind wings of insects are a valuable source of inspiration for biomimetic construction of active facade constructions.

The principle component of the arthropod exoskeleton, cuticle, represents a natural fiber-reinforced composite material that spans an astonishing variety of material properties. A multitude of performance requirements are met by altering arrangements of chitin fibrils and the composition of matrix proteins, most notably by the incorporation of the near-ideally rubber-like protein resilin.

We analyzed the structural composition of the wings of the true bug, *Graphosoma italicum*, using light microscopy, wide field and laser scanning fluorescence microscopy, scanning and transmission electron microscopy on whole-mounts and serial sectionings to gain an understanding of the arrangement of chitin fibrils and its relation to the distribution of regions of varying mechanical properties, as well as the distribution of resilin-containing structures in the wing.

Our analysis shows that upper and lower lamella of the membranous regions differ considerably in structure and properties. Additionally, the load-bearing anterior vein of the hind wing contains a tubular inner sheath of chitin fibrils and a peculiar arrangement of elastic components.

Possible mechanical advantages of the analysed structures are discussed together with implications for biomimetic constructions using modern fibre-reinforced materials.

**Keywords:** insect wing, cuticle, structure

**PP-MO-37**

**3D micro-anatomy of the calcaneal tendon enthesis in mice [*Mus musculus*]**

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As entheses are transitions between compliant tendons and stiff bones, they could be expected to be the weakest link in the force exchange between muscle and bone. At such interfaces peak stresses can emerge from several phenomena: (1) tensile stresses transferred by the tendon and compressive stresses due to its contact with stiffer materials may sum up. (2) Loads may concentrate in a part of the enthesis, leaving another part of the tendon fibers relaxed, e.g. due to an oblique orientation of the transition zone relative to the force vector. However, clinical data shows that entheses are not the most common site of failure of the muscle-tendon-bone chain. Over the last decades anatomical and histological studies identified structural features potentially contributing to their robustness. One explanation is the "stretching brake model": Fibers, which loop over cartilage chondrons, deform those chondrons, whenever the structure is stretched. In this scenario the chondrons influence the stiffness and damping of the transition zone by their material properties - and could create a stiffness gradient by an increase in sphericity towards the bone. Our study aims at (a) evaluating whether enthesis structure fulfills the requirements for this model and (b) identifying further structural factors of robustness. We examined one PTA-stained and one cell-macerated, demineralized and critical-point dried mouse calcaneal tendon enthesis [C57BL/6J] by micro-CT. In the enthesial fibrocartilage parallel fiber courses prevailed, their curvatures were mainly corresponding to the curvature of the complete tendon. We conclude that this macroscopic curvature of fibers is a major parameter for the recruitment of chondrons as stretching brake elements.

**Keywords:** tendon-bone insertion, functional morphology, micro-computed tomography

PP-MO-38

**Fine structural investigations of the central nervous system in camel spiders**

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The central nervous system of arachnids surely is the least studied among arthropods, a fact that is especially true for camel spiders. As a result of the entirely fused supra- and subesophageal parts of the central nervous system, camel spiders possess a compact prosomal ganglion. Little is known about fine structural organization of this large ganglion, nor about sensory projection areas of eyes, chemosensory input or secondary processing areas such as the mushroom bodies - to name few apparent examples. Here, we analyze the organization of the prosomal ganglion based on X-ray microcomputed tomography (microCT), 3D reconstruction of serial paraffin sections, and backfill preparations. Backfill experiments concentrated on (the mostly chemo-) sensory input from the malleoli, fan-shaped organs located on the proximal hind leg articles that contain presumably tens of thousands of sensory neurons. Their projection area is intriguingly located in the anteriormost ventral part of the prosomal ganglion, next to chemosensory input projections from the pedipalps. Our results depict the first detailed neuroanatomical data on a camel spider's central nervous system and thus provide the basis for a comparative approach and further neuroanatomical studies in the arachnids.

**Keywords:** Solifugae, Arachnida, Neuroanatomy

PP-MO-39

**Ultrastructure and phylogenetic evaluation of the Tömösváry organ in *Craterostigma tasmanianus* Pocock, 1902 (Myriapoda: Chilopoda)**

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All centipedes share cuticular sensilla of various morphologies and functions. However, more complex sense organs are only present on the head and associated appendages of some chilopod subgroups. For instance, postantennal organs, termed Tömösváry organs in Myriapoda, were only known from Scutigermorpha and Lithobiomorpha. Here, Tömösváry organs are located in small excavations/depressions of the cuticle at either head flank, posterior to the antennal base and, if present, the anterioventral margin of the eye. Tömösváry organs were assumed to be present in Craterostigmomorpha but solid anatomical evidence was missing. With the present contribution, its existence in *Craterostigma tasmanianus* is documented for the first time, based on light and electron microscopy. TEM reveals that two distinct groups of altogether 8–12 biciliated receptor cells are nested in an epithelium made up by hundreds of sheath cells surrounding and supplying a huge common but strongly diversified receptor lymph space. Each receptor cell projects two elongated, locally convoluted cilia that pass through a pore canal in the cuticle, branch and finally abut to the sensory plate lining the pore canal with a very thin cuticle. Axons of receptor cells project into the nervus tömösváryi, which innervates the lateral protocerebrum. Homology of Tömösváry organs in Chilopoda is further strengthened by common presence of receptor cells each projecting two cilia that branch apically. However, many characters, such as lacking a cuticular excavation or the asymmetric distribution pattern of receptor cells and their cilia represent further apomorphies of Craterostigmomorpha.

**Keywords:** Sense organs, Evolution, Systematics

## Neurobiology – invited talks

### Emergence and refinement of phase invariant coding in the electrosensory system

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**Introduction:** Neural representations that are invariant to identity preserving transformations of natural stimuli (i.e. looking at the same object from different angles) have been observed ubiquitously across systems and species and are thought to be essential for context independent object recognition. The common wisdom is that such invariance emerges because neurons transform their inputs through “OR-like” logical operations, enabling them to give similar responses to stimulus waveforms associated with a given feature and that such representations are further refined along ascending sensory pathways. However, whether and, if so, how the brain implements such “OR-like” operations remain unknown to this day.

**Objectives:** The neural coding strategies used by the electrosensory system to process natural communication stimuli of heterogeneous waveforms and behavioral responses to these have been investigated.

**Materials & methods:** A systems level approach was used combining electrophysiology and behavioral assays in the electrosensory system of *Apteronotus leptorhynchus*.

**Results:** The results show that this system exploits the fact that correlated peripheral neuron activity provides a phase invariant representation through decoding synchronized excitation and inhibition by ON and OFF-type pyramidal neurons, respectively. Midbrain neurons receiving input from both types of pyramidal neurons displayed the most phase invariant responses and likely provide a neural correlate of the invariant perception seen at the organismal level.

**Conclusion:** The results provide insight into neurobiological mechanisms and the underlying sensory.

### Neural computations underlying acoustic communication in *Drosophila*

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Acoustic communication is pervasive in the animal kingdom, ranging from human language over bird song to the songs produced by many insects. Yet, the neural basis of this complex behavior is only poorly understood. Here, we use courtship behavior in the fruit fly *Drosophila melanogaster* as a model system for studying acoustic communication. *Drosophila* is well suited to study acoustic communication: automated, high-throughput behavioral assays facilitate the characterization of communication signals and of the behaviors they evoke; genetic tools allow to manipulate and visualize neuronal activity underlying acoustic communication.

During courtship, the male fly chases the female and produces a courtship song. The female in turn evaluates the song's pattern to inform her mating decision. *Drosophila* courtship song constitutes a surprisingly complex communication signal with structure on multiple time scales. Song is produced in bouts that can last several seconds and whose structure is shaped by the dynamical interactions between male and female during courtship. Individual bouts are usually composed of two modes - sine and pulse mode - each with species-specific parameters. Sine mode corresponds to a sinusoidal oscillation and pulse mode consists of trains of short, stereotypical sound pulses.

I will first provide a comprehensive description of the song features driving behavioral responses in female and in male flies. A novel behavioral assay reveals sex-specific selectivity for the species-specific parameters of song. In addition, females are also sensitive to the dynamical bout structure. Lastly, I will talk about experiments in which we begin to examine how the behaviorally relevant song features are extracted and represented in the fly's auditory system.

## Neurobiology – oral presentations

### OP-NB-01

#### How do birds predict the value of novel objects?

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Animals can effortlessly categorise diverse objects according to some shared value. Objects vary along multiple dimensions, (e.g. shape, size, and colour), some of which are relevant to decisions about whether a novel object belongs to say, a palatable or an unpalatable category, while others are irrelevant. How do animals learn which variations are relevant to successfully categorize novel stimuli? We train young poultry chicks to discriminate rewarded from unrewarded stimuli, where the two categories are specified by their position in a two dimensional colour space, but where only one dimension is relevant for categorization (the one separating the two categories). Chicks are trained in two different groups: One group is trained with equal variation along the two colour dimensions whereas the other group is trained with greater variation along the irrelevant dimension. We then test how this training generalises to novel colours. Comparing generalisation gradients between the two groups allows us to determine if variation along the irrelevant dimension influences generalization along the relevant dimension. The shape of the generalisation gradients allows us to distinguish between a number of classical mathematical models of learning and generalisation in humans and non-human animals.

**Keywords:** categorization, generalisation, learning

### OP-NB-02

#### Revealing the neuronal substrate mediating 3D vision in the praying mantis

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The praying mantis is a predatory insect that catches prey with a rapid strike of its two front legs. It relies on stereoscopic ("3D") vision, the ability to combine images from the two eyes to compute depth. This enables it to accurately judge the range of a target in space and to decide whether it is in reach or not.

We study the mechanisms underlying 3D vision by means of behavioural, neuro-anatomical and electrophysiological approaches. We provide visual stimuli by using anaglyph 3D technology. This means that the images intended for left and right eyes are presented in different colours. Spectral filters ensure that each eye sees only its intended image. For studying the neuronal substrate underlying stereoscopic computations we map the gross anatomical architecture of the mantis brain with particular emphasis on the visual information processing machinery. Moreover, we target and stain individual neurons via sharp electrodes and test them for their tuning to particular binocular disparities. We map monocular and binocular receptive fields by presenting vertical bars at different azimuthal positions.

By presenting a moving disc seemingly floating in front a computer screen and in catching distance the mantises strike during behavioural testing. This clearly shows that the animals possess stereoscopic vision. One of our anatomical findings is that the lobula complex, a component of the insect optic lobe, is highly structured. Therein we find neurons tuned to specific combinations of bars shown to the left and right eye corresponding specific distances in space.

I will present results of all stages of our praying mantis stereovision project with main focus on the neuronal machinery.

**Keywords:** stereoscopic vision, praying mantis, insect vision

**OP-NB-03**

**Proprioceptive signaling determines visuomotor gain in flying *Drosophila***

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The integration of multiple sensory signals is critical for effective locomotor control in most animals. The impressive aerial performance of flies, in particular, relies on the integration of visual signaling and mechanosensory feedback within milliseconds. During flight, the compound eyes produce graded neural potentials that are continuously fused with spikes from mechanoreceptors distributed over wings and gyroscopic halteres. This output activates wing steering muscles (WSM) for flight control within narrow temporal phase bands of the stroke cycle. To determine how phase-locked activation of WSM depends on proprioception, we mechanically silenced halteres and laser-ablated wing nerves in tethered flying fruit flies. We studied the consequences in a flight simulator, evaluating visual object fixation behavior, optomotor altitude control, and saccadic escape reflexes. Data show that the two sensory sources have an antagonistic effect on visuomotor gain control. Suppression of haltere feedback attenuates, while suppression of wing feedback enhances the animal's wing steering range. Mechanosensory feedback thus balances the temporal activation of flight muscles during vision-controlled manoeuvring, potentially favouring a behaviour with optimal trade-off between body stability and flight agility. Sensory integration in flies conceptually represents a neural *local sensory feedback* circuitry for motor control that has also been found in cats and humans.

**Keywords:** *Drosophila*, Sensory integration, Flight control

**OP-NB-04**

**VISUAL AND SPATIAL REVERSAL LEARNING IN *OCTOPUS VULGARIS***

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Reversal learning tasks require an animal to learn to discriminate between two stimuli but reverse its responses after it has reached a predefined learning criterion. In a serial reversal learning experiment, the signs of the stimuli are reversed repeatedly to test if the animal will need fewer errors the more reversals experienced. Reversal learning including visual stimuli has been extensively studied in octopus. However, in these studies, experimental procedures such as pretraining on the new positive stimulus after a reversal, the possibility of secondary cueing by the experimenter or the involvement of strong negative reinforcement might have affected the results. Thus we revisited visual reversal learning in octopus excluding previous limitations and using positive reinforcement alone. One animal completed four reversals and showed progressive improvement, whereas other animals only completed one reversal or did not even learn the original task. For comparison, we conducted a spatial reversal learning experiment which, for many species, has been shown to be easier than a visual reversal task. However, the octopuses did not show much better reversal learning abilities with a spatial task. This changed drastically when the animals were gently pushed away from the location they had incorrectly chosen in combination with positive reinforcement for a correct response: the octopuses completed several reversals and showed progressive improvement. Our results indicate that octopuses are able to perform successfully in reversal learning experiments showing progressive improvement over reversals. Thus octopus can indeed show behavioural flexibility usually associated with advanced cognitive abilities. The refined methodology adds to the amelioration of existing protocols for working with cephalopods in behavioural experiments.

**Keywords:** cephalopods, cognition, learning

**OP-NB-05**

**Cross-modal object recognition and dynamic weighting of sensory inputs in a fish**

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Within a multisensory system cross-modal object recognition increases flexibility, allowing an animal to react quickly to environmental changes. Dynamic weighting of sensory inputs enables the system to integrate multisensory information efficiently and to obtain a reliable overall percept. So far both abilities have only been shown in mammals, raising the question as to whether such high-level functions may be absent in animals lacking complex mammalian brain structures.

We tested whether a non-mammalian vertebrate, the weakly electric fish *Gnathonemus petersii*, is capable of cross-modal object recognition and dynamic weighting of sensory inputs.

The fish were trained to discriminate between two objects at a distance of 1 cm using either only vision, only the active electric sense or both senses. Subsequently, object discrimination at varying distances was tested in uni-modal trials (visually, electrically).

When trained with both senses available, electrolocation dominated vision, leading to an inability/decreased ability to fulfil the visual tests at 1 cm distance. Fish trained with only vision or only the electric sense were subsequently able to solve the task using only the untrained sense, demonstrating cross-modal object recognition. In the electrically trained fish the electrosensory input dominated vision at short distances but with decreasing reliability of the electric input at longer distances, the performance increased, showing that the sensory inputs are weighted dynamically.

Our results show for the first time that a fish is capable of cross-modal object recognition and dynamic weighting of sensory inputs and suggest that these cognitive abilities may be phylogenetically ancient mechanisms of vertebrates.

**Keywords:** sensory transfer, multisensing, sensory conflict

**OP-NB-06**

**Olfactory-visual integration in mushroom body output neurons**

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Brains are fascinating miracles with a multitude of adaptations across the animal kingdom. They receive a tangle of multi-modal input and hold the capacity to simultaneously select adequate stimuli while ignoring others. The resulting percept reflects a multi-modal construct rather than the neural representation of a single modality.

Multi-modal integration involves convergence of different sensory pathways at a higher brain level. The bee's mushroom body (MB) represents such a level. Its ~170.000 Kenyon Cells are organized in layers each receiving input from a different modality. MB output is conveyed to ~400 MB extrinsic neurons (MBON), which we record from on a reliable basis. We established an experimental design allowing characterization of olfactory, visual, as well as olfactory-visual (OV) induced activity in the same MBONs. Preliminary results show that the layered input of the MB is represented in a subpopulation of MBONs responding to either odors (11%) or light stimulation (34%), whereas a substantial proportion of MBONs was sensitive to both modalities (45%) and thus integrated OV information across MB input layers. A subpopulation of MBONs (10%) did not respond to any of the presented stimuli. Previously we showed that such units become recruited after a classical conditioning experiment. We therefore propose that reward association to an OV compound stimulus may elicit the same result. In future experiments we will address this question and examine if the neural activity of a single modality of the reward associated compound stimulus may substitute for the other modality or if the multi-modal stimulus acts always as a compound.

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**Keywords:** multi-modal integration, insects, mushroom body output neurons

OP-NB-07

**Serotonin mediates behavioural depression after “mobbing” - a lesson from crickets**

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Some individuals are consistently more active and aggressive than others, that tend to be behaviourally depressed, but the proximate causes are unclear. We report that inter-individual differences in aggression and motility in crickets can arise from early social experience and require serotonin (5HT). Using video-tracking software (*Ethovision*) we evaluated motility and attraction to conspecifics in 110 adult male crickets after 48 h isolation, after which all known behavioural effects of social experience have abated. We nonetheless found significant behavioural differences between individuals that were to win or lose fights staged 24 h later - future losers being generally behaviourally depressed. These differences seem to result from early socially experience. 1. The differences become more pronounced after winning or losing. 2. Adult crickets isolated since larval life are consistently more aggressive. 3. While crickets that experience 1 defeat exhibit depressed aggression for only 3 h, 6 multiple defeats leads to long term depression (>24 h). Finally, while treatment with the 5HT synthesis inhibitor AMTP or 5HT receptor antagonist ketanserin had no effect on fighting behaviour, or recovery of aggression after 1-2 defeats, AMTP and ketanserin each prohibited long-term depression of aggression after multiple defeats. We conclude that repeated social subjugation (“mobbing”) of some individuals during crowded culture conditions leads to long-term behavioural depression via the action of 5HT. While this amine is renowned for its aggression-depressing effects in mammals and man, to our knowledge, this is the first demonstration of a specific behavioural function for 5HT in aggression. Supported by the DFG (STE 714/4-1).

**Keywords:** aggression, serotonin, social defeat

OP-NB-08

**Population encoding of social signals in the medulla of a weakly electric fish.**

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**Introduction:** Behavioral responses are typically triggered by the activity of neural ensembles. Correlations between the activities and the variability of the activities of multiple cells, introduce redundancy which should be minimized for an efficient representation of natural stimuli. Neuronal correlations, however, can be found almost ubiquitously in the brain and a growing body of evidence suggest that they might contribute to information transmission or even carry information not encoded by the classical aspects of neural activity (i.e. spike rate or latency).

**Objectives:** We investigate neuronal correlations in the Gymnotiform ELL for their contribution to the encoding of social signals.

**Methods:** We simultaneously record the activities of pyramidal neurons in the ELL of the weakly electric fish *Apteronotus leptorhynchus* in vivo, while stimulating with natural social electrosensory signals. We analyze correlations that are attributable to stimulation (trial to trial activity, “signal correlations”) as well as correlations that arise from common neural input (trial to trial variability of activity, “noise correlations”) for their contribution to signal encoding.

**Results & Conclusions:** Our preliminary results show that the amount of correlations of simultaneous recorded cells depends on stimulus context, i.e. the electrosensory envelope or 2<sup>nd</sup> order of the signal. Decorrelation via reduction of noise correlations seems to be the driving mechanism which are presumably modulated via the ELL feedback pathways. This will be the future focus of our investigations.

**Keywords:** Population Coding, Correlations, Weakly Electric Fish

## Neurobiology – posters

### PP-NB-01

#### A retinal connectomics study using a combination of mechanical and FIB-based BFSEM

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Understanding neural networks requires detailed knowledge about the morphology and synaptic connectivity of every single neuron involved. Combining 3D electron microscopy, digital imaging, and structural analyses this is rendered possible just recently. Nevertheless, it is a challenge requiring (1) acquisition of 3D image data of a tissue volume (VOI) large enough to contain all cells of a subcircuit entirely, with (2) a quality that allows to track their finest dendritic ramifications to the tips and to identify synaptic sites unequivocally, and (3) laborious manual segmentation of hundreds of intertwined neurons. Covering several hundred  $\mu\text{m}$  in three space dimensions at a resolution of only few nm per pixel is a scale-gap that can be overcome with block-face scanning electron microscopy (BFSEM) at sufficient contrast and, most important, virtually free of distortions.

We aim at the exploration of the wiring rules of the vertebrate retina using teleosts with their geometrically regular cell patterns. Subcircuits are arranged repetitively in this organ and comprise a VOI of e.g.  $60 \times 60 \times 150 \mu\text{m}^3$  in the region of highest photoreceptor density. As a first step of a comprehensive study we try to combine two BFSEM methods on the same tissue block to (1) cover the VOI required (mechanical cutting: 3View at  $11 \times 11 \times 30 \text{ nm}^3$ ) and to (2) get maximal resolution in the outer plexiform layer with their exceptionally fine bipolar cell dendrites (ion beam milling: FIB at  $8 \times 8 \times 8 \text{ nm}^3$ ).

We succeeded in getting two well aligned 3View stacks ( $5 \times 13 \times 3 \text{ kpx}$  each) and a FIB stack ( $4 \times 3 \times 4 \text{ kpx}$ ) covering the OPL in the lower 3View stack, gluing them and reconstructing a group of 5 bipolar cells spanning all three stacks. Now the data are ready for reconstruction of all cells in the VOI.

**Keywords:** retina, connectomics, 3d

### PP-NB-02

#### Functional regeneration in the locust olfactory system

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We study regeneration of olfactory receptor neurons (ORN) into the locust (*Locusta migratoria*) brain after damaging the antennal nerve. After injury, ORN axons grow back into the first olfactory integration centre, the antennal lobe (AL), within 4 days, and establish a mature appearance similar to the untreated side within 2 weeks. Quantitative immunofluorescence of the cell surface marker Fasciclin I which is expressed by ORN axons, revealed quicker regeneration in juveniles than in adult locusts (Wasser et al., submitted). We now investigate functionality in the regenerated system electrophysiologically. We record intracellularly from olfactory projection neurons, while stimulating the antenna with odor pulses. Whereas in control ALs 40% of all projection neurons respond to the food plant odor cis-3-hexenal, and 30% respond to the aggregation pheromone odor guaiacol, responses are absent in ALs after nerve damage. After 7 days, first responses can be measured on the regenerating side, and after 3 weeks no differences to controls remain. Again, regeneration is faster in juveniles than in adults. These findings are confirmed by measurements of local field potentials in the mushroom body, the second olfactory integration centre, where odor stimulation is responded to by characteristic 20 Hz oscillations. These oscillations are caused by precisely coinciding action potentials in several projection neurons responding to the same odor, and are a strong sign for specific synaptic connections in the AL. These stimulus-induced oscillations are absent directly after damage, begin to return 1 week later, and are back to normal after 2 weeks. Thus, regeneration can be assumed to be both functional and specific within the locust antennal lobe.

**Keywords:** olfactory system, regeneration, insect brain

**PP-NB-03**

**Immunolocalization of arthropsin in the onychophoran *Euperipatoides rowelli* (Peripatopsidae)**

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Opsins are light-sensitive proteins that play a key role in animal vision and are related to the ancient photoreceptive molecule rhodopsin found in unicellular organisms. In general, opsins comprise two major groups: the rhabdomic (r-opsins) and the ciliary opsins (c-opsins). The functionality of opsins, which is dependent on their protein structure, may have changed during evolution. In arthropods, typically r-opsins are responsible for vision, whereas in vertebrates c-opsins are components of visual photoreceptors. Recently, an enigmatic r-opsin-like protein called arthropsin has been identified in various bilaterian taxa, including arthropods, lophotrochozoans and chordates, by performing transcriptomic and genomic analyses. Since the role of arthropsin and its distribution within the body are unknown, we immunolocalized this protein in a representative of Onychophora - *Euperipatoides rowelli* - an ecdysozoan taxon which is regarded as one of the closest relatives of Arthropoda. Our data show that arthropsin is expressed in the central nervous system of *E. rowelli*, including the brain and the ventral nerve cords, but not in the eyes. These findings are consistent with previous results based on reverse transcription PCR in a closely related onychophoran species and suggest that arthropsin is a non-visual protein. Based on its distribution in the central brain region and the mushroom bodies, we speculate that the onychophoran arthropsin might be either a photosensitive molecule playing a role in the circadian clock, or a non-photosensitive protein involved in olfactory pathways, or both.

**Keywords:** Onychophora, opsins, mushroom bodies

**PP-NB-04**

**Receptive fields of polarization-sensitive neurons of the central complex in the desert locust**

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The desert locust *Schistocerca gregaria* is able to perceive the polarization pattern of the sky, which is characterized by electric field vectors, *E*-vectors, arranged tangentially along concentric circles around the sun. This pattern depends directly on the sun's position in the sky and may be used to determine geographic directions.

Specialized photoreceptors in the dorsal rim area of the compound eyes are sensitive to the plane of oscillation (polarization) of light. The central complex plays a key role in the integration of this information: Parallel pathways innervate the protocerebral bridge as well as the lower and upper divisions of the central body in the locust brain. Within the central complex, columnar and tangential neurons establish connections between and within the neuropils. The protocerebral bridge is innervated such that *E*-vector orientation is represented topographically, mapping 180° variability over each brain hemisphere. While the *E*-vector tuning of the involved neuron types is relatively well known, their receptive fields regarding the celestial position of polarized light stimuli have not been determined yet.

In order to map these receptive fields, we recorded intracellularly from polarized-light sensitive neurons of the central complex while presenting blue light stimuli using a rotating polarizer at different positions on the hemisphere. Neurobiotin tracer injection allowed for identification of neuron types and reconstruction of anatomical relationships. We found that individual columnar neurons have receptive fields directed at different parts of the sky, which might indicate that the protocerebral bridge topography maps the solar azimuth over the complete horizon around the animal.

**Keywords:** polarization vision, central complex, sky compass orientation

PP-NB-05

**Integration of polarized and chromatic sky-compass cues in the central complex of the desert locust**

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Like other migratory insects, the desert locust likely uses a sky compass mechanism for spatial orientation. In the sky, several cues including direct sunlight, the polarization pattern of the sky and the chromatic and intensity gradient can be exploited for compass orientation. Previous work showed that the central complex in the locust brain holds a polarotopic internal representation of celestial *E*-vectors and may therefore act as an internal sky compass (Heinze and Homberg 2007, *Science* 315:995). To explore whether other celestial cues contribute to this internal compass, we examined whether polarization-sensitive (POL) neurons of the central complex receive additional input from the chromatic gradient of the sky. The intensity gradient of long wavelengths (green light) and the uniform distribution of short wavelengths (UV light) across the sky lead to a chromatic gradient with highest intensity difference between long and short wavelengths near the sun and smallest difference in the antisolar hemisphere (Coemans et al. 1994, *Vision Res* 34:1461). We tested the responses of central-complex neurons to zenithal polarized light and a green- and UV light spot rotating at an elevation of 45° around the head of the animal. Sensitivity to the unpolarized light spots was found in various neurons of the CX-network. In many neurons the tunings to both wavelengths were in the same position or close to each other. It might therefore be possible, that the light spot represents the sun, independent of its wavelength. The preferred position of the unpolarized light spots and the innervated slice of the protocerebral bridge (PB) were linearly correlated in certain columnar cell types, suggesting a topographic organization of solar azimuth positions in the PB.

**Keywords:** orientation, sky-compass, central complex

PP-NB-06

**To climb, surmount or pass below: Tactually guided obstacle negotiation in a stick insect.**

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As a nocturnal obligatory walker, the stick insect *Carausius morosus* relies on tactile cues when negotiating obstacles. Stick insects continuously sample their environment with their antennae, their main sense organs for touch. Stick insects are known to exploit antennal tactile cues to redirect ongoing swing movements of a front leg towards a touched obstacle [1]. Here, we analyse tactually induced obstacle negotiation in blindfolded, walking insects. The objectives were to explore the height dependence of behavioural choice in a paradigm where animals can climb, surmount or pass below a horizontal rod, and to identify height-dependent effects of tactile cues on front leg reaching and body inclination. Experiments were done with a pair of video cameras (10 heights, n=500(10)), or with a Vicon motion capture system (2 heights, n=120(3)). Contact events and movement types were annotated during video inspection. Kinematic analyses were done in Matlab.

Animals detected the rod reliably up to 30 mm (= 1 antenna length) and with efficacy dropping to 0 at 50 mm. Up to 25 mm, the likelihood to climb the rod increased from 0.3 to nearly 1, while the likelihood to surmount it dropped from 0.7 to 0. Beyond 25 mm the likelihood to pass below increased to 0.15, with a corresponding drop of the likelihood to climb. In climbing trials, ventral antennal contacts seem most efficient in eliciting aimed retargeting of a front leg. During reaching, front legs are levated more than during swing, with the increase depending on obstacle height. Similarly, thorax elevation depends on obstacle height. As the second front leg is levated less than the first, animals seem to take into account their body elevation during reaching.

[1] Schütz & Dürr (2011) *Phil Trans R Soc Lond B* 366

**Keywords:** insect antennae, tactile sense, climbing

**PP-NB-07**

**Active tactile exploration in a walking insect: Adaptation of the antennal beating-field according to speed and curvature**

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During walking, many insects explore the ambient space by continuously moving their antennae. Since antennal contacts can inform the insect about mechanical object features and potential footholds, antennal touch is particularly relevant for nocturnal, flightless species such as the stick insect *Carausius morosus*. As tactile information can be acquired only from the space traversed by the antenna, we expected that the antennal movement pattern is adapted context-dependently. Previously we found that tethered walking stick insects shift their antennal beating-field during visually induced turning [1]. Here we explore this shift during spontaneous turning and visual orientation behaviour of freely walking animals. Animals were released in a circular arena with black bars on white background serving as visual landmarks. The same animals were re-tested after unilateral and bilateral blindfolding with black paint. Sighted animals tended to turn towards and approach one of the landmarks, whereas blindfolded animals walked in circles of varying size and direction. During walking, the movement of both antennae and front legs, head and thorax was video-recorded using a custom-built motion capture gantry that allowed us to track freely walking animals at high spatial resolution. We found a strong shift of the median antennal pointing direction (ca. 30 deg on both sides) over a turning velocity range of 80 deg/s. The effect was similar in blind and sighted animals. During turning, bilateral temporal coordination of the antennae was generally weak and the width of the beating-field often asymmetric. The results show how antennal exploration movements are adapted to walking direction and turning velocity.

[1] Dürr & Ebeling (2005) *J Exp Biol* 208

**Keywords:** insect antenna, active sensing, motion capture

**PP-NB-08**

**A special “trinity” of sensilla on distal tarsal segments in insects**

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In the locust species *Locusta migratoria* and *Schistocerca gregaria* we found a conspicuous combination of two campaniform sensilla and one hair sensillum located very close together. These special combinations of sensilla were found ventrally on the distal rim of the third tarsomeres, and on both anterior and posterior sides. They occur in all three pairs of legs. Using light and scanning electron microscopy we found similar arrangements of three sensilla in comparable locations in several other insect species such as dragonflies, crickets, leafhoppers, planthoppers, and flour beetles. In cockroaches and stick insects, only the campaniform sensilla were found, the setae appeared to be missing in these species. Based on these observations we started a search for these structures in other insect orders. In locusts, with electrophysiological techniques we investigated possible functions of this special arrangement of three sensilla.

**Keywords:** insect, mechanoreception, walking

PP-NB-09

**Passive versus active sensing: a giant descending interneuron in a stick insect conveying information about antennal movement.**

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Stick insects use their antennae to continuously search and sample the environment ahead during walking. *Carausius morosus* executes aimed front leg movements towards obstacles shortly after tactile localization by its antennae. The information required for this behavior could be conveyed by previously identified descending interneurons that connect the brain to the thoracic ganglia. For example, the contralateral on-type velocity-sensitive neuron (cONv) encodes contralateral antennal joint angle velocity but also responds to low amplitude substrate vibration. How can cONv reliably encode single-trial joint movement in the presence of its strongly fluctuating spontaneous activity and how does it respond depending on the behavioral state of the animal and the mode of stimulation (movement or vibration)? These questions were studied by electrophysiology and antennal motion tracking in otherwise stationary animals. Substrate taps at a rate comparable to stepping during walking are reliably encoded by a single spike per tap, while suppressing spontaneous (i.e., irregular) spike activity. Thus, the presence of substrate vibration may improve the encoding of antennal movement cues. The response of cONv to passive deflection of the antenna is reliable, strong and velocity-dependent. However, spontaneous activity of cONv is unchanged or even suppressed during active transient or rhythmic exploratory antennal movements, while its sensitivity to passive deflection persists. Provided that the response to passive deflection is similar to the response to interrupted active movement, cONv could serve as a reliable antennal contact detector under behaviorally relevant conditions.

**Keywords:** Stick insects, Descending interneurons, Active sensing

PP-NB-10

**Biogenic amines modulate Dh44 signalling in *Drosophila melanogaster***

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The diuretic hormone 44 (Dh44), the *Drosophila* homolog of the mammalian corticotropin-releasing hormone, is involved in a variety of different physiological processes. Albeit Dh44 contribution is reported for diuresis, metabolism and locomotion rhythmicity, our knowledge on upstream regulatory pathways is poor. In the adult fly brain, the major source of Dh44 are only six neurons located in the *Pars intercerebralis* (PI). In our study, we focus on the dopaminergic and tyramineric control of Dh44 signalling within the PI.

IHC was used to visualize the expression patterns of tyramine receptor I (TyrR), dopamine receptor I (DopR) and Dh44 in the fly brain. Life cell imaging of Dh44<sup>+</sup> cells was used to examine cAMP responses upon dopamine (DA) and tyramine (TA) application and Ca<sup>2+</sup>-transients in response to TA application. Receptor function in Dh44<sup>+</sup> cells was analysed by cell-specific RNAi. Moreover, DopR-signalling in DH44 cells was mimicked by using optogenetic tools to manipulate the intracellular cAMP level. To investigate the influence of the TyrR and cAMP signalling in Dh44<sup>+</sup> cells on the activity of flies, we employed the *Drosophila* activity monitoring system. The impact on the fat storage was determined by measuring the triglyceride content in flies.

We found that the DopR and the TyrR are coexpressed in Dh44<sup>+</sup> cells in the PI and that DA and TA application induced a specific cAMP response in these cells, while TA application also induced Ca<sup>2+</sup>-transients. We can show that diminished expression of the TyrR as well as increased cAMP levels in Dh44 cells lead to numerous changes in metabolism and behavior. Taken together, our results indicate that DA and TA exert some of their physiological actions via modulation of Dh44 signalling in the PI.

**Keywords:** *Drosophila*, Dh44, Biogenic amines

PP-NB-11

**Are leg chordotonal organs simplified in a cave-dwelling insect? Comparative neuroanatomy of the subgenual organ complex in the cave cricket *Dolichopoda* (Orthoptera: Rhaphidophoridae)**

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**Question:** Leg chordotonal organs in insects occur in various morphologies. In Orthopteran, the subgenual organ complex in the proximal tibia can contain 2 - 4 sensory organs. These organs are physiologically adapted to detect vibration stimuli and/ or airborne sound. In Ensifera (long-horned grasshoppers), multiple evolutionary losses of sound production and hearing organs in the leg's tibia were suggested from molecular phylogenetic analysis (Jost and Shaw 2006, Mol Phyl Evol 38:510). Such losses could be adaptive in the repeated changes to a burying life style and the parallel loss of wings. Cave-living animals usually show extensive changes in sensory organs with reduction of optic structures and elaboration of chemosensory and touch receptors. We study the evolutionary changes in the subgenual organ complex in a mainly troglobitic cave cricket, *Dolichopoda* spec. Particular focus is on neuroanatomical differences to the troglomorphic cave cricket *Troglophilus* indicative of advanced evolutionary regression in the troglobitic species.

**Materials & methods:** Axonal tracing was used to reveal sensory organs in the tibia and their neuronal innervation pattern.

**Results:** The subgenual organ complex in *Dolichopoda* consists of three scolopidial organs which are well developed. The innervation pattern is similar to other Ensifera including *Troglophilus*. We did not find indications of an evolutionary regression.

**Conclusion:** The subgenual organ complex appears highly similar in distinct cave cricket genera, arguing against a strong pressure for reduction in the cave habitat. We discuss whether the subgenual organ complex in cave crickets is a reduced hearing organ or may represent the plesiomorphic organisation in Ensifera.

**Keywords:** Neuroanatomy, Evolution, Mechanosensation

PP-NB-12

**Responses to the neurotransmitter GABA in circadian pacemaker neurons of the Madeira cockroach *Rhyparobia maderae***

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The accessory medulla (AME) is the circadian pacemaker center that coordinates daily physiological and behavioral rhythms in the cockroach *Rhyparobia maderae*. The GABA-ergic distal tract that connects the noduli of the AME with the medulla is suggested to relay light entrainment to the clock. Consistent with a role of GABA in photic entrainment behavioral analysis revealed light-like phase-delays at dusk and phase-advances at dawn for GABA-injections. In addition, GABA plays other important roles in the circadian clockwork since extracellular recordings from the AME *in vitro* and *in vivo* revealed GABA- as well as neuropeptide-dependent ensemble-formation. To further analyze GABA functions in the circadian clock we performed Fura-2-dependent calcium imaging with primary cell cultures and extracellular recordings of the adult AME *in vivo* and *in vitro*. Application of GABA either inhibited or excited clock neurons either in the intact AME network, or isolated in primary cell cultures. Interestingly, long-term recordings from single circadian pacemakers revealed that GABA-responses of a cell could switch during the course of the recording. Preliminary pharmacological experiments hint that chloride transporter expression could allow for this switch from excitatory to inhibitory GABA-responses. Current studies examine whether circadian clock neurons change GABA-responses daytime-dependently via changes in internal chloride concentrations. [Supported by DFG grants STE 531/18-1,2,3]

**Keywords:** Chronobiology, GABA, circadian pacemaker

**PP-NB-13**

**GABA-immunoreactivity in the scorpion brain**

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Patterns of GABA-immunoreactivity (GABA<sub>ir</sub>) observed in the scorpion central nervous system are reminiscent of those in other arthropods, namely hexapods and malacostracan crustaceans (GABA<sub>ir</sub> is presumed to label inhibitory neurons using **gamma-amino-butyric acid** as transmitter). This holds for the fused **subesophageal** ganglion that supplies pedipalps, walking legs, genital opening, and pectines (Wolf & Harzsch 2002, doi 10.1016/S1467-8039(02)00044-0). The **supraesophageal** neuromeres (loosely termed brain) that supply eyes and chelicers had not yet been studied. The present results are thus of particular interest regarding brain structures not present in the more posterior neuromeres, such as mushroom bodies and acuate body. Immunocytochemistry for GABA was according to standard procedures (ibid).

Most brain neuropil areas exhibit low and rather homogeneous levels of GABA<sub>ir</sub>, like in the subesophageal ganglion, resulting from profuse fine neuron branchings. GABA<sub>ir</sub> is undetectable only in the mushroom bodies and most parts of the arcuate body, while the posterior ventralmost portion of the arcuate body exhibits clear GABA<sub>ir</sub>. This neuropil is located next to a band of GABA<sub>ir</sub> somata running along the lower posterior margin of the brain. Distinctly elevated levels of GABA<sub>ir</sub> are further observed in the optic ganglia and the anterior portion of the chelicer neuromer. Notable clusters of GABA<sub>ir</sub> somata occur in the following places: (i) a collar-shaped band of cell bodies antero-dorsal of the chelicer nerve entry, reminiscent of the segmental GABA<sub>ir</sub> clusters in the walking leg neuromeres, (ii) bilateral dorsal clusters located antero-laterally close to the optic ganglia, (iii) postero-ventral to the arcuate body, as noted above.

**Keywords:** scorpion brain, immunocytochemistry, GABA

**PP-NB-14**

**Brain serotonergic neurons control reproduction in *Daphnia magna*: evidence from adverse antidepressant actions and feeding regimes.**

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Serotonin reuptake inhibitors (SSRIs) are currently the treatment of choice against human major depression. After use SSRIs end up as endocrine disruptive contaminants in freshwater environments affecting reproduction of a variety of aquatic organisms incl. primary grazers such as water fleas. We investigated whether a known food ration-dependent increase in offspring production by the SSRI fluoxetine is brought about by serotonin-producing neurons newly identified by us in *Daphnia magna*. Strong evidence is provided for exogenous SSRI fluoxetine selectively increasing serotonin-immunoreactivity in brain neurons under limiting food conditions. This leads to maladaptive offspring production. At low food conditions, fluoxetine increases serotonin-immunoreactivity to similar maximal levels as observed under high food conditions and concomitantly enhances offspring production. The neurotoxin 5,7-dihydroxytryptamine known to specifically ablate serotonin-neurons markedly decreases serotonin-immunoreactivity and offspring production in sublethal amounts. This strongly supports the effect to be serotonin-specific by reversing the reproductive phenotype attained under fluoxetine. As first distinct candidate target neurons of serotonergic neurons with overlapping branches in central neuropils, we discovered neurons immunoreactive for crustacean hyperglycemic hormone and SIFamide, known to be involved in reproduction control of decapod crustaceans and insects, respectively. Thus, SSRIs impair serotonin-regulation of reproductive investment in a planktonic key organism causing adversely increased reproduction with potentially severe ecological impact.

**Keywords:** serotonin neurons, reproduction, *Daphnia magna*

**PP-NB-15**

**Neuropeptidergic modulation of adaptive locomotor behavior in *Carausius morosus***

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**Introduction:** In the past few years, an increasing number of studies have focused on the identification of neuropeptides in the central nervous system of insects, which represent one of the largest classes of signalling molecules. Besides the regulation of a wide range of physiological processes, neuropeptides can act as a neuromodulator or cotransmitter modulating the neuronal activity within neuronal circuits. One of the most thoroughly studied insect species with respect to locomotion is the indian stick insect *Carausius morosus*. In the stick insect, detailed information exists on premotor networks in controlling walking. Little knowledge exists, however, on the set of neuropeptides that are involved in the generation and modulation of motor activity, e.g. locomotion.

**Objectives:** In the present study a biochemical approach called Imaging Mass Spectrometry (IMS) will be used to map the spatial distribution of neuropeptides in the thoracic ganglia, which contain the neuronal microcircuits for the generation of locomotion. However, IMS requires that the neuropeptidome of the animal is biochemically characterized, but so far only 15 neuropeptides were described. In order to investigate the distribution of neuropeptides, first a neuropeptidomic analysis will be conducted. Subsequently, the spatial distribution of neuropeptides in the thoracic ganglia will be examined and, hence, the peptidergic content of single neurons that belong to the locomotor system (premotor interneurons) will be in focus of investigation. This information shall then be used to provide insight into the neuropeptidergic modulation of motor neurons and the premotor microcircuitry that drives locomotion.

**Keywords:** MALDI Imaging, Neuromodulation, Locomotion

**PP-NB-16**

**Assessing segmental versus non-segmental features in the ventral nervous system of onychophorans (velvet worms)**

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Due to their phylogenetic position as one of the closest arthropod relatives, studies of the organisation of the nervous system in onychophorans play a key role for understanding the evolution of body segmentation in arthropods. Previous studies revealed that, in contrast to the arthropods, segmentally repeated ganglia are not present within the onychophoran ventral nerve cords, suggesting that segmentation is either reduced or might be incomplete in the onychophoran ventral nervous system. To assess segmental versus non-segmental features in the ventral nervous system of onychophorans, we screened the nerve cords of two representative species for various markers, including synapsin, serotonin, gamma-aminobutyric acid, RFamide, dopamine, tyramine and octopamine. In addition, we performed retrograde fills of serially repeated commissures and leg nerves to localise the position of neuronal somata supplying these nerves. Our data revealed a mixture of segmental and non-segmental elements within the onychophoran nervous system. Thus, we suggest that the segmental ganglia of arthropods evolved by a gradual condensation of subsets of neurons either in the arthropod or the arthropod-tardigrade lineage. These findings are in line with the hypothesis of gradual evolution of segmentation in panarthropods and thus contradict a loss of ancestral segmentation within the onychophoran lineage.

**Keywords:** segmentation, nerve cord, ganglia

PP-NB-17

**Marker-less motion capture of antennal movements in honeybees and bumblebees**

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Bees extensively use their antennae for active tactile exploration, pattern recognition and learning. To date, the honeybee (*Apis mellifera*) is the only insect species that has been investigated systematically in both non-associative motor learning and associative conditioning paradigms. In each of these paradigms, bees actively sample the ambient space with both antennae. For investigating the role of antennal movement sequences in tactile learning, a posture tracking system is needed for resolving antennal kinematics. In our earlier work, we proposed a system for automatic tracking of the antennal tip position [1]. Here, we present a method for automated and reliable marker-less posture-tracking of both antennae in hymenopterans with geniculate antennae, honeybees in particular. To this end, we captured stereo videos of spontaneous antennal movements in honeybees and bumblebees under various conditions. Bees were fixed in metal tubes and blindfolded with paint. Videos were recorded at 100 fps, using macro lenses. For automated posture tracking, videos were processed by subtracting a mean image, thresholding and filtering, yielding pixel clusters that correspond to parts of the antennae. The head coordinate system was determined by manual labelling of morphological landmarks in a single frame. The tracking algorithm uses a virtual model with 4 DoF per antenna and calculates the correspondence between the projections of the model into both camera views and the pixel clusters of the processed video. The correspondence is optimised by a particle swarm algorithm that adjusts the 2x4 DoF. The precision and robustness of the algorithm was evaluated by comparison with three manually tracked videos.

[1] Mujagic et al. (2012) *JoVE* e50179

**Keywords:** insect antenna, tactile sense, motion capture

PP-NB-18

**Morphological characterization of neurons in the central complex of the honeybee *Apis mellifera***

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Honeybees are able to use the polarization pattern and the color gradient of the sky for spatial orientation. Polarization-sensitive photoreceptors in the dorsal rim area of the compound eye provide input to transmedulla neurons that presumably integrate polarization and color information and project to the anterior optic tubercle. Information is then passed via the bulbs of the lateral complex (LX) to neurons of the central complex (CX).

To identify neuronal cell types in the CX, we injected a tracer into the central brain using electroporation. We morphologically identified five types of neuron, that have previously been described in the sky-compass network of other insect species and a hitherto unknown type of neuron.

We stained two different types of tangential (TL) neuron that connect the bulbs of the LX to the lower division of the central body (CBL) and are the likely input to the sky-compass network of the CX. The CBL is linked to the protocerebral bridge (PB) via different types of columnar neurons (CL1, CL2). CL1 neurons connect the CBL to the PB and have ramifications in the *Gall*. CL2 neurons are intrinsic to the CX. They connect the CBL and the PB to a distinct region in one of the two noduli. We found two types of CPU1 neuron that projected from the PB via the upper unit of the central body to the LX.

We further identified a previously unknown type of TL neuron. This neuron innervated the entire CBL and had a large field of processes in the posterior protocerebrum and a distinct region along the esophageal foramen.

Our data suggest that the morphology of polarization-sensitive neurons is highly conserved in different insect species but that the sky-compass network of the honeybee might receive additional input via a, so far unique, type of neuron.

**Keywords:** Central Complex, Navigation, Sky-Compass

PP-NB-19

**Postmetamorphic plasticity of the mushroom bodies**

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With its fully sequenced genome and the susceptibility for reverse genetics based upon RNA interference (RNAi), *Tribolium castaneum* is best suited to study the development and plasticity of the nervous system. While plasticity can be provided by various mechanisms, we focus on ongoing cell proliferation in the adult brain. It is well established that neurogenesis persists in the mushroom bodies (MB) of adult insects, including beetle *T. castaneum* where neuroblasts giving birth to MB Kenyon-cells remain active for more than one month after adult eclosion. To label cell proliferation in the adult beetle we successfully adapted the 5-ethyl-2'-deoxyuridine (EdU) technique to living beetles. Combined with immunohistochemistry against the glia-cell marker reversed-polarity and the use of transgenic lines expressing neuron- and/or glia-specific markers, we labeled the progenies of adult persisting neuroblasts, determined their identity and counted the newborn Kenyon cells in within the first week after adult eclosion to determine the proliferation rate.

In several studies it was proposed that newborn neurons of MBs may play a role during olfactory processing and learning. We combined the EdU-staining with olfactory stimulation using the leaf alcohol cis-3-hexen-1-ol and again determined the proliferation rate. Our data suggest at least two phases. Direct after adult eclosion, proliferation is independent from stimulation with the leaf alcohol, while after about three days, proliferation is influenced by olfactory stimulation.

To further investigate MB plasticity, we plan to use other odors, including the beetle's aggregation pheromone 4,8-dimethyldodecanal (DMD), odor deprivation and knockdown of Orco via systemic RNAi.

**Keywords:** insect, adult neurogenesis, olfaction

PP-NB-20

**Identification and quantification of biogenic amines from individual *Drosophila somata* by MALDI-TOF MS**

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**Question:** Biogenic amines represent a diverse group of neurotransmitters, -modulators and -hormones which are synthesized and released by neurons, influencing physiological processes and shaping behavioral patterns in organisms. Detection of biogenic amines by mass spectrometry from a small sample size such as a single cell body is still a challenging analytical task. While a MALDI-TOF MS-based method for detection of neuropeptides on single cell level has been published [1], an equivalent approach for the detection and quantification of smaller neurotransmitter such as biogenic amines is lacking to date.

**Methods:** Here, we introduce a robust and reproducible protocol by using on-plate chemical derivatization with 4-hydroxy-3-methoxycinnamaldehyde to decrease the limit of detection; first focusing on octopamine (OA) and tyramine (TA) (limit of detection OA 1 fmol/μl, TA 2.5 fmol/μl); without interruption of the detection of putative neuropeptides in the same sample set. The strategy contains quantification experiments with internal standards which shows an excellent linearity ( $R^2 > 0.999$ ) and a limit of quantification of 10 fmol/μl for OA and TA, respectively.

**Results:** Analyzes of individual dissected somata from two discrete tyraminergetic/octopaminergic neuron populations, the VL cluster at the protocerebrum and the VMlb cluster of the suboesophageal ganglion, revealed a highly significant difference in OA level between the two cell population (t-test,  $p = 4.373e-8$ , VL  $n = 12$ , VMlb  $n = 7$ ).

**Conclusions:** Further experiments will include behavioral assays to study putative differences in OA/TA expression on soma level to get a more detailed understanding about their influence in the nervous system.

**Keywords:** biogenic amines, single cell, MALDI-TOF MS

PP-NB-21

**Mechanoreceptor arrangement at the antennal base helps crickets to differentiate between active and passive antennal touch**

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Crickets use their antennae as tactile sense organs to actively explore their surroundings. The antennal-tactile sense enables them to overcome obstacles, discriminate surface structures, and also react to approaching predators and conspecifics. I used light and electron microscopy to systematically map the distribution of mechanoreceptors in the two antennal base segments (scape and pedicel) and traced sensory fibres in the antennal nerve to reveal the central projection patterns of different antennal sensilla and proprioceptors in the cricket brain. A total of about 600 sensilla were counted on the surface of the scape and about 250 on the pedicel. Based on their distinctive morphologies they can be classified as sensilla campaniformia, basiconica, coeloconica and chaetica. Chaetic sensilla are arranged in hair fields at the actively moveable head-scape and scape-pedicel joints to monitor the actual position and active movement of the antenna. Large and small campaniform sensilla are arranged in a band at the distal edge of the pedicel to detect deflection of the flagellum. Retrograde nerve labelling demonstrated a single mechanosensory cell innervating each chaetic and campaniform sensillum. Basiconic and coeloconic sensilla, however, have several sensory cells and appeared to be randomly scattered on both, scape and pedicel. Furthermore, anterograde and retrograde staining revealed about 40 sensory neurons forming a chordotonal organ in the ventral pedicel and 5 somata of pedicellar strand receptors in each side of the brain. The anatomical findings suggest that the specific arrangement of sensilla and internal proprioceptors at the antennal base can be used to differentiate between active and passive antennal touch.

**Keywords:** insect, antenna, mechanoreceptor

PP-NB-22

**Eclosion rhythmicity in wildtype and clock-related mutants of the fruit fly *Drosophila melanogaster* under natural abiotic conditions**

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Adequate timing of behaviour allows animals to adapt to temporally variable environmental conditions and is thought to optimise fitness. A classical model for a circadian-timed behaviour is eclosion in fruit flies of the genus *Drosophila*. In *Drosophila melanogaster*, eclosion is gated to the morning hours which is commonly assumed to be an adaptive behaviour to reduce water loss and facilitate wing spreading.

Laboratory studies have shown that the *Drosophila* eclosion rhythm can be entrained by different abiotic Zeitgebers like photoperiod or temperature. The eclosion rhythm depends on a functional central clock in the brain and a peripheral clock in the prothoracic gland. Very little, however, is known about *Drosophila* eclosion rhythms in nature. A major question here is whether and to what extent the circadian clock and abiotic Zeitgebers contribute to ensure that flies eclose at the right time of the day.

Using a newly developed eclosion monitor (WEclMon), we monitored eclosion timing in wildtype and clock-related mutant fruit flies under natural abiotic conditions. Our results show that a functioning molecular clock but not PDF-signalling is required for properly timed eclosion even in presence of all Zeitgebers. This is in contrast to what has recently been found for locomotor rhythms under semi-natural or nature-like conditions. Fitting an extended statistical model to the data revealed that the circadian clock under natural conditions is the major determinant for rhythmic eclosion, while temperature seems to be much more important than light to determine at which time during the eclosion gate the flies emerge. Light, however, appears to be the key Zeitgeber for clock entrainment under natural conditions.

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**Keywords:** circadian clock, behavioural timing, insect emergence

### PP-NB-23

#### **Coding of time varying stimuli in ampullary afferents of *Gnathonemus petersii***

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Weakly electric fish detect prey and navigate using their electrosensory system. This consists of the active and a passive system. The ampullary receptors of the passive system are sensitive to the low frequency and amplitude electric signals characteristic for prey. Such signals can be easily mimicked in the lab using either a stationary or a moving DC dipole source. While the encoding at the level of the afferents is considered to function as an amplitude-sensitive rate-encoder, it is not apparent such a system can cope with natural time varying stimuli. For example, a DC dipole source moving towards a fish (looming stimulus) contains information on speed and distance to the source that are confounded by a rate-coding system. It has been proposed (Clarke et al., 2013) that the South American brown ghost knifefish are able to disambiguate speed and distance in the active system by having the corresponding receptors implementing power law adaptation. In the present study we investigate whether this mechanism is also used in the passive system of an African fish *Gnathonemus petersii* an evolutionarily unrelated species. As a first step we show that the ampullary receptors exhibit multiple time scales of adaptation best explained by a power law function. However, the exponent in this adaptation is smaller than the one that has been proposed to be optimal for disambiguation. Hence we measure the response to moving DC stimuli of different speeds and analyze whether distance and speed are encoded unambiguously. Indeed, dipole-speed and discharge rate are slightly correlated, indicating a weak ambiguity. In a modeling approach we now investigate if this is the result of imperfect power-law adaptation and/or further shaped by the known frequency tuning of the afferents.

**Keywords:** Electric fish, Adaptation, Neuronal coding

### PP-NB-24

#### **HRTF processing in barn owls**

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**Introduction:** The American barn owl (*Tyto furcata pratincola*) has developed an excellent hearing capacity to catch its prey. Sound localization is driven by interaural time difference (ITD), interaural level difference (ILD) and possibly further monaural parameters. These parameters are in turn influenced by the morphology of the ruff and the ear flaps. The influence of these structures on the auditory signals is described by head related transfer functions (HRTF).

**Objectives:** HRTFs of owls will be recorded, analyzed and the influence of sound-localization parameters on behavior and neural tuning will be investigated. It will especially be examined how the auditory system of barn owls deals with ambiguous information in auditory signals.

**Material & Methods:** HRTFs are recorded, while auditory signals are presented via a movable loudspeaker. The auditory signals are filtered with recorded HRTFs and presented via headphones in the behavioral and electrophysiological experiments.

**Results:** Owls can easily locate HRTF filtered stimuli. Preliminary data with stimuli originating from different spatial locations but containing the same broadband ITD and broadband ILD suggest that it is difficult for the birds to discriminate between such locations.

**Conclusion:** The absent discrimination of spatial locations containing the same ITD and ILD indicates that barn owls didn't use further monaural cues to disambiguate such locations.

**Keywords:** HRTF, barn owl, auditory system

PP-NB-25

**Effects of chronic THC exposure on brain aging in the zebrafish**

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**Introduction:** Considering the increasing number of elderly in the world's population today, investigation of the aging process represents one of the biggest challenges in biomedical research. To attenuate or decelerate the consequences of senescence, animal models may help identifying key factors of cellular aging contributing to the cognitive decline at elevated ages. The zebrafish (*D. rerio*) represents a promising model organism in this research. During natural aging, zebrafish undergo a gradual decline in cognitive abilities between the age of 1-2 years. Concurrently, the oxidation of cellular macromolecules in the animals' brains increases, suggesting that enhanced oxidative stress may contribute to cognitive impairments. Phytocannabinoids like THC ( $\Delta^9$ -tetrahydrocannabinol) are known to possess direct and indirect anti-oxidative properties.

**Objective:** Our study aimed to investigate the anti-oxidative properties of THC on age dependent learning deficits and cellular aging in zebrafish.

**Methods:** We performed chronic THC-treatment of 1 and 2 years old zebrafish and tested the animals in color discrimination and active-avoidance conditioning. Afterwards, we determined the levels of oxidized macromolecules in the animals' brains.

**Results:** We found that chronic THC treatment in zebrafish accelerated learning without increasing behavioral performances compared with untreated controls. This effect was considerably stronger in the one year old animals. Furthermore, level of oxidation was reduced in THC treated animals.

**Conclusion:** Experimental evidences show cannabinoid's neuroprotective activity. Elevation of cannabinoid level could be a promising strategy for slowing down the progression of brain aging.

**Keywords:** Zebrafish, Aging, Endocannabinoid System

PP-NB-26

**Neuroendocrine correlates of reproductive status in female Damaraland mole-rats**

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Damaraland mole-rats (*Fukomys damarensis*) are eusocial, subterranean mammals, which exhibit an extreme reproductive skew with a single female (queen) monopolizing reproduction in each colony. Non-reproductive females in the presence of the queen are physiologically suppressed to the extent that they are anovulatory. This blockade is thought to be caused by a disruption in the normal gonadotropin-releasing hormone (GnRH) secretion from the hypothalamus. In female mammals, GnRH release is under the control of feedback mechanisms of  $17\beta$ -estradiol, mediated by the estrogen receptor  $\alpha$  (ER $\alpha$ ). In order to understand the physiological mechanisms of reproductive suppression in subordinate females we studied the mRNA expression of steroid hormone receptors, of the androgen-converting enzyme aromatase and of GnRH in forebrain regions involved in the control of reproductive behaviour. Quantification of the hybridisation signal revealed that breeding females had increased ER $\alpha$  expression in the anteroventral periventricular nucleus (AVPV) and in the medial amygdala, while aromatase expression in the AVPV was significantly reduced compared to non-breeders. Gene expression of androgen receptors was significantly increased in breeders in most brain regions examined. Interestingly, breeders and non-breeders did not differ in the area covered by GnRH mRNA, but breeders had elevated expression in the region of the diagonal band of Broca/organum vasculosum of the lamina terminalis, which constitutes a major GnRH cell cluster in rodents. These data show that breeding status differentially affects the neuroendocrine phenotype of females and they suggest that the GnRH system of subordinates may be inhibited at the level of gene expression.

**Keywords:** in situ hybridization, GnRH, social status

**PP-NB-27**

**Distance reproduction in harbor seals**

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In the open ocean, marine mammals, such as harbor seals, commute regularly between haul-out places and feeding grounds. The mechanisms they use in order to orientate themselves in the open ocean, which seems low structured at first glance, are still largely unknown. As the open ocean hardly provides external cues for orientation in general or under certain circumstances, internal cues gain importance. A mechanism for orientation that could be based solely on internal cues is path integration. When using path integration, an animal has to document and thus estimate distances and directions in order to integrate them in to a goal-directed vector. Until now, it is unknown if marine mammals use path integration. In a first approach to path integration, we trained a male harbor seal to estimate and reproduce a specific sample distance. The seal was supposed to swim a specific sample distance interval marked on a belt-system and to reproduce it afterwards by swimming the same distance along the belt keeping the same swimming direction. The sample distance interval was presented at various positions along the belt and with reversed swimming direction in one control session to avoid that the animal uses absolute cues defining the end point of the reproduction interval for solving the task. The seal was indeed able to estimate a distance of 5m irrespective of the absolute position in space, but it needs to be investigated if seals can reproduce any distance. In conclusion our results provide first evidence for precise distance estimation abilities on a marine mammal which would be a prerequisite for path integration.

**Keywords:** Distance reproduction, Path Integration, Marine Mammal

**PP-NB-29**

**The use of optic flow in the zebrafish *Danio rerio*: Comparison of neuronal velocity tuning and swimming behavior**

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Fish navigate through their three-dimensional environment at remarkable speed. Besides other modalities, vision seems to be used extensively in this challenging behavior (Rosenthal et al., 2015). Correspondingly we found neurons in the tectum opticum of adult zebrafish that respond highly specialized, i.e., responses were tuned for directionality and velocity. Our physiological studies revealed that these tuning properties are plastic on a short-term scale. The optic tectum is known to generate motor output directly from its visual input, making it an ideal substrate to study sensorimotor integration. For this, a sensory variable known to be of importance is optic flow (Koenderink, 1986). We here test how visual adaptation to grating patterns influences a well-studied compensatory behavior common to insects, birds and fish. When facing unbalanced optic flow, these animals behave as if perceiving objects at differing depth and reposition themselves with respect to the perceived (imaginary) distance. Notably zebrafish were shown to differ from other animals by swimming closer to illusionary objects (Scholtyssek et al., 2014). We here exploit this tendency to investigate how adaptation to a fixed spatial frequency influences this behavior. For this, we analyze positions and speed of single fish passing a tunnel with varying spatial frequencies after adaptation with a fixed spatial frequency. Finally, we investigate if our behavioral results can be linked to the plasticity tuning characteristics of tectal neurons and provide further insight into the use of optic flow in fish.

**Keywords:** optic flow, neuronal tuning, adaptation

**PP-NB-30**

**Medullary lateral line units of rudd, *Scardinius erythrophthalmus* and nase, *Chondrostoma nasus* are sensitive to Kármán vortex streets of different intensities, shed by upstream objects in different distances**

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Primary lateral line afferents of fish respond to bulk water flow and to the vortices caused by an upstream object. In running water vortices occur downstream of an object and in the wake of undulatory swimming fish. Until now it was not known whether and how medullary lateral line units of fish respond to the vortices shed by an upstream object. To study this, we recorded single units from the medullary medial octavolateralis nucleus (MON) of 29 common rudd, *Scardinius erythrophthalmus* (total length 6-9 cm) and 23 common nase, *Chondrostoma nasus* (8-12 cm) to bulk water flow and to the Kármán vortex street (KVS) shed by an upstream D-shaped cylinder. Vortex shedding frequency (VSF) of the KVS was determined with particle image velocimetry. Autocorrelation was used to uncover the repetition rate of burst patterns. In both fish species some MON-units showed a burst-like discharge pattern if the fish was exposed to a KVS. In these units the burst frequency matched the VSF. In all of these units, response strength decreased with increasing distance of the fish from the cylinder. Since the burst frequency depends on cylinder size and bulk flow velocity, fish not only should have the ability to detect an upstream cylinder but also to determine its size.

**Keywords:** lateral line, MON, Vortex

**PP-NB-31**

**Adaptive responses of Lateral Line primary afferents to repetitive dipole stimuli**

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Neuronal adaptation has been described for all sensory systems except the mechanosensory lateral line. We investigated whether primary afferent nerve fibers in the Posterior Lateral Line Nerve (PLLN) of goldfish, *Carassius auratus*, adapt to a series of identical hydrodynamic stimuli and whether presentation of a novel stimulus can change an adapted firing activity. We also studied the possible involvement of efferent fibers in neuronal adaptation by recordings from fibers after cutting the PLLN close to the brainstem.

Series consisting of ten identical stimuli (1 s duration) were presented with Inter Stimulus Intervals of 0.1 s. Over a series of ten 100 Hz stimuli, discharge rates of PLLN fibers decreased (adapted) in 83 (43.5 %) recordings, did not change in 100 (52 %) and increased in 8 (4.5 %) recordings. Over the course of ten noise stimuli (1/f, bandwidth 0-150 Hz) discharge rates decreased in 54 (63 %) recordings and did not change in 32 (27 %) recordings. Discharge rates to the novel stimuli (95 Hz, equal acceleration amplitude) presented after a 100 Hz series were greater than the adapted firing rates but still suppressed compared to reference (response to novel stimulus presented prior to the adaptation series). In 21 (78 %) recordings from a severed PLLN discharge rates decreased (adapted) and in 6 (22 %) recordings discharge rate did not change across a stimulus series.

Our data show that PLLN fibers can adapt to a series of identical hydrodynamic stimuli. Most likely, this is due to an adaptive process that shifts a unit's sensitivity but not to sensory learning. Our data also indicate that adaptation to a stimulus series is not dependent on efferent fibers.

**Keywords:** Neuronal Adaptation, Lateral Line, Repetitive Stimulation

PP-NB-32

**From behavior to brain: inducing the Immediate Early Genes *egr-1* and *c-fos* in the grey bamboo shark (*Chiloscyllium griseum*) and the Malawi cichlid *Pseudotropheus zebra*.**

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This study aims to reveal the relevant neuronal substrate allowing fish to perform learning and long-term memory retention with respect to selected visual discrimination abilities in bamboo sharks (*Chiloscyllium griseum*) and Malawi cichlids (*Pseudotropheus zebra*), using the expression of the immediate-early genes *egr-1* and *c-fos* as metabolic markers. Sharks showed a significant up-regulation of *egr-1* mRNA expression levels in a small telencephalic region. Expression patterns between different training regimes (early/late learning stages, long-term memory retention) showed distinct variations in size and strength. Although up-regulation in individuals exposed to acute stress occurred within the same telencephalic region, *egr-1* labeling patterns were significantly different compared to individuals subjected to higher cognitive tasks. *Egr-1* activity was virtually absent in unstimulated control sharks. In cichlids, expression of *egr-1* and *c-fos* was not limited to the telencephalon but occurred extensively throughout most of the brain. Moreover, expression patterns did not vary significantly in size or strength across groups (control, stress, early/late learning stages), barring identification of relevant neural substrates for learning. The observed differences across shark groups (but not cichlids) point to important, evolutionarily conserved mechanisms regarding the processing and neuronal plasticity of the elasmobranch brain with respect to learning and long-term memory retention, a pattern consistent with that observed in other vertebrate groups. Our data support findings from lesion experiments in sharks, showing that selected cognitive functions are processed in the telencephalon lacking a neocortex.

**Keywords:** Immediate Early Genes, *Chiloscyllium griseum*, *Pseudotropheus zebra*

## Physiology – invited talks

### Sleep, rhythm and stress in developing barn owls in nature

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Understanding the function of variation in sleep requires studies in the natural ecological conditions in which sleep evolved. Sleep has an impact on individual performance and hence may integrate the costs and benefits of life history decisions. Dark and pale melanistic animals differentially regulate energy homeostasis, immunity and stress hormone levels, thus the amount and/or organization of sleep may covary with melanin-based color. Wild nestling barn owls (*Tyto alba*) from mothers displaying more black spots had shorter non-REM (rapid eye movement) sleep bouts, a shorter latency until the occurrence of REM sleep after a bout of wakefulness and more wakefulness bouts. Therefore, nestlings of more heavily spotted mothers switched sleep-wakefulness states more frequently and were behaviorally more vigilant. Furthermore, the ontogeny of rhythmicity (period length and level of rhythmicity) were strongly related to the nestlings' pigmentation. Rhythmicity was more intense in small spotted nestlings for all three sleep-wakefulness states. Previously, we found that, nestlings with higher expression levels of a gene implicated in melanogenesis (*PCSK2*) followed a more precocial pattern of development regarding the ontogeny of sleep states, which are thought to be related to the developmental changes in the brain. Given its role in brain development, variation in nestling REM sleep may lead to variation in adult brain organization, and thereby contribute to the behavioral and physiological differences observed between adults expressing different degrees of melanism. We conclude that different strategies of the regulation of brain activity have evolved and are correlated with melanin-based coloration.

### Dietary lipids and eco-physiological constraints

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A dietary deficiency in essential lipids has serious consequences for life history traits of invertebrate consumers. Polyunsaturated fatty acids (PUFA) and sterols are indispensable structural components of eukaryotic cell membranes and serve as precursors for a number of bioactive molecules, such as eicosanoids and ecdysteroids. Eicosanoids are known to modulate reproduction and immunity while ecdysteroids are involved in the process of molting. PUFA are involved in the homeoviscous adaptation of membranes to varying temperatures and the dietary PUFA supply may thus affect the ability of ectothermic animals to cope with low environmental temperatures. PUFA-derived eicosanoids have been shown to influence invertebrate immune responses and there are indications that the dietary PUFA supply can affect the outcome of parasite-host interactions and the susceptibility to pathogens. Sterol auxotrophy is widespread among invertebrates. In contrast to animals, which predominantly contain cholesterol, plants and especially algae contain a great diversity of phytosterols. Consequently, herbivorous invertebrates have to metabolize dietary phytosterols to cholesterol to cover their physiological demands. Dietary phytosterols, however, differ substantially in their potential to support growth and reproduction of invertebrates. Investigating the physiological constraints associated with an inadequate dietary lipid supply is thus crucial for understanding the performance of animals under various environmental conditions. Aim of this talk is to highlight recent advances in biochemical food quality research and to point out gaps in knowledge and new avenues for future research.

Physiology – oral presentations

OP-P-01

**EVOLUTION OF UCP1 AND BROWN ADIPOSE TISSUE**

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Brown adipose tissue (BAT) is a unique evolutionary outcome enabling adaptive thermoregulation in eutherian mammals through heat production catalyzed by mitochondrial uncoupling protein 1 (UCP1). Despite the presence of UCP1 orthologs prior to the divergence of teleost fish and mammalian lineages, UCP1's significance for thermogenic adipose tissue emerged at later evolutionary stages. In marsupials, UCP1 is expressed in adipose tissue of 'brownish' appearance but noradrenaline does not trigger the classical adaptive excitation of thermogenesis. Here, we show progressively increasing UCP1 gene expression during juvenile development of the grey short-tailed opossum, *Monodelphis domestica*. To determine the molecular identity of UCP1-positive adipose tissue in marsupials, we assessed the global transcriptome of the interscapular adipose tissue and characterized gene program changes associating with UCP1 gene expression. We annotated gene products to the respective modern eutherian orthologs to answer the question which pathways were already wiring UCP1 biology in adipocytes about 140 MYA. Although UCP1-positive marsupial adipose tissue resembles eutherian brown fat-like molecular signatures, ectopically expressed marsupial UCP1 does not catalyze proton conductance. Current work in our laboratory aims to unravel the functional origin of thermogenic UCP1 by determining specific metabolite transport prior to thermogenic uncoupling.

**Keywords:** ucp1, brown adipose tissue, marsupials

OP-P-02

**Functional analysis of the peritrophic matrix in *Tribolium castaneum***

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The peritrophic matrix (PM) is an extracellular barrier made of chitin nanofibers and PM proteins (PMPs) which lines the midgut epithelium of most insects. It protects the intestine from invasion by microorganisms and parasites, and is thought to facilitate digestion. To analyze PM function, we performed *in-situ* permeability assays (feeding fluorescein-isothiocyanate dextrans of various sizes) in combination with systemic RNAi in larvae of the red flour beetle, *Tribolium castaneum*. Our analyses revealed an anterior-to-posterior gradient in PM permeability. Moreover, we demonstrated that chitin is a major determinant in maintaining the PM's barrier function, as RNAi to knock-down the gene encoding chitin synthase 2 as well as feeding of the chitin synthesis inhibitor diflubenzuron (DFB) significantly increased PM permeability. We further analyzed the function of eleven PMPs, which are differentially expressed along the larval midgut and have various numbers of peritrophin-A-type chitin-binding domain (CBDs). RNAi for two of these genes, *TcPMP3* and *TcPMP5-B*, resulted in depletion of fat body, growth arrest, molting defects and mortality due to the disruption of the PM's barrier function. As particularly these two PMPs are extensively glycosylated, we suggest that proteoglycans mainly determine PM permeability. Interestingly, structural analyses of the 45 CBDs found in the eleven PMPs revealed variations in the polymer binding pockets indicating differences in binding affinities and/or specificities. Taken together, our findings suggest that chitin and specific *TcPMPs* are critical for maintaining the PM's barrier function, and that a gradient of PM permeability is essential for nutrition and survival.

**Keywords:** Chitin, Peritrophic matrix proteins, Permeability

**OP-P-03**

**Multidrug resistance transporters - Key players of cardiac glycoside sequestration in a highly specialized bug?**

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*Oncopeltus fasciatus* sequesters cardiac glycosides (CGs) derived from its host plant (*Asclepias* sp.) in a specialized thoracic compartment. This sequestration requires selective CG trafficking and thus influx and efflux carriers to facilitate their transport across membranes. Multidrug resistance transporters (MDRs) are known to transport CGs in mammals and are widely distributed in eukaryotes. Here we investigate the potential role of these efflux carriers in CG trafficking in *O. fasciatus*.

Two MDR-like sequences (ABCB1, ABCB2) related to insect and human MDRs were identified by transcriptome searches. Western blots using an MDR-specific antibody (C219) confirmed the presence of MDRs in *O. fasciatus* and the detected ~130kDa protein band (range of predicted MWs) was restricted to the membrane fraction. Both proteins were expressed in tissues known to be important for adaptation to CGs: the thoracic storage compartment and the nervous system. Fluorescent IHC with C219 confirmed the presence of MDR-like proteins in the nervous system and that they are localized in the brain periphery. The expression of ABCB2 was 2.5 fold higher in bugs fed on a CG containing diet vs. bugs fed on a CG free diet. ABCB1 expression, on the other hand, was not altered. HPLC analysis of sequestered defense fluids revealed that ouabain uptake occurs rapidly: as fast as 1h *post* injection, highlighting the importance of temporal dynamics for MDR expression under CG exposure.

We confirmed the presence of MDR-like proteins on the transcript and protein level in *O. fasciatus*. The CG induced up-regulation of expression as well as MDR localization in the perineurium points towards an eminent role of MDRs in physiological adaptations to CGs.

**Keywords:** multidrug transporters, cardiac glycosides, *Oncopeltus fasciatus*

**OP-P-04**

**Influence of JAK/STAT signaling on the cell homeostasis in the fruit fly's airway epithelium**

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Worldwide, 235 million people suffer from chronic respiratory diseases like asthma. Especially the genetic predisposition plays an essential role in developing this chronic disease. But more and more other risk factors like allergens, tobacco smoke and air pollution are involved in promoting the disease progression. However, the signaling components relevant for pathogenesis are not yet fully understood. Key members of the evolutionary highly conserved JAK/STAT pathway (STAT3/6) are known to mediate susceptibility to asthma. We investigated the role of JAK/STAT signaling in remodeling the airway epithelium. On one hand we used different stressors like UV radiation, hypoxia and oxidative stress to trigger the pathway, on the other hand we were interested in the influence of upd secretion. Upds build a group of chemokines that behave as endogenous ligands of the JAK/STAT pathway. We wanted to know if all three members (upd, upd2 and upd3) are regulated and if their enhanced expression can effect a structural change of the epithelial cells of the fly's respiratory system. Affirming our conclusion our results demonstrate a time dependent expression of two of the chemokine ligands, *upd2* and *upd3* under hypoxic conditions in wildtype flies. This implicates an autocrine activation of the JAK/STAT pathway in the airway epithelium. In addition, we could observe dramatic structural changes as a result of ectopic overexpression in the whole tracheal system. We were able to detect a strong effect on the epithelial plasticity as represented by epithelial thickening of the dorsal trunks. Furthermore, we were able to link that the Wnt signaling pathway is a downstream target of the JAK/STAT pathway, what may probably implicate Wnt as a critical key player for the structural change of the epithelial cells. JAK/STAT appears to be a key factor in maintaining the epithelial homeostasis of the fruit fly's respiratory system.

**Keywords:** *Drosophila*, JAK/STAT, Asthma

OP-P-05

**Structure and function of the adipokinetic hormones of the cabbage pest insect, *Pieris brassicae***

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The cabbage white butterfly is a pest insect in South Africa: the larvae of *Pieris brassicae* feed on cruciferous crops. Adult *P. brassicae* undertake dispersal flights. Metabolic fuel for flight muscle contraction is usually supplied from the fat body, and regulated by peptides of the adipokinetic hormone (AKH) family, which is made in the corpus cardiacum (CC).

We aimed to elucidate and characterise AKH peptides in *P. brassicae* as part of a database on potential targets for biorational, integrated pest management.

Circulating lipid and carbohydrate levels were measured in resting butterflies; lipid is their preferred fuel. CC extracts were tested in butterflies in an *in vivo* bioassay for lipid mobilisation. LC-ESI MS was used to identify and sequence an AKH in the CC; the synthetically made AKH was tested *in vivo*. We measured lipid levels after free flight.

Three AKH peptides are in the CC of *P. brassicae*, one of which has a novel sequence: an octapeptide pELTFSSGW amide (denoted Piebr-AKH); the nonapeptide pELTFTSSWG amide (Manse-AKH) and the non-amidated undecapeptide pELTFTSSWGGK OH (Vanca-AKH). Injections of Piebr-AKH and Manse-AKH caused hyperlipaemia in *P. brassicae*, whereas Vanca-AKH did not. After flight and a short period of rest the circulating lipid level increased. Thus, AKHs are released from the CC to provide energy via lipid oxidation. Vanca-AKH is an incompletely-processed precursor of Manse-AKH.

Support: NRF (RSA) and UCT staff awards. ESI-MS by Dr P. Šimek (Czech Rep.).

**Keywords:** Adipokinetic peptides, cabbage white butterfly, adipokinetic bioassay

OP-P-06

**The GATA transcription factor ELT-2 mediates strain-specific immune responses in *Caenorhabditis elegans***

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Invertebrates were believed to rely exclusively on common responses of the innate immune system to fight the great diversity of pathogenic threats they encounter. However, recent evidence suggests that invertebrate taxa are able to mount pathogen- and even strain-specific immune responses, though the underlying molecular mechanisms are unknown. To test the hypothesis that the *C. elegans* immune response is pathogen strain-specific, we analyzed the transcriptomes of worms infected with two pathogenic (BT18247 and BT18679) and one non-pathogenic (BT18407) *Bacillus thuringiensis* (BT) strains. We found that while the expression of the majority of genes was generally regulated by infection with both pathogenic BT strains, 9,2% of infection responsive genes were differentially regulated between BT18247 and BT18679. To further investigate the molecular mechanisms underlying this strain-specific response, we searched for transcription factors regulating general and strain-specific expression changes. We found that the AP-1 component gene *jun-1* regulates the general response to pathogenic BT. *In contrast*; the GATA transcription factor gene *elt-2* mediates strain-specific responses to BT18247 and BT18679: *elt-2* RNAi knockdown worms were highly resistant to BT18247 infection, but highly susceptible to BT18679. Through epistasis analysis, we further found that the p38-MAPK pathway acts either in parallel to or directly interacts with *elt-2* in response to the pathogen BT18679, but is not required for the resistance to BT18247. The response of *C. elegans* to BT infection is thus strain-specific. Our results further suggest that ELT-2 mediates the specificity of the response, likely in the interaction with different signaling cascades.

**Keywords:** innate immunity, immune specificity, *Caenorhabditis elegans*

OP-P-07

**Temporal expression of the biological clock protein PERIOD in the brain of *Daphnia pulex***

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Many biological processes in organisms exhibit daily rhythms that are controlled by circadian clocks. These clocks are formed by interacting molecular feedback loops consisting of core clock genes and proteins. An essential feature of PER protein, encoded by the clock gene *period* (*per*), is its cycling in nuclear abundance.

Previous work showed that *per* mRNA and PER protein are rhythmic in the whole bodies of *Daphnia*. However, the localization of the central oscillator in this species is not known. Also there is no data about temporal changes of clock components expression in the brain in *Daphnia*. Thus the aim of our study was to characterize the temporal and spatial expression of PER protein in the *Daphnia* central nervous system.

To reach this goal we performed experiments on animals reared in light-dark (LD) conditions, constant darkness (DD) and continuous light (LL). To characterize PER localization, *D. pulex* brains were immunohistochemically processed with anti-PER primary antibody followed by analysis in the confocal microscope.

We found that PER is produced only in six neurons in the *Daphnia deutocerebrum*. One pair of these cells displays strong immunofluorescence, while staining of another two pairs remains much weaker. We observed circadian changes in the PER protein distribution in the cytoplasm and nuclei of labeled neurons under both LD and DD conditions whereas in LL this rhythm was abolished. Keeping the rhythm in DD confirms endogenous character of the observed phenomenon.

Identification of PER protein expression that oscillates over the course of the day in the population of brain neurons is important as it indicates the presence of locally active molecular oscillators in this organ which might drive rhythmic behavior of *Daphnia*.

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**Keywords:** *Daphnia*, circadian clock, period

OP-P-08

**Strong ion regulatory abilities enable the crab *Xenograpsus testudinatus* to inhabit the world's most acidic vents systems**

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**Introduction:** The underwater volcano of Turtle island off the coast of Taiwan has been described as one of the most acidic marine vent systems in the world, discharging water with a minimum pH of 1.25. This challenging hydrothermal vent habitat is inhabited by *Xenograpsus testudinatus*, a crab species that is endemic to shallow-water vent systems.

**Objectives:** To survive in this highly acidified environment, this species must have evolved substantial acid-base regulatory abilities which are unexplored, to date.

**Materials & Methods:** Determinations of extracellular acid-base parameters in combination with biochemical and gene expression analyses during exposure to hypercapnic conditions (pH 6.5; 1.78 kPa pCO<sub>2</sub>) were used to characterize the branchial pH regulatory machinery.

**Results:** Within few hours *X. testudinatus* restores extracellular pH in response to environmental acidification accompanied by a substantial increase in extracellular HCO<sub>3</sub><sup>-</sup> levels. Branchial Na<sup>+</sup>/K<sup>+</sup>-ATPase (NKA) and V-type H<sup>+</sup>-ATPase (VHA) increased in response to acidified conditions on the mRNA, protein and activity level. A high timely resolution of the compensation reaction demonstrates a time lag between mRNA expression and synthesis of the NKA and VHA, respectively. Immunohistochemical analyses demonstrate the presence of NKA in basolateral membranes whereas the VHA has a predominantly cytoplasmic localization in branchial epithelia suggest pH regulatory mechanisms of the VHA via vesicular pathways.

**Conclusion:** Our results suggest a strong coupling between osmo- and pH regulatory abilities in marine crustaceans and demonstrated that strong pH regulatory abilities represent a key feature of this crab species to successfully inhabit one of the world's most acidic marine environments.

**Keywords:** pH regulation, hydrothermal vent, gill

## Physiology – posters

### PP-P-01

#### **Webspinners - the forgotten insect order. Characterization of the first neuropeptide of webspinners.**

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Webspinners are the only group of animals that spins silk via numerous unicellular spinning glands situated in the substantially enlarged basitarsomer of the forelegs. This cryptic and not well-researched order of insects, the Embioptera, lives in silk-spun galleries on the bark of trees. We investigated *Oligotoma saundersii*, which is indigenous to India, but was collected off trees in Durban, South Africa.

Objectives: to elucidate and characterise a neuropeptide for the first time from this overlooked insect order.

The retrocerebral neurohaemal corpora cardiaca (CC) were dissected, and peptides extracted. The CC extracts were tested in cockroaches *in vivo* for carbohydrate mobilisation. Electrospray ionization mass spectrometry (MS) was performed with the CC extract to identify and sequence an adipokinetic hormone (AKH). A synthetic neuropeptide and a scrambled analogue was then tested in the *in vivo* assay to compare biological activity and learn something about the AKH receptor requirements.

The webspinner CC extract had a high hyperglycaemic potency in cockroaches. MS identified one decapeptide of the AKH family with a novel sequence: pEVNFSPNWGG amide. The synthetic peptide is very active in the cockroach and this can easily be explained by the sequence identity of the cockroach hypertrehalosaemic hormone with the first eight residues of the novel webspinner AKH, denoted Olisa-AKH. An analogue of Olisa-AKH where the positions of Pro and Asn were changed (...Asn<sup>6</sup>-Pro<sup>7</sup>....) had no biological activity at low concentrations demonstrating the importance of certain amino acid residues in the molecule at the correct position for receptor interaction.

Supported by the National Research Foundation of RSA and UCT staff awards.

**Keywords:** Embioptera, Adipokinetic hormone, Polyneoptera

### PP-P-02

#### **Lipid homeostasis in the *Drosophila* oenocyte: dual effect of starvation and cAMP activation.**

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Lipid metabolism is fundamental for development and produces much of the energy needed through periods of fasting. In the fruit fly *Drosophila melanogaster*, specialized hepatocyte-like cells (oenocytes) are principal cell type accumulating fat droplets during periods of starvation. The major goal of this project is to unravel the hormonal regulation of this complex process. For this, we manipulated the cAMP level in oenocytes in order to evaluate if hormonal signals converging onto cAMP level modify their physiology. It is evident that short-term starvation results in a significant increase in both, number and size of accumulated lipid droplets. Light induced activation of a bacterial adenylate cyclase that is exclusively expressed in oenocytes enhanced this effect significantly. Moreover, even under well-fed conditions, light-induced cAMP production induced the occurrence of lipid droplets. Furthermore, there is an obvious association between amount of lipid droplets in oenocytes and the sensitivity to starvation. The observed phenotype mirrors the situation found in humans with hepatosteatosis (fatty liver). Our results could pave the way for better understanding of the complex regulatory network that controls the activity of these hepatocyte-like cells and to understand molecular events underlying the pathogenesis of metabolic inflammation of the liver.

**Keywords:** oenocyte, lipid droplets, cAMP

**PP-P-03**

**Activation of different branches of the unfolded protein response induces massive changes in different organs of the fruit fly *Drosophila***

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In eukaryotic cells, endoplasmic reticulum (ER) stress occurs when misfolded proteins accumulate in the lumen of the ER, it is observed in many tissues in human diseases including cancer, diabetes, obesity, and neurodegeneration. The unfolded protein response (UPR) is an intracellular signal transduction pathway, which is activated to respond to ER-Stress to restore homeostasis. *Drosophila* is becoming a powerful tool for studying the role of ER stress and the UPR. The UPR consists of three main signaling branches, mediated by inositol-requiring protein-1 (IRE1/XBP1), activating transcription factor-6 (ATF6) or protein kinase RNA (PKR)-like ER kinase (PERK).

Using *Drosophila melanogaster* as a model, we studied the role of the three branches of the unfolded protein response by their ectopic activation. For this, we enhanced expression of IRE1, XBP1s, PERK, or ATF6 respectively. Overexpression of XBP1s and of PERK in the fat body induced striking structural changes in cell shapes and nuclear sizes, while expression of IRE1 and ATF6 had only minor effects. Activation of XBP1s and of PERK in the trachea was lethal. Moreover, we could find that ectopic activation of XBP1s and of PERK, both in trachea and in the fat body induced expression of antimicrobial peptide genes, namely that of the AMP *drosomycin*. Thus, a strong activation of the innate immune response might be part of the UPR in these tissues.

**Keywords:** *Drosophila*, UPR, ER-stress

**PP-P-04**

**Nutritional effects on the progression of intestinal cancer in *Drosophila***

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*Drosophila* is a well established model for colorectal cancer. Nutrition is the main factor interfering with the midgut epithelium. Therefore, we are using the fruit fly to investigate the influence of high fat dieting and caloric restriction, conditions that industrialized and developing countries are encountering, respectively.

We are investigating hyperplasia in the fly's midgut by elucidating the role of the EGFR MAPK signaling in tissue remodeling and cancer progression. Flies expressing the oncogene *raf* develop colorectal cancer. The tumor growth was qualified and monitored over time by microscopy and by luciferase analysis. Additionally, the effects of the progressing cancer on different aspects of metabolism and lifespan were investigated.

A constitutive activation of the EGFR MAPK cascade leads to the formation of stem cell nests and impacts the lifespan of flies. An early onset of cancer impairs larval development and is lethal during pupation. Stem cell nests in flies feeding on a high fat diet are enlarged and densely packed, indicating an increased proliferative rate. Additionally, these flies exhibit a reduced lifespan. In contrast, caloric restriction results in small, sporadic stem cell nests. A reduced lifespan is observed in these flies although hyperplasia is reduced, indicating that they might suffer from wasting syndrome.

Our results highlight the striking role of nutrition in cancer progression. Calorically restricted flies are starving while the tumor grows, whereas flies feeding on a high fat diet exhibit a somewhat similar phenotype due to the fast progression of cancer and its devastating effects on the epithelium's integrity. We suggest that alternating food regimes might rescue the observed phenotype.

**Keywords:** *Drosophila*, Cancer, Intestinal Epithelium

**PP-P-05**

**Ectopic activation of EGFR signaling induces lung cancer-like phenotypes in the airway epithelium of *Drosophila***

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Lung cancer is one of the most aggressive types of cancer with an extremely high overall fatality rate due to late state detection and the lack of late state treatment options. *Drosophila* is a model for studying chronic inflammatory diseases of the lung, its tracheal system shares comprehensive structural and functional similarities with the human lung, thus making it an ideal model for studying the molecular framework underlying lung cancer development.

Targeted overexpression of human oncogenes and their *Drosophila* homologs in the airway epithelium was chosen to induce cancer-like phenotypes in *Drosophila*. The larvae were analyzed regarding hyper- and metaplasia of the epithelium. For this, we measured e.g. thickening of the epithelium or a change in number and size of the nuclei. Larvae showing a strong cancer-like phenotype were selected for treatment with potential anti-cancer drugs in a 96-well format.

A number of oncogenes were able to induce epithelial meta- and hyperplasia indicating that they can induce tumor formation in the airway system. A thickening of the epithelium and an increased number of nuclei are showing the proliferating state of the tissue. Ectopic overexpression of a constitutively active version of the EGFR gene in larval airway epithelia is lethal in early developmental stages. When treated with specific EGFR inhibitors these larvae can successfully develop into adult flies.

The results highlight the potential of *Drosophila* as a model in cancer research and its usefulness in high-throughput anti-cancer drug screenings. It is our goal to use *Drosophila* lung cancer models to understand the molecular underlying tumor formation and progression and to identify compounds that can be used as therapeutic agents.

**Keywords:** *Drosophila*, Cancer, Drug Screening

**PP-P-06**

**Chitosan-based delivery of mRNA to human airway epithelial cells for cystic fibrosis therapy**

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The lethal genetic disorder cystic fibrosis (CF) is caused by a dysfunction of the epithelial chloride channel *cystic fibrosis transmembrane conductance regulator* (CFTR). In recent years, clinical approaches for CF gene therapies mostly failed due to increased unwanted immune responses towards the vectors. Therefore, it is essential to develop suitable vehicles for the optimal delivery of genes to target cells at the expense of minimal toxicity. This study evaluates chitosans (CS) as potential non-viral carrier for wtCFTR-mRNA to transfect human airway epithelial cells to specifically address CF. CS are natural biocompatible cationic polymers, which are able to form interpolyelectrolyte complexes with nucleic acids via self-assembly. Hence, primary human airway epithelial (HNE) cells were transfected with CS-wtCFTR-mRNA complexes at (+/-) charge ratio 30. Twenty-four hours after transfection, electrophysiological Ussing chamber measurements were conducted. HNE cells showed an increase in the cAMP-stimulated current as compared with the non-transfected cells, which indicates a functional expression of CFTR. This study demonstrates that transfection of HNE cells with wtCFTR-mRNA using chitosan as a carrier results in increased CFTR function. In conclusion, CS-wtCFTR-mRNA complexes are a promising alternative for future CF therapies.

**Keywords:** Chitosan, Cystic Fibrosis, Transfection

PP-P-07

**Effect of cigarette smoke exposure on the airway epithelium of the fruit fly *Drosophila melanogaster***

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Cigarette smoke with over 4000 different components is the primary risk factor of a disease called chronic obstructive pulmonary disease (COPD). COPD is predicted by the WHO to become the third leading cause of death in 2030 and already today over 64 million people suffer from it. The term COPD comprises all diseases resulting in an airflow limitation due to the destruction of lung tissue (emphysema), fibrotic changes in the lung tissue (fibrosis) and mucus hypersecretion. As there is no cure yet, the need to understand this disease in its full complexity is great, to counteract the postulated effects.

In order to understand the responses of the airway epithelium to prolonged cigarette smoke exposure (CSE), we used the fruit fly *Drosophila melanogaster* as a model. For this, the tracheal epithelium was subjected to CSE with smoke of three cigarettes at an interval of three hours on two consecutive days each. After manual dissection of the tracheal system, RNA sequencing and qRT-PCR was performed. Daily low dose CSE (1 cigarette per day) reduced the lifespan of adult *Drosophila* significantly in comparison to matching controls. In addition, cigarette smoke exposed *Drosophila* larvae showed an increase in tracheal epithelial thickness. Results of RNA sequencing suggest the involvement of the Keap1/Nrf2 and JAK/STAT pathway in the reaction to CS exposure.

Among the regulated genes are those encoding for the cytochrome P450 family, Glutathione S-transferases and Mucin-like proteins. Based on these results, we will further expand the *Drosophila* COPD model to better understand the molecular framework underlying COPD development.

**Keywords:** *Drosophila*, COPD, Signalling

PP-P-08

**Role of FoxO and nutritional stressors for maintaining epithelial homeostasis in the *Drosophila* intestine**

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Maintaining intestinal homeostasis is essential for organismal health and to prevent premature death. Previous findings suggested that FoxO is a key player for keeping homeostasis in different epithelia of the fruit fly *Drosophila melanogaster*. On the other hand, different nutritional stressors, such as malnutrition, high fat dieting, starvation or caloric restriction are believed to disturb the epithelial homeostasis and consequently the intestinal architecture.

In our studies we examined the impact of deregulated FoxO expression and of different nutritional regimes on the physiology and structure in the intestine of *Drosophila*. Moreover, the response of *upd3*, a cytokine relevant for activation of stem cell activity, upon FoxO overexpression and nutritional stress was investigated.

In order to analyze the role of FoxO in the gut epithelium, we used the binary expression system Gal4/UAS to specifically overexpress FoxO in different intestinal cell types. The influence of FoxO on the gut morphology was elucidated by using immunohistochemical methods. RT-qPCR was used to show FoxO-mediated regulation of *upd3*. The impact of nutritional stressors on the gut of *Drosophila* was tested by rearing the flies on different, chemically well-defined food sources.

Based on these studies, it can be assumed that FoxO plays an important role in intestinal epithelial homeostasis. Moreover, FoxO appears to regulate *upd3* regulation. Nutritional stress, like high fat, affects the intestinal cell composition. Taken together, FoxO is a key factor that is responsible for keeping a homeostatic situation in the intestinal epithelium.

**Keywords:** *Drosophila*, gut, nutrition

PP-P-09

**Substitutions in the cardenolide target site and  $\beta$  subunits together determine the kinetic behavior of the *Drosophila* Na,K-ATPase**

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Cardenolides, like ouabain, are specific inhibitors of the ubiquitous Na,K-ATPase. Substitutions within the cardenolide target site of several insects' Na,K-ATPase  $\alpha$ -subunits have been shown to confer increased insensitivity towards these toxins. The cardenolide-adapted milkweed bug *Oncopeltus fasciatus* for example has three isoforms of the  $\alpha$ -subunit (A, B, and C) that differ in the number and identity of resistance conferring substitutions. However, the extent to which these substitutions alter the kinetic properties of insect Na,K-ATPase is not clear. We investigated the impact of these different combinations of substitutions by introducing them into the  $\alpha$ -subunit of *Drosophila melanogaster* and combined these mimics with two different  $\beta$ -subunits, Nrv2.2 and Nrv3. While the substitutions Q111T-N122H-F786N-T797A (A-isoform mimic) and Q111T-N122H-F786N (B-isoform mimic) mediated a high insensitivity to ouabain compared to the wild type, they also exhibited a drastically lowered ATPase activity with both  $\beta$ -subunits. Remarkably, the identity of the  $\beta$ -subunit was also decisive and mimics combined with Nrv3 were significantly less active than those combined with Nrv2.2. Measurements of K<sup>+</sup>-, Na<sup>+</sup>- and ATP-dependent ATPase activities of the recombinant enzymes revealed that the substitutions strongly altered the substrate affinities of the recombinant enzymes. The affinities were also considerably influenced by the co-expressed  $\beta$ -subunit. Our results demonstrate that naturally observed resistance against cardenolides comes at the cost of significantly altered kinetic properties of the Na,K-ATPase. The  $\beta$ -subunit can strongly modulate these properties but cannot fully compensate for the effect of the substitutions.

**Keywords:** Na,K-ATPase, Cardenolide target site, Substitutions

PP-P-10

**Cation-entry through *S. aureus* alpha-toxin pores depolarizes membrane potential and activates p38 MAP kinase in human airway epithelial cells**

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One of the major virulence factors expressed by most strains of *Staphylococcus aureus* is the pore-forming alpha-toxin (alpha-hemolysin, hemolysin A, Hla). To determine whether the Hla pore is directly permeable to mono- or divalent cations (Na<sup>+</sup>, Ca<sup>2+</sup>) we treated immortalized human airway epithelial cells with recombinant Hla (rHla), a mutated form of rHla, rHla-H35L, which forms oligomers in the plasma membranes of eukaryotic cells but fails to form functional transmembrane pores, or the cyclodextrin-derivative IB201, a blocker of the Hla-pore, and used membrane potential ( $V_m$ )-, Na<sup>+</sup>- or Ca<sup>2+</sup>-sensitive fluorescent dyes to analyze changes in  $V_m$  or intracellular ion concentrations. Our data indicate that Na<sup>+</sup>- as well as Ca<sup>2+</sup>-ions were able to pass through the rHla-pore and accumulated in the cytosol. The rHla-H35L oligomer, however, did not allow ion influx. Our finding that pre-treatment of cells with IB201 prevented the rHla-mediated increase in [Ca<sup>2+</sup>]<sub>i</sub> provided additional evidence for the conclusion that Ca<sup>2+</sup>-ions enter the cells directly through the Hla pores. Hla-mediated ion fluxes were accompanied by depolarization of the plasma membrane to the same degree as achieved upon treatment of cells with gramicidin which forms transmembrane channels permeable to monovalent cations. Both treatments resulted in increases in p38 MAP kinase phosphorylation in the cells. Our results indicate that formation of functional Hla-pores in the plasma membrane of airway epithelial cells activate the p38 MAP kinase signal transduction module through changes in ion equilibria and plasma membrane depolarization. Such stress conditions may activate defense mechanisms of the cells directed against the bacterial attack.

**Keywords:** bacterial toxin, airway epithelial cells, ion equilibrium

PP-P-11

**Hirudins and hirudin-like factors in *Hirudinidae*: implications for function and phylogenetic relationships**

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Haematophagous leeches express a broad variety of bioactive factors that are released from the salivary gland cells into the wound of a host during feeding. Among these, hirudin is probably the best studied factor and, moreover, the only one that has successfully made the transition from nature to clinical use. Many components of the leech saliva still remain either poorly characterized or yet completely unknown. Only recently a new class of leech-derived factors has been discovered in *Hirudo medicinalis*, the hirudin-like factors (HLFs). HLFs comprise typical structural features of hirudin, but lack others. We were able to verify the expression of HLFs not only in two additional species of the genus *Hirudo*, but also in *Hirudinaria manillensis*. Various phylogenetic analyses based on gene and protein sequences support a sister group relationship between hirudins and HLFs. Although potential molecular targets of HLFs remain unknown, the presence of multiple isoforms in individual leeches of different genera points to key functions in the regulation of several processes associated with the blood-sucking life style of leeches.

**Keywords:** Hirudinidae, Hirudin, Phylogeny

PP-P-12

**Digestion physiology predicts sensitivity of marine invertebrate larvae to ocean acidification**

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**Questions:** Anthropogenic emission of CO<sub>2</sub> is predicted to decrease ocean surface pH by 0.4 pH units in the coming century, termed ocean acidification (OA). Marine larval stages were identified to be the weakest link when a species is confronted with acidified seawater. Because of OA related changes in seawater carbonate system chemistry, special attention has been dedicated to marine calcifiers, but recent studies demonstrated that some non-calcifying species also respond sensitively to acidified seawater. The underlying physiological processes remain unexplored.

**Methods:** We used larvae of a hemichordate (*Ptychodera flava*) and a sea star (*Archaster typicus*) to access the effects of OA levels on the morphology and physiology in these non-calcifying marine organisms. We measured growth, survival, gastric pH, extracellular matrix pH and metabolic rates in response to simulated OA.

**Results:** Two contrasting physiological mechanisms were observed in these two species. Larvae of the hemichordate *P. flava* respond highly sensitive (100% mortality after 8 days) to simulated near-future acidification levels and have highly regulated alkaline (pH 10.13± 0.04) digestive systems. Metabolic rates increased 4-fold in response to acidified seawater. In contrast, the sea star *A. typicus* displayed no increased mortality, but a slight developmental delay and did not regulate gastric pH.

**Conclusions:** Non-calcifying marine larvae may respond very differently to simulated ocean acidification. Digestion physiology can be regarded as one of several key process that determines the degree of sensitivity. Our results highlight the importance to better understand physiological processes in marine larval stages and suggest that our current knowledge underestimates the severity of ocean acidification on marine biota as many non-calcifying species were neglected.

**Keywords:** environmental change, pH regulation, energetics

**PP-P-13**

**Biochemical and bioinformatic analyses of the chitin synthase**

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Chitin synthases (CHSs) belong to family 2 of membrane-integral glycosyltransferases (GT2), which also include hyaluronan synthases and cellulose synthases (CSs). While catalysis of the polymerization reaction occurs in the cytosol, the polymers are deposited at the extracellular site indicating that they are translocated across the plasma membrane. A major breakthrough in understanding this process was achieved by the crystallization of the BcsA-BcsB CS complex from *Rhodobacter sphaeroides*, which revealed a cellulose-conducting channel formed by six transmembrane helices. The overall structure was in line with a previously suggested model according to which polymerization and translocation are tightly coupled processes in GT2 enzymes. Current knowledge on the mode of action of CHSs is limited due to the lack of structural data. However, several transmembrane helices of the presumed translocation channel are highly conserved in CHSs too, and thus may be involved in chitin translocation. To analyze this process, we investigated the chitin synthase Chs3 in the genetic model *Saccharomyces cerevisiae*. Based on amino acid sequence alignments, computational structure predictions and proteinase accessibility assays, we generated a topological model for Chs3. Interestingly, GT2 enzymes may facilitate fibrillogenesis by the assembly of several catalytic units, and also chitin synthases have been shown to form oligomeric complexes. To analyze the significance of Chs3 oligomerization *in vivo*, we used bimolecular fluorescence complementation. We detected oligomeric complexes at the bud neck, in the membranes of Golgi vesicles, and in the membranes of the endoplasmic reticulum (ER) when using mutant cells defective in the ER exit.

**Keywords:** chitin synthase, oligomeric complexes, chitin translocation

**PP-P-14**

**How leaf beetles exploit poisonous plants  
- Functional profiling of their ABCB transporters -**

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We chose the specialized leaf beetle *Chrysochus auratus* to elucidate the essential physiological and molecular mechanisms involved in insect resistance to plant toxins. This leaf beetle is specialized to feed on cardenolide containing host-plant and deploys these potent plant toxins for its own defense. We assume that ABCB (ATP-binding cassette, subfamily B) transmembrane proteins play a key role in the evolution of host-plant derived toxin sequestration and test this hypothesis using *C. auratus* as a model system.

A bioinformatic screen of the transcriptome of *C. auratus* revealed three different ABCB transporters (*Ca*\_ABCB). Using a baculovirus system we managed to express the beetle's ABCB transporters heterologously in Sf9 cells. In order to investigate their function, we established different transport assays. As ABCB transporters rely on ATP hydrolysis, ATPase assays of isolated membranes of *Ca*\_ABCB overexpressing cells can be used as a screening tool for ABCB transporter substrates. Furthermore, we tested inside-out membrane vesicles (MV) from *Ca*\_ABCB overexpressing cells. Subsequently, quantitative fluorescence or radiolabeled substrates were used to evaluate directly the transport activity by quantifying the compounds in vesicular accumulation assays.

Our data show that one *Ca*\_ABCB transporter imports radiolabeled cardenolides from the outside of the cell membrane vesicles to the inside. In summary, our results support that the leaf beetle's ABCB transporters located at cellular and physiological tissue barriers may contribute to/ be decisive for selective cardenolide sequestration.

**Keywords:** ABCB transporter, leaf beetles, Cardenolides

PP-P-15

**Exploring the role of C-type lectin-like domain gene *clec-4* and its paralogs in *C. elegans* immunity**

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*Caenorhabditis elegans* has a highly diverse and large number of 283 genes encoding C-type lectin-like domain proteins (*clec* genes). The differential expression of *clec* genes in response to pathogen infection has led to a generalized assumption of their role in immunity, although their exact function is completely unknown. In this study we asked whether pathogen responsive *clec* genes indeed function in *C. elegans* immunity.

We analyzed microbe-induced expression of *clec* genes and identified *clec-4* as being highly responsive to infection with different pathogens. We thus focused on *clec-4* for subsequent functional analyses. Contrary to our expectations, *clec-4* knock-out had no effect on worm survival on *Pseudomonas aeruginosa*, whereas *clec-4(ok2050)* mutants were either more susceptible or more resistant after infection with different strains of *Bacillus thuringiensis* (BT). By looking at the expression of *clec-4* paralogs, we identified co-expressed *clec-41*. We further found that *clec-41* acts redundantly with *clec-42*. Knocking-down both genes by RNAi resulted in a higher susceptibility to infection by both BT strains and revealed a genetic interaction between *clec-4*, *clec-41*, and *clec-42* on BT. Analysis of transgenic reporter strains showed that all three *clec* genes are expressed in the intestine, in the case of *clec-4* also in amphid neurons.

We conclude that the three pathogen responsive *clec* genes function in *C. elegans* immunity. However, while *clec-41* and *clec-42* are required for resistance against BT infection, the role of *clec-4* is less clear. Thus, the function of *clec* genes in *C. elegans* immunity cannot be assigned purely based on their transcriptional up-regulation upon infection.

**Keywords:** *C. elegans*, immunity, C-type lectin-like domain gene

PP-P-16

**Inhibitors of P2X-receptors interfere with  $\alpha$ -toxin binding and toxicity**

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The  $\alpha$ -toxin from *S.aureus* is one of the most-studied toxins. Still, the basic mechanism of membrane-protein interactions is poorly understood. The toxin is able to lyse pure lipid membranes if they contain either sphingomyelin or phosphatidylcholine, since these two lipids seem to constitute the primary binding partner. Concentrations necessary to lyse liposomes are 200 nM and above, depending on the composition. In particular, sphingomyelin in the liquid-disordered phase increase oligomerisation efficiency (Schwiering 2013). In contrast, certain cells are lysed at low or sub-nanomolar concentrations. In the last years experimental evidence is accumulating which points towards a role of ATP-gated P2X-channels in enhancing lysis (Skals 2011). Is this concept a general one in the context of toxin-induced lysis? A study of the effect of various P2X-receptor antagonists on hemolysis induced by  $\alpha$ -toxin from *S.aureus* showed that the inhibitory concentrations of antagonists like PPADS, MRS2159 and BBG are in a similar range as reported for other erythrocytes and other toxins. However, treatment with hexokinase, oxATP or ATP did not alter lysis nor did changes in extracellular calcium concentration. Furthermore, inhibitors PPADS and MRS2159 interfere also with the interaction of the toxin with pure-lipid membranes, as evidenced by efflux-measurements, gel-electrophoresis and fluorescence microscopy and PPADS inhibits binding of Hla to HaCaT cells. Thus, these results point more towards lipid/toxin/membrane effect than towards an involvement of P2X7-receptors in the action of  $\alpha$ -toxin induced hemolysis.

Schwiering, M., Brack, A., Stork, R. et al. (2013), *Biochim Biophys Acta* 1828, 1962-72.

Skals, M., Leipziger, J., Praetorius, H.A. (2011), *Pflugers Arch* 462, 669-79.

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**Keywords:** pore forming toxin, *s.aureus*, P2X

**PP-P-17**

**Primary lateral line afferents of *Xiphister mucosus* respond to thermal stimuli**

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The marine teleost *Xiphister mucosus* (Stichaeidae) inhabits the intertidal zone of the Pacific coastline. *Xiphister* has four trunk lateral line canals on each body side, each of which has many side branches (tubuli). A tubulus can have up to five pores, thus *Xiphister* may have over 1500 lateral line canal pores on each body side. The functional significance of the *Xiphister* lateral line has not yet been fully understood. In an attempt to close this gap, we recorded from primary lateral line afferents while stimulating the lateral line of *Xiphister* with local water movements. None of the primary lateral line afferents responded to mechanical stimuli. Instead, afferents responded to thermal stimuli: while the ongoing activity of all afferents increased if the water temperature slowly increased, sudden temperature changes resulted in a reversed response. Cooling increased and sudden warming decreased neuronal activity. This paradoxical response has also been reported for the lateral line system of rays and frogs. However, the present study is the first that documents the phenomenon in bony fishes. We will discuss our finding with respect to the natural habitat of *Xiphister mucosus*.

**Keywords:** Xiphister, lateral line, temperature

**PP-P-18**

**Hemoglobin and its role in temperature acclimation in *Daphnia*:  
A comparative approach between and within species**

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For poikilothermic aquatic animals, elevated temperatures are correlated with rising oxygen demand and decreasing oxygen supply. Consequently, raising the hemoglobin concentration and thus increasing the oxygen transport capacity of the hemolymph is an important adjustment during temperature acclimation of the small planktonic crustaceans *Daphnia*.

The potential to induce hemoglobin under warm conditions shows large differences between the species of the genus. *Daphnia magna* increases the hemoglobin concentration in the hemolymph to a significantly higher amount than *Daphnia pulex*, which is correlated with a lesser degree of thermotolerance in the latter species (Lamkemeyer et al, 2003, Can J Zool 81:237; Gerke et al, 2011, Comp Biochem Physiol A 159:56). Comparing *Daphnia galeata* and *Daphnia hyalina*, the different potential to induce hemoglobin at elevated temperature (Pinkhaus et al, 2007, Freshwater Biol 52:1537) can be assigned to habitat preferences: Only specimen with up-regulated hemoglobin expression are found in the deeper water layers with low oxygen content.

But also within a species, considerable variation of the temperature-induced hemoglobin accumulation is observed. A study of 39 clonal lines of *Daphnia magna* reveals intraspecific differences in hemoglobin concentration in animals raised at 20°C and 30°C ambient temperature. The adjustments at elevated temperature include strong increases, constant levels and even slight decreases of hemoglobin concentrations. The impact for the animals' thermotolerance is subject of the present analyses. Along with common garden competition experiments, trade-offs of resource allocation to hemoglobin induction can be estimated. The results can add important puzzle pieces to our understanding of the role of hemoglobin in temperature acclimation of poikilothermic animals.

## Zoological Systematics – invited talks

### Complex speciation and irresolvable branches in the avian Tree of Life

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**Introduction:** Birds have arguably been the most intensely studied animal group for their phylogenetic relationships. However, the recent advent of genome-scale phylogenomics has made the forest of bird phylogenies even more complex and confusing.

**Objectives:** I will show here that most parts of the avian Tree of Life are now firmly established as reproducible phylogenetic hypotheses. This is to the exception of the deepest relationships among Neoaves.

**Materials & methods:** Using phylogenetic networks and simulations, I argue that the very onset of the super-rapid neoavian radiation is irresolvable because of eight near-simultaneous speciation events.

**Results:** Such a hard polytomy of nine taxa translates into 2,027,025 possible rooted bifurcating trees. Accordingly, recent genome-scale phylogenies show extremely complex conflicts in this (and only this) part of the avian Tree of Life. The early neoavian polytomy coincides with the Cretaceous-Paleogene (K-Pg) mass extinction and is, to my knowledge, the first empirical example of a hard polytomy.

**Conclusion:** This example illustrates the necessity for three paradigm shifts avian phylogenomics as well as genome-scale phylogenomics in general: 1) Bootstrap and conventional Bayesian posterior probabilities should not be the only measures for topological support. 2) Every phylogenetic tree hypothesis should be accompanied by a phylogenetic network for visualization of conflicts. 3) Hard polytomies exist in nature and should be treated as the null hypothesis in the absence of reproducible tree topologies.

### Detecting convergence – Computational biomechanics refines our view on insect head evolution

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Convergence is a common phenomenon that might bias phylogenetic reconstruction. Functional demands, or constraints, influencing the evolution of morphological characters, may promote that convergence. If characters are functionally dependent to each other, this can even result in concerted convergence - the convergent evolution of whole groups of characters. Here, a novel biomechanical approach is introduced to detect convergence in a set of cephalic characters focused on the deep level relationships of winged insects, i.e. mayflies, dragonflies and neopterans. Musculoskeletal modelling combined with finite element analysis allows biologically realistic simulations of insect biting and predictions of head loading. The resulting strain patterns allow an assessment of whether characters are mechanically interdependent which might be used as an independent measure of convergence. Biting simulations reveal functional interactions of a suite of structures in the insect head capsule, mainly ridges, endoskeletal elements and joints, which are indeed mechanically connected to each other. Phylogenetic tree reconstruction excluding these functionally interdependent characters, based on the mechanical data, supports a sistergroup relationship of dragonflies and mayflies. Mechanically induced concerted convergence is a potentially widespread phenomenon within organisms. With a combination of biomechanics and phylogenetics, such as the one proposed here, we should be able to explain functional dependencies, common selective pressures, and thus concerted convergence in a wide array of characters complexes and lifeforms.

## Zoological Systematics – oral presentations

### OP-ZS-01

#### These legs were made for walking... - Three dimensional analysis of the spider locomotory system

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Although an impressive body of knowledge exists, detailed comparative studies of structural and spatial aspects of the complex locomotory apparatus in Arachnida have produced contradictory results. In the course of a comparative survey recently started on this topic, we therefore studied three representative species of spiders (*Liphisitus malayanus*, *Cupiennius salei*, *Araneus diadematus*). One major aim of this study was to establish visualization methods and terminology to be easily and consistently applied to all arachnid taxa.

Spiders comprise over 45,000 species and, in some features, show a fascinating disparity. Other features, such as the locomotory system, however, seem to be highly conserved. Generally, the locomotory system in spiders consists of the prosoma and its four pairs of walking legs, each comprising seven cuticular podomeres. The locomotory musculature can be subdivided into the extrinsic musculature situated in the prosoma and the intrinsic musculature located inside the walking legs.

Here we present the first three-dimensional analysis of the locomotory system in spiders. Cuticular structures, muscles and tendons are visualized and described using state of the art morphological methods. To unify the nomenclature of the investigated structures, results are compared to published data and a position-based nomenclature of muscles is established which does not refer to homology in order to avoid *a priori* misconceptions. On the basis of these comparisons, homology hypotheses are formulated in order to synthesize all current morphological knowledge. This in combination with interactive 3D representations confer our results a high degree of reproducibility.

**Keywords:** Araneae, musculature, cuticular exoskeleton

### OP-ZS-02

#### The importance of the Paleo-Tethys Ocean for the evolution of *Stygocapitella* (Parergodrilidae, Annelida)

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Many interstitial species with limited dispersal capacity are complexes of cryptic species showing a seemingly cosmopolitan distribution. Mainly two hypotheses have been put forward explaining the global distribution of such complexes. The first hypothesis assumes that vicariance following plate tectonics has driven their distribution and the strong similarities would be cases of morphological stasis lasting for millions of years. The second one stresses the importance of dispersal over long distances during the last thousands of years. The interstitial annelid *Stygocapitella subterranea* is such a complex with populations in Northern America, Europe, Australia, and South Africa and a tropical distribution gap. Using specimens from both hemispheres and morphological, nuclear and mitochondrial data we show that the origin of this complex is within the Southern hemisphere. About 260 million years ago the complex split into Panthalassic and Paleo-Tethys parts and the Northern hemisphere was colonized from the Australian region via the Paleo-Tethys Ocean about 80 million years ago. Hence, the distribution of this complex was not driven by recent distributions, but rather it showed a strong case of morphological stasis. On the other hand, our analyses also indicate that the distribution did not strictly follow vicariant events, but only generally the formation of the Paleo-Tethys Ocean and then its disappearance. More important was the Paleo-Tethys Ocean and, therefore, in the distribution of marine, especially interstitial, species it should be considered more often.

**Keywords:** Phylogeography, Meiofauna, Vicariance

OP-ZS-03

**The oldest velvet worm in amber reveals early migration patterns of Gondwanan onychophorans into Southeast Asia**

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The anomalous occurrence of supposedly Gondwanan taxa in Laurasian-derived regions remains an intriguing chapter of the palaeobiogeographical history of velvet worms (Onychophora). In particular, extant representatives of the subgroup Peripatidae show a disjointed distribution in the neotropics, tropical Africa, and Southeast Asia, with the latter being the only landmass previously associated to Laurasia. The arrival of peripatids in Southeast Asia has been controversially explained by either an early migration via Europe before continental drift (Eurogondwana hypothesis) or transportation via insular India during the Cretaceous/Paleogene (“Out-of-India” hypothesis) — a hypothesis based on a single extant species of Peripatidae, *Typhloperipatus williamsoni*, in India. To clarify this issue, we studied †*Cretoperipatus burmiticus* from Myanmar — the oldest fossil onychophoran found in amber and crucial for clarifying how Gondwanan lineages of these animals reached Southeast Asia, as it dates to sometime between these two conflicting scenarios. Based on anatomical reconstruction using synchrotron radiation-based X-ray microtomography (SRμCT) and comparisons with SEM data from extant taxa, we resolved the hitherto unclear position of †*C. burmiticus* within Onychophora, in particular, within Peripatidae with *T. williamsoni* as its closest extant relative. These findings suggest that the Eurogondwanan migration is the most likely scenario in this case, as Burmese amber is too old to be compatible with the “Out-of-India” hypothesis. Consequently, representatives of Peripatidae probably colonized India only recently from Myanmar, thus refuting the putative Gondwanan relict status of Indian onychophorans.

**Keywords:** Onychophora, Biogeography, Fossil

OP-ZS-04

**Spotting specifics in nature’s look-alike contest: Evolutionary systematics of Thai marsupial snails**

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**Introduction:** A major challenge of evolutionary systematics is the delimitation of species and species groups. This is especially true for taxa that either exhibit characters similar to those of their closest relatives or cases where a high plasticity of characters is present. The latter case is exhibited within and between several genera of the viviparous thiarid snails (Gastropoda, Cerithioidea).

**Objectives:** Aiming at a clear delimitation of Thai thiarid taxa, we here examine three morphologically particular similar snail genera: *Neoradina*, *Stenomelania* and *Melanoides*. Shell morphology of these species groups is highly confusable, hampering the delimitation and species identification.

**Material and Methods:** We examined specimens of all three genera by means of molecular biology, geometric morphometrics of the shell, examination of radula morphology and brood pouch content (viz. veliger larvae or juveniles).

**Results:** We found all three groups to genetically cluster in distinct clades. These are only recognizable by a combination of morphological characters whereas any single morphological character is indifferent at least for one of the species and genus pairs.

**Conclusion:** Our findings emphasize the general necessity to use evolutionary systematics approaches rather than only spotlighting particular genetic or morphological characters for taxon delimitation.

**Keywords:** Gastropoda, Evolutionary Systematics, Viviparity

**OP-ZS-05**

**Pancrustacean phylogenomics: New insights into pancrustacean evolution from large-scale transcriptome analyses**

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Molecular phylogenetic analyses have led to profound changes in our understanding of crustacean phylogenetics and evolution. Probably the most important finding was that Hexapoda are terrestrial Crustacea (a taxon termed Pancrustacea or Tetraconata). However, the phylogenetic relationships among several pancrustacean main groups, including Hexapods, are still not fully resolved. One of the underlying problems in determining these relationships has been that two key taxa - Remipedia and Cephalocarida - were either missing or represented by single species each in previous studies.

We present the most detailed transcriptome-based pancrustacean phylogenetic study to date. We focus on resolving the phylogenetic relationships of Hexapoda by including three species of Remipedia and two of Cephalocarida. To further resolve the phylogenetic relationships among crustacean main taxa and especially within Malacostraca and Branchiopoda more than 80 crustacean transcriptomes and genomes were included. The majority of transcriptomes were newly sequenced for this study.

Most of our phylogenetic analyses support monophyletic Xenocarida (Remipedia + Cephalocarida) as sister group to Hexapoda with Branchiopoda being the sister group to Xenocarida + Hexapoda. Yet, a few analyses suggest that either Remipedia alone or Branchiopoda are hexapod's closest sister group or Branchiopoda as the sister group to a monophyletic clade comprising Malacostraca + Cirripedia + Copepoda. Differences in evolutionary rates among genes may explain some of the conflicts.

**Keywords:** Pancrustacea, Phylogenomics, Transcriptomes

**OP-ZS-06**

**The power of sex pheromones in systematics**

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The delimitation of taxa is a constant challenge in taxonomic and phylogenetic research. The most commonly used methods, morphological and molecular studies (e.g. "barcoding"), allow only indirect conclusions with respect to reproductive isolation between taxa as required by the biological species concept, the most accepted species concept today. Here we show the reliability of using sex pheromones as markers for species delimitation. Using an integrative taxonomic approach to revise the click beetle genus *Idolus*, we applied molecular analysis of COI (mtDNA), CAD, and ITS2 (nDNA) genetic markers, as well as a multivariate ratio analysis (MRA) to numerous body measurements. The results are compared to earlier findings on the composition of the sex pheromones in the studied taxa. Our results demonstrate that molecular and morphological methods both fail to separate some taxa, which have different sex pheromones and are therefore sexually isolated from each other. This demonstrates the ability to resolve questionable species delimitations or to separate cryptic (molecular and/or morphologic) species.

**Keywords:** Sex pheromone, Systematic, Species concept

OP-ZS-07

**Comparative morphology of euplantular ultrastructures in Phasmatodea (Hexapoda)**

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Attachment organs with different ultrastructure have been evolved on the tarsi of hexapods. The phylogenetic relevance of these attachment systems have been previously demonstrated not only for Hexapoda, but also for subgroups, such as Dermaptera and Plecoptera. Although different adhesive structures on phasmid euplantulae are richly present in taxonomical descriptions, no attempt has been made yet to compare attachment structures for the purpose of internal systematic of this animal group. Here we studied the euplantular surface microstructure in 18 phasmid species from six families and discussed these morphological results according to their phylogenetic relevance and possible functional importance. This work is the first systematical overview of these features.

Using scanning electron microscopy (SEM), we observed six different types of adhesive microstructure, two of them for the first time. Eight studied species bear euplantulae with nubby surface microstructure, two of them have distinctly longer nubs. The euplantulae of seven species are smooth, without any micromorphological features. Pointed acanthae, flat pads, and hexagonal patterns were found in only one species each.

A correlation of micromorphological features with the biology of species can be assumed. As a plesiomorphy, nubby structures occur in ground dwelling species and represent a conserved character state in many taxa. The adaptation to habitats, located at certain height above the ground, is presumably responsible for evolution of smooth pads as an apomorphy, which is supposed to occur convergently in different taxa.

**Keywords:** Stick insects, Tarsal attachment structures, Adhesive microstructure

OP-ZS-08

**Museomics and  $\mu$ CT: The use of non-destructive tools for integrative taxonomy of insects, exemplified with the revision of the genus *Prasinocyma* (Lepidoptera, Geometridae)**

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So far, the taxonomically difficult geometrid genus *Prasinocyma* Warren, 1897 (Lepidoptera, Geometridae) contained 94 described species in the Afrotropical region. Since many new and undescribed species were expected in this genus, the aims of the present study were to test how new approaches and modern techniques can foster integrative revisions in particularly large and difficult cases.

For our study, we used 'conventional' morphological approaches as well as three-dimensional  $\mu$ CT-scanning and molecular methods, including DNA barcoding of old type specimens using the Sanger approach and Next Generation Sequencing (NGS) protocols. The identification of the known biodiversity (described species and synonyms) was based on type photographs and genitalia dissection of type specimens as well as on DNA barcodes from type specimens, using a single leg, with tissue recovery after DNA extraction.

DNA barcoding of comprehensive material at the Bavarian State Collection of Zoology, Munich (ZSM) revealed the existence of more than 100 additional genetic clusters ('BINs') for African members of the genus *Prasinocyma*, likely referring to undescribed species. Genitalia dissections confirmed this diagnosis.  $\mu$ CT-scans can provide similar information as 'conventional' genitalia dissections in a non-destructive way.

Based on this example, we show how integrative taxonomic revisions can profit from using minimal invasive methods like three-dimensional  $\mu$ CT-scanning and molecular methods, including DNA barcoding of old type specimens. Though being non-destructive,  $\mu$ CT-scanning is time-consuming. We therefore recommend 'in situ' screen-diagnosis of the genitalia of the holotype and comparison with a dissected paratype. The  $\mu$ CT image data should be deposited in appropriate databases for potentially being used for further digital processing.

**Keywords:** taxonomy,  $\mu$ CT, insects

## Zoological Systematics – posters

### PP-ZS-01

#### Invertebrate diversity in Icelandic freshwater springs

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Freshwater springs may be considered as ecotones between surface and subsurface water habitats and have the potential to house a diverse and highly specialized invertebrate fauna. Cold and thermal springs are common feature in Iceland, which makes the country a perfect place to study temperature influences on stygobiont and crenobiont invertebrates. The objective of the study is to analyze microfauna and invertebrate community composition in Icelandic freshwater springs at the surface-subsurface water interface and assess temporal, environmental, and spatial influences on them. In order to achieve this, aim we compare classical species identification methods based on morphological characteristics with genetic species identification through a metabarcoding approach.

Over 35 freshwater springs have been sampled, both at the surface of each spring and within the subsurface, i.e. the groundwater. We developed a novel method for sampling the groundwater, based on a modified electric fishing gear which is inserted into the spring opening. Invertebrates were identified to as low taxonomic levels as available keys allowed. Additionally, environmental DNA (eDNA) has been extracted from water samples of the springs. We amplified the eDNA with primers targeting bacteria, protozoans, fungi, and eukaryotes, and sequenced them via Illumina MiSeq.

First results indicate that Icelandic spring habitats are highly diverse, with the groups Chironomidae, Ostracoda and Copepoda in general being the most abundant taxa. In warm springs, the thermophilic *Scatella thermarum* (Diptera, Ephydriidae) can be found in great numbers. From several sampling sites we collected the groundwater amphipod *Crangonyx islandicus*, which is endemic to Iceland.

**Keywords:** groundwater, invertebrates, metabarcoding

### PP-ZS-02

#### Resolving a case of taxonomic mistaken identity in *Synchaeta* (Rotifera)?

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*Synchaeta* is an important, cosmopolitan genus of rotifers comprising over 40 known species. However, species within this genus are often difficult to identify and distinguish from one another morphologically. Indeed, a few valid species descriptions within *Synchaeta* remain doubtful because of inadequate initial descriptions combined with the species never being discovered again. In this project, we focus on the morphologically similar species *S. tremula* and *S. tremuloida*. The latter was first described in 1965 by Pourriot, who noted its strong similarity to the model species *S. tremula* and differing only slightly in body shape and toe length. *S. tremuloida* was not rediscovered again until individuals were detected nearly fifty years later in the winter of 2014 in a puddle in Oldenburg; Germany. In light of its strong morphological similarity to *S. tremula*, we conducted molecular analyses (of CO1 and 18S) of both species combined with reinvestigations of their habitus and trophus morphology using light and electron microscopy to exclude the possibility that these specimens belonged to a phenotypically varying population of *S. tremula*. Comparing our new morphological data for *S. tremuloida* to the first description of *S. tremula* revealed several identical morphological characters, but also that this first description of *S. tremula* is often morphologically inconsistent to what is commonly recognized as *S. tremula* today. Thus, we assume that Müller originally described specimens of what is now recognized as *S. tremuloida*, but that his description has been mistakenly applied to the highly similar and more common *S. tremula*. If further examinations can confirm our hypothesis, some form of taxonomical correction will be needed.

**Keywords:** Rotifera, species delineation, phenotypic variation

**PP-ZS-03**

**Correlation of trophus morphology and feeding behaviour within *Synchaeta* (Rotifera)**

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**Question:** The rotifer genus *Synchaeta* is a group of species that occurs in limnic, brackish or marine environments. Previous studies about their feeding behaviour and associated morphological adaptations revealed that the morphology of the trophus and the feeding habit are clearly associated in limnic *Synchaeta*: herbivorous specimens have one main tooth and several separated parateeth, whereas carnivorous specimens show only one main tooth with no parateeth. In this study, we examined several marine and brackish species of *Synchaeta* to ascertain whether this pattern can be expanded beyond only the limnic occurring species.

**Methods:** Samples were taken over a period of four months at three different sampling locations that differed in their salinity. Specimens were isolated and prepared for scanning electron microscopy (SEM). In addition, preparations of the trophus were done by dissolving the animal until the trophus was free of tissue and was either examined by using light microscopy or by SEM after further processing.

**Results:** We found that herbivorous specimens have one main tooth and several, clearly separated parateeth in line with previous observations for limnic species. By contrast, although the carnivorous specimens possess a trophus with one main tooth, the parateeth show great variation in shape and manifestation. For instance, whereas *S. vorax* has serrated parateeth, those of *S. baltica* are clearly separated.

**Conclusions:** In summary, there does not appear to be a general correlation between feeding behaviour and trophus morphology across habitats in *Synchaeta* and an interesting question is why limnic carnivorous species in the genus have uniformly lost the parateeth in contrast to the remaining groups.

**Keywords:** Rotifera, *Synchaeta*, trophi

**PP-ZS-04**

**Investigating the evolution of nuptial gifts and sexual dimorphism in *Oedothorax* dwarf spiders: a taxonomic case study**

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Nuptial gifts, items or substances that are transferred by the male to the female, have evolved independently in several animal taxa. The gifts and the traits involved have been shown to be sexually selected. Previous studies have shown that the prosomal structures that occur only in male dwarf spiders possess glands that produce a nuptial gift. In most dwarf spider genera there is little intrageneric variety among these structures. However, the genus *Oedothorax* comprises species with elaborate hunches, sulci, pits and/or grooves on the male prosoma as well as species that lack such structures. Therefore, the genus lends itself in particular for investigating the evolutionary history of dimorphic head structures.

Our objective is to infer the evolutionary history of sexual dimorphic prosomal structure in *Oedothorax* by means of phylogenetic analysis.

We have inspected somatic and genitalic morphological characters of both sexes from 51 of 76 known *Oedothorax* species and several outgroup taxa and present a preliminary phylogenetic hypothesis.

The robustness of Erigonine, as well as certain species groups at lower level, is supported by multiple synapomorphies. Although the relationships among major groups of *Oedothorax* and their close relatives are mainly supported by homoplastic characters, the results show that species currently placed in *Oedothorax* are not monophyletic and thus the genus requires a taxonomic revision.

Our results shed light on the evolutionary pattern of dimorphic structures in these spiders, and also provide insight into the taxonomy of this genus and its closely related taxa.

**Keywords:** Erigoninae, nuptial gifts, phylogeny

PP-ZS-05

**Molecular barcoding, species delimitation and biogeography of *Antarctomysis Coutière, 1906*, a mysid genus endemic to the Southern Ocean**

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The Southern Ocean is characterized by a highly unique taxonomic composition of abundant taxa, many niches in the Southern Ocean are occupied by taxa that are rare or absent outside the Southern and vice versa. Amongst the benthic crustaceans, decapods are almost absent in the Southern Ocean and functionally replaced by peracarids. Mysids (Crustacea, Peracarida) are amongst the best studied invertebrates of the Antarctic on account of their high abundance and their importance as food for fishes, penguins and seals. *Antarctomysis* currently comprises three species, all endemic to different regions of the Southern Ocean: *Antarctomysis maxima* (Holt & Tattersall, 1906), *Antarctomysis ohlinii* Hansen, 1908, *Antarctomysis profunda* Ledoyer, 1990. Nevertheless, a recent molecular barcoding survey provided evidence for the existence of several undescribed species of *Antarctomysis*, a genus endemic to the Antarctic.

Here we investigate the molecular phylogeography of the *Antarctomysis* species complex in the West Antarctic using nucleotide sequence variation from both mitochondrial (cytochrome *c* oxidase subunit I, COI) and nuclear (18S) genes in combination with morphology. We have studied the distribution and phylogenetics of cryptic species in the West Antarctic (Antarctic Peninsula, Bellingshausen Sea, Amundsen Sea, Ross Sea), which except for the northernmost tip of the Antarctic Peninsula is largely unstudied.

**Keywords:** Mysis, Antarctic, phylogeography

PP-ZS-06

**Genetic diversity of rice hopper parasitoids is independent of habitat complexity**

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Natural enemies are key organisms to promote sustainable agriculture and reduce pesticide use in agricultural landscapes. Among others, parasitoids can play a major role in controlling pests effectively. Two of the major pests in the rice agroecosystem of Southeast Asia are the brown planthopper (BPH) (*Nilaparvata lugens*, Stål) and the green leafhopper (GLH, *Nephotettix* spp.). They are naturally controlled by four genera of egg parasitoids. However, little is known about these organisms, as morphological identification is challenging due to their small size (<2mm).

This research addresses the question, whether different levels of habitat complexity influence the genetic diversity of the egg parasitoids and explores the possibility of DNA barcoding to better investigate parasitoids in the rice agroecosystem.

We included agroforests, rice fields adjacent to these agroforests and rice monocultures in our analysis to mirror the varying landscape complexity of the rice production system. Parasitoids were caught by infesting rice plants with hopper eggs and placing them within the different landscapes, allowing parasitisation by the local populations. Segments of the COI and 28S genes were sequenced in a total of 207 individuals.

We did not find significant differences in genetic diversity between the three habitat types but found big discrepancies between the genetic and the morphological identification of the parasitoids.

With this work, we hope to promote the use of DNA barcoding as an additional tool to investigate parasitoid diversity, which cannot be apprehended by morphological analyses only. We also want to emphasize the great potential these insects have to control two major pests of one of the world's most prevailing crops.

**Keywords:** Parasitoids, Rice, DNA barcoding

PP-ZS-07

**Visual orientation in three dimension - observations on the structure and ultrastructure of eyes in salps (Thaliacea, Tunicata, Chordata)**

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Salps are marine planktonic chordates that possess an obligatory alteration of reproductive modes in subsequent generations. Within tunicates, salps represent a derived life cycle and are of interest in considerations of the evolutionary origin of complex life history strategies. In the present study eyes of the sexual, aggregate blastozoid stage of *Thalia democratica* (Forsskal, 1775) were reconstructed and examined based on serial sectioning for transmission electron microscopy and light microscopy. The blastozoid stage of *T. democratica* possesses three pigment cup eyes, situated in the anterior part of the brain. The eyes are arranged in a way that the optical axes of the three eyes resemble the Cartesian coordinate system, where the eyes are oriented obliquely ventro-posteriorly, to the right, and obliquely antero-dorsally towards the water surface. Each eye is an inverse eye that consists of two different cell types, pigment cells (pigc) and rhabdomeric photoreceptor cells (prcs). The pigc are filled with numerous vesicles, possess a dense cytoplasm, and extend cell processes around and between prcs. Prcs possess apical microvilli that form a densely packed presumably photosensitive receptor part adjacent to the concave side formed by the pigc. Basally, prcs possess a single efferent neurite. The relatively large aperture, short focal length, and low number of photoreceptor cells indicate that each eye is capable of directional photoreception. While the structure of individual eyes indicates the lack of spatial vision, the elaborate arrangement of the three eyes may result in low-resolution spatial vision. Potential roles of the three eyes for the behaviour of *T. democratica* are discussed, remain however largely speculative.

**Keywords:** neurophylogeny, morphology, 3D-TEM

PP-ZS-08

**Molecular systematics and conservation biology of the cartilaginous fish (Chondrichthyes)**

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Despite the fascination and/or abhorrence with which many people view sharks and their relatives, this interest has not translated to unraveling the evolutionary relationships among all members of the group. Large parts of the tree remain poorly investigated (especially at less inclusive levels) and there is often large disagreement between studies, and those based on morphology in particular. In this study, we present a time-calibrated, multi-gene phylogeny encompassing over 700 of the roughly 1000 extant species belonging to the group. Our results uphold the traditional divisions within cartilaginous fish, with chimaeras (Holocephalii) forming the sister group to the clade of sharks (Selachii) and skates and rays (Batoidea) (collectively, Elasmobranchii). Beyond this, we highlight several instances of the non-monophyly of historically recognized taxa as well as confirm the monophyly of others. We also indicate areas of the tree in need of increased exploration (both in terms of increasing sampling of species and/or genes) and examine the effects of missing data on the stability of our phylogenetic results. Finally, within the constraints of these limitations, we provide an initial attempt to summarize the evolutionary distribution of conservation threat within cartilaginous fish as well as highlighting those species in greatest need of conservation effort based on the combination of threat and evolutionary distinctiveness.

**Keywords:** Chondrichthyes, molecular phylogenetics, conservation biology

PP-ZS-09

**How to incorporate results of molecular phylogenetics into morphometrics**

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Phylogenetic distances estimated by use of molecular data are more suited for the reconstruction of evolutionary trees than morphometric distances. If there are only three extant species (for instance *Homo sapiens*, *Pan troglodytes* and *Gorilla gorilla*) the result of the reconstruction is a bifurcating Y-shaped unrooted tree. The three extant species are situated at the ends (called terminal nodes or terminal vertices) of the three legs (called terminal edges) of the Y. The point where the three legs meet is called an interior node in mathematics and is a missing link in biology (for instance a "proto-chimp"). If we want to know something about the shape (for instance simply the length and the width of the thumbnail) of the missing link, we cannot stop by considering an evolutionary tree reconstructed by use of molecular data. For instance, we can depict the result of measuring the length  $x$  and the width  $y$  of our thumbnail in a double logarithmic plot as a single point A with coordinates  $[X=\ln(x), Y=\ln(y)]$ . For a chimpanzee we get a second point B and for a gorilla a third point C. In such a way we get a triangle DABC. The square roots of the three molecular distances between the species A, B, C are the edges of another triangle DA'B'C' in a coordinate system (X',Y'). It is possible to transform the coordinate system (X,Y) in such a way that the DABC becomes congruent to the DA'B'C'. We generalize these simple features observed for only one specimen per species, two measurements and only three species to many measurements and many species. In such a way we get morphometric distances measuring the change of shape in units of accepted point mutations. Then we can include fossils in a morphometric study of the skulls of hominoid primates and reconstruct skulls of missing links.

**Keywords:** evolutionary trees, morphometry, biometrics

Mini Symposium on animal-microbe symbioses – invited talks

**KEYNOTE**

**Evolutionary origin and maintenance of the nutritional symbiosis in firebugs**

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Evolutionary adaptations for the exploitation of nutritionally challenging or toxic host plants represent a major force driving the diversification of phytophagous insects. Although symbiotic bacteria are known to have essential nutritional roles for insects, examples of radiations into novel ecological niches following the acquisition of specific symbionts remain scarce. Bugs of the family Pyrrhocoridae harbor a community of Actinobacteria, Firmicutes, and Proteobacteria in the anoxic M3 region of their mid-gut. The symbionts are transmitted vertically via egg-smearing, but horizontal transmission can also occur by the uptake of symbionts from the feces of conspecific individuals. By targeted manipulation of the microbial community, we were able to demonstrate that the actinobacterial symbionts play an important role for the hosts' fitness by supplementing B vitamins that are limiting in the bugs' natural diet of Malvales plant seeds. Concordantly, symbiont-free bugs show slower growth rates, increased mortality, and lower reproductive success than symbiont-containing bugs. A broad survey of microbial communities associated with 22 different Pyrrhocoridae and closely related bug species revealed the evolutionary origin of the symbiosis with vitamin-supplementing Actinobacteria in the late Cretaceous, coinciding with the evolution of their host plant order Malvales. Thus, the symbionts may have facilitated their hosts' adaptation to this imbalanced nutritional resource and enabled the subsequent diversification in a competition-poor ecological niche. In addition, the resident microbes in the firebug gut appear to play an important role in suppressing proliferation of intestinal parasites, providing their host with an extended immune defense against antagonists. Due to its amenability to experimental manipulation, the firebug symbiosis provides an excellent model system to investigate the molecular basis of host-symbiont interactions as well as the ecological and evolutionary implications of symbiotic associations between animals and extracellular gut microbes.

**Hydra modifies bacterial quorum sensing and thereby maintains symbiotic functions of its colonizers**

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Epithelial surfaces of most animals are colonized by specific bacterial communities. Several factors, including the innate immune system, mucus composition, and diet have been identified as determinants of host-associated bacterial communities. Here we show that the early branching metazoan *Hydra* is able to regulate the behavior of its bacterial colonizers. We identified a new eukaryotic quorum quenching mechanism, which enables *Hydra* to specifically modify long-chain 3-oxo-homoserine lactones into their 3-hydroxy-HSL counterparts. Functional characterization of the QS system of *Hydra*'s main bacterial colonizer *Curvibacter* sp. showed that both, the host-modified and the non-modified quorum sensing signal, were recognized by the same bacterial receptors. Remarkably, even though both quorum sensing signals were recognized by the same receptors, the gene expression induced by the different signals led the induction of different bacterial phenotypes. While the host-modified signal represses bacterial genes involved in the biosynthesis of the flagellum, the non-modified signal induces the flagellar machinery *in vitro* and *in vivo*. Investigating the impacts of the different quorum sensing signals on metaorganism assembly *in vivo* elucidated, that the host-modified signal promotes, while the non-modified signal represses symbiont colonization. These results show for the first time, that an animal can manipulate bacterial quorum sensing signals *in vivo*. The animal thereby not only maintains the symbiotic function of its bacterial colonizers, but also supports the homeostasis of the metaorganism.

### **Male pregnancy, immune defence & microbes**

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In the animal kingdom, various strategies exist how parents allocate their resources into the future generation. This can range from a mere investment into the production of gametes (eggs and sperm) to complex mechanisms aiming to support the offspring before and after birth. The most extreme form of costly parental investment is viviparity, which has evolved multiple times independently and can be found in most vertebrate groups. In all but one case of this convergent evolution, females are the pregnant sex, only in Syngnathids (i.e. seahorses and pipefishes) male pregnancy has evolved.

The evolution of female pregnancy and placentation required specific morphological reorganizations. Only the co-adaptation of parental investment with major changes in the immune system and the microbial composition permitted its evolution.

To gain insight why in Syngnathids males are the pregnant sex and to understand if male pregnancy comes with similar adaptations, we sequenced the genome of the sex-role reversed pipefish *Syngnathus typhle* and addressed the genes that are differentially expressed during male pregnancy. We further genotyped the microbial composition both on female eggs and in the pouch of males.

Our data suggest an impressive rearrangement of the immune system in *S. typhle*, and we identified over a hundred homologous genes with a function both in female and male pregnancy. The development of the embryonal microbiota seems to be facilitated by biparental sex-specific microbial contribution.

### **Zero waste and no known diseases in fungus farming termites**

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Thirty million years ago, the ancestors of the termite sub-family Macrotermitinae and the basidiomycete Termitomyces joined forces in what became one of the most sophisticated plant-biomass decomposition symbioses on Earth. Through intricate interactions between an external fungus garden and the termite host and its accompanying gut microbes, this symbiosis manages to fully decompose nearly any plant polysaccharides and has no apparent problems with infectious diseases. 16S rRNA 454 pyro-sequencing portraying community compositions of the Macrotermitinae core gut microbiota and Illumina HiSeq metagenome sequencing show that the innovation of fungiculture induced a compositional and functional shift in the Macrotermitinae gut microbiota. Gut bacteria contribute fungolytic enzymes and enzymes needed for final plant decomposition after Termitomyces degrades complex carbohydrates. This implies that the shift in gut microbial capacity after Termitomyces domestication involved the evolution of complementary division of symbiont labour. A second gut passage of the fungus comb thereby ensures that all polysaccharides are utilized. Obligate gut passage of the plant substrate may also assure that potential antagonists are efficiently suppressed before entering termite nests, and I will end with a discussion of evidence for this hypothesis.

Mini Symposium on animal-microbe symbioses – oral presentations

OP-MS-01

**Bacterial but not protist gut microbiota align with ecological specialization in lower termites**

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All known metazoans are associated with microbes. These microbes can be important facilitators of adaptation of their metazoan host. However, most studies that investigate how organisms adapt focus on the target organism alone, but neglect the contribution of microbes to the adaptative capacity of the host. Lower termites are a textbook example of adaptation facilitated by symbioses with microbes. They require symbiotic gut protists and bacteria to thrive on wood. In order to better understand the role of microbes in host adaptation, we profiled the gut microbiota of a set of lower termite species that are adapted to different life styles and diets using illumina based 16S/18S rRNA gene sequencing as well as metagenomic shotgun sequencing. Our results suggest that bacteria contribute to life style and substrate adaptation, whereas protists seem to play a less important role.

**Keywords:** metagenomics, symbiosis, termites

OP-MS-02

**Probiotic *Enterococcus mundtii* isolate protects *Tribolium castaneum* against *Bacillus thuringiensis***

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**Introduction:** Storage food pests are eating, oviposit and defecating in the same environment resulting in a constant exposure to their own feces. Insect feces again are known to have protective function against pathogens, partly based on symbionts. Furthermore, newly hatched offspring can directly acquire beneficial microbes from this feces in the environment.

**Objectives:** Isolation of protective microorganism from the feces of the Mediterranean flour moth larvae, *Ephesia kuehniella*, and further characterization of the isolates.

**Materials & methods:** *In vitro* assays to characterize the probiotic profile of the isolates. *In vivo* characterization of the isolates' protective effect was done in the model organisms *Tribolium castaneum*. Isolates and corresponding supernatant (CFS) were orally exposed to *T. castaneum* larvae and after additional infection with entomopathogenic bacteria survival was recorded.

**Results:** Isolated *Enterococcus mundtii* strains showed antimicrobial activity against a broad spectrum of bacteria. The *in vitro* characterization of one of the isolates revealed a high auto-aggregation score, a hydrophilic cell surface, a tolerance for low pH, no hemolytic activity and susceptibility to all tested antibiotics. *T. castaneum* larvae exposed to *E. mundtii* or the corresponding CFS showed an increase survival after exposure to entomopathogenic bacteria. Heat treatment or treatment with proteinase K reduced the protective effect of the CFS.

**Conclusion:** Feces of food pests provide an alternative source for new probiotic strains. *E. mundtii* isolates showed good probiotic properties both *in vitro* and *in vivo*. *T. castaneum* is a suitable insect model for screenings of probiotic microorganisms.

**Keywords:** Probiotic, *T. castaneum*, *E. mundtii*

**OP-MS-03**

**A sponge fluorescent secondary metabolite increases O<sub>2</sub> concentrations in cultures of blue green algae of the genus *Synechococcus* via increased light harvesting and reduced respiration**

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Marine sponges harbor many microorganisms of different origin. One of the mostly abundant symbiont groups are blue-green algae of the genus *Synechococcus*, which generate carbohydrates and O<sub>2</sub> by photosynthesis. Cyanobacteria use chlorophyll A as an important light harvesting molecule. In water, the absorption of red light is determined strongly by the depth of the sponge and its symbionts, as infrared and red light are attenuated quickly with depth. Even though 470nm (blue) is the wavelength which can travel the longest distances in water, a majority of radiation transmitted over long distances belong to the UV and blue light spectras, with both not being very efficiently absorbed by chlorophyll A.

The sponge derived brominated pyrrole alkaloid Ageladine A was synthesized at AWI and previously used as pH sensitive fluorescent dye in live imaging experiments. Because of its membrane permeability and its long time staining, paralleled by low toxicity it was effectively implemented in experiments with different organisms as well as single cells. The absorbance of Ageladine A is in the UV range and its fluorescence is blue. Ageladine A most likely acts as an additional light harvesting molecule used by the sponge symbionts. Mathematical modelling hints to an additional effect of Ageladine A as an inhibitor of cellular respiration, supported by observations that Ageladine A is a potent kinase inhibitor.

**Keywords:** secondary metabolites, marine sponges, fluorescence

**OP-MS-04**

**How does a gut get lost? Development of the symbiotic gutless oligochaete *Olavius algarvensis***

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*Olavius algarvensis* belongs to a monophyletic clade of around one hundred known species within the tubificid annelids that all live in symbioses with consortia of sulfur-oxidising and sulfate-reducing bacteria and inhabit reducing, sulfidic layers of marine shallow-water sediments. The bacterial symbionts reside between the worm epidermis and cuticle and provide the host with nutrients gained by chemosynthesis. The worm hosts have in turn completely reduced both their intestinal tracts and metanephridial excretory organs.

The aim of this study is to investigate how, in the course of the evolution of an obligate nutritional symbiotic relationship, developmental patterns have changed to generate such drastic morphological alterations and whether the symbionts play an active role in inducing new host phenotypes.

Gravid *O. algarvensis* worms were kept in aquaria under conditions mimicking the natural habitat. Gametogenesis, oviposition, and embryonic development were documented using light microscopy, fluorescent staining with confocal microscopy, histology with computerised 3D reconstruction, and transmission electron microscopy.

Comparisons to closely related non-symbiotic annelids reveal stages very similar to normal tubificid gastrulae. Internalised yolk-rich endodermal cells, however, do not differentiate an intestinal lumen but become completely resorbed until juvenile worms hatch after ~35 days. Development of a buccal cavity is not evident at any stage. Symbionts were present inside the cocoons directly after oviposition but remained sparse until hatching. We conclude that embryonic development can rely on internal yolk and even proceed under conditions unfavourable for symbiont metabolism.

**Keywords:** Symbiosis, Development, Morphology

Mini Symposium on animal-microbe symbioses – posters

PP-MS-01

**Skin bacteria in hybridizing European freshwater fish are shaped by environmental and host genetic factors**

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Natural hybrid zones often emerge at habitat clines where distinct populations meet, mate and hybridize. The possible factors that govern the dynamics of a hybrid zone are insufficiently explored. For example, symbiotic bacteria can induce selection pressure by influencing the host's immune system, nutrition, development and behavior. These interactions are in turn influenced by environmental factors making it difficult to disentangle all involved components. Here we use a secondary contact zone where two populations of European freshwater fish, *Cottus rhenanus* and invasive *Cottus*, hybridize at a habitat ecotone. This system enables to study the association of symbiotic microbiota, habitat and host genotype to infer whether host-bacterial interaction may act as evolutionary force. We extracted genomic DNA from fin samples of wild caught fish and assessed bacteria through pyrosequencing of 16S rRNA markers. The host genetic makeup was inferred based on 80 nuclear SNP markers that permit to classify all fish into parental forms and recent hybrids. By means of additional laboratory experiments we examined the host genetic influence on bacterial communities under controlled environments. Phylogenetic and statistical analyses revealed major differences in bacterial diversity and abundance in distinct habitats. However, we also identified minor host-specific variation independent from the surrounding indicating some core bacterial microbiota. These results indicate that bacterial communities in our system are shaped by both, host genetic and environmental factors, and can at least not solely act as selective force against migrants in a *Cottus* spp. hybrid zone.

**Keywords:** microbiota, hybrid speciation, fish

PP-MS-02

**Beyond nutrition: macronutrient dietary preference in the cockroach *Blatta orientalis* is driven by pathogen infection**

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Diverse animal species consume toxins, minerals or secondary compounds as an adaptive response to pathogen infection - a process termed self-medication. Recent studies have also shown that macronutrients can play an important role in an individual's response to infection. For instance, African army worm caterpillars select a diet rich in protein and low in carbohydrate upon viral infection. Here we investigate whether dietary preference for macronutrients also plays a role in immunity in the omnivorous cockroach: *Blatta orientalis*. After challenging individual cockroaches with a common entomopathogenic soil bacterium, *Pseudomonas entomophila*, we conducted food-choice experiments using artificial diets differing in their relative protein to carbohydrate ratio. We show that cockroaches self-select a protein-enriched diet as a response to infection. This is driven by a sharp decline in carbohydrate intake rather than an increase in protein intake, which is also consistent with an illness-induced anorexia-like response. The macronutrient consumption pattern of infected individuals returned to normal approximately 4 days after challenge. We also investigated whether cockroach survival and hemolymph immune activity are enhanced in individuals when restricted to a protein-rich vs. carbohydrate-rich diet. In combination with findings from other insect study systems, our results indicate the presence of a general pattern of macronutrient use in response to infection. Furthermore, we show that interactions between nutrition and immunity may be highly conserved during evolution, highlighted by the fact that caterpillars and cockroaches diverged some 386 million years ago.

**Keywords:** Self-medication, Nutrition, Cockroach

**PP-MS-03**

**The guts of blood-group antigens: *B4galnt2* alters pathogen susceptibility through the intestinal microbiome**

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Glycans play important roles in host-microbe interactions. Tissue-specific expression patterns of the blood group glycosyltransferase *B4galnt2* are variable in wild mouse populations and underlie strong balancing selection. Alleles driving endothelial expression lead to a loss of glycosylation in the intestine and to a naturally occurring bleeding disorder. We hypothesize that variation in *B4galnt2* alters the intestinal microbiota and susceptibility to intestinal pathogens.

In this project we aimed to test the hypothesis that modulation of intestinal microbial communities through *B4galnt2* contributes to resistance against gastrointestinal pathogens.

We challenged mice expressing *B4galnt2* in a tissue-specific manner with a *Salmonella* infection model and analyzed the taxonomic- and functional genomic differences in the intestinal microbiota with respect to disease susceptibility and genotype.

Differences in *B4galnt2* expression cause strong differences in bacterial community composition and pathology upon *Salmonella* infection. Fecal transfer experiments demonstrate a crucial role of the *B4galnt2*-dependent microbiota in conferring susceptibility to intestinal inflammation, while epithelial *B4galnt2* expression facilitates invasion of *Salmonella*. Specific compositional- and functional adaptations of the *B4galnt2*-dependent microbial communities and their resistance to disturbance have a strong influence on infection and inflammation.

**Keywords:** Microbiome, Blood-group antigens, Pathogen susceptibility

**PP-MS-04**

**The evolution of the nervous system: does it play a role in host-microbe interactions?**

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Accumulating data indicate that symbiotic microbes communicate with the central nervous system, possibly through neural, endocrine and immune pathways, thereby influencing brain function and behavior. This bi-directional communication is known as the “microbiota-gut-brain axis” and has been mainly studied in vertebrate models, in particular mouse. However, the complexity of the vertebrate nervous system, the interaction among the proposed pathways and the still poorly understood vertebrate microbiota composition impose difficulties for advancing in the study of this field.

Contrary to the mouse, the fresh-water cnidarian polyp *Hydra* possesses an anatomically simple nerve net consisting of only two cell types: sensory and ganglion neurons. The nerve net is nevertheless complex enough to coordinate several stereotypical behaviors including the spontaneous contraction of the polyp's body column. Moreover, *Hydra*'s core microbiota is composed of less than ten bacterial strains that are cultivable. As both *Hydra*'s microbiota and behavior are amenable to study in the lab, *Hydra* appears to be a suitable model to mechanistically understand the impact of microbes on animal behavior. Finally, due to its phylogenetic position *Hydra* allows to assess the microbiota-gut-brain-axis from an evolutionary perspective.

By comparing germ-free and wild-type polyps here we show that symbiotic bacteria influence *Hydra's* spontaneous body contractions, a vital behavior that resembles intestine peristalsis. These data suggest an important role of microbes in the neuronal signaling underlying behavior in an early branching metazoan. The results suggest that the microbiota-gut-brain axis is an ancient evolutionary trait.

**Keywords:** Gut-brain-axis, Microbiota, Nerve net

#### PP-MS-05

##### Dissecting microbial community interactions in *Hydra*

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Recent studies of microbes associated with animal hosts have not only dramatically altered our understanding of the outbreak of complex diseases but have also shed light on metazoan development and their various physiological functions. Yet little is known about the establishment and the ecological forces that are at play in defining the composition of such host-associated communities and the different types of interactions among community members. Using a synthetic microbial ecology approach we gain insights into the qualitative and quantitative nature of the interactions between the different microbial species colonizing *Hydra*. Growth kinetics and invasion experiments (*in vitro* and *in vivo*) point to host mechanisms modulating species interactions at the glycocalyx-microbiota interface. As microbiomes consist of many different species it is difficult for a host to control each species independently. Disentangling the ecological interactions within these microbial communities will help to understand how stability is maintained and how microbiomes can be manipulated.

**Keywords:** metaorganism, microbiome, microbial interactions

#### PP-MS-06

##### Neuron-derived antimicrobial peptides are involved in maintaining host-bacterial associations in *Hydra*

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All multicellular animals evolved in the presence of microbes, developing long-lasting symbiotic relationships with them. The freshwater polyp *Hydra* is stably associated with species-specific bacterial communities, which provide beneficial effects such as antifungal resistance to their host.

A previous study Fraune *et al.* demonstrated that the composition of *Hydra's* microbiota significantly changes after the removal of nerve cells. Thus, we hypothesized that neuron-derived factors are involved in shaping *Hydra's* microbiota. We analyzed the antimicrobial activity of three different members of the well-characterized neuropeptide classes, Hym-357, Hym-370 and RFamide III. Strikingly, all peptides showed antibacterial activity mainly against Gram-positive bacteria. Whereas the microbiota of adult polyps is dominated by Gram-negative bacteria, *Hydra* hatchlings are colonized by Gram-positive bacteria, too. Here, we discuss a function of neuron-derived antimicrobial peptides in removing Gram-positive bacteria during ontogenetic establishment of the microbiota.

Furthermore, we report the finding of a non-conventional neuropeptide, which is expressed in ganglion and sensory neurons concentrated at the basal disc of the foot and in the head. In contrast to the other neuropeptides, "neuron derived antimicrobial peptide 1" (NDA-1), showed a strong antibacterial activity not only against Gram-positive strains, but also against *Curvibacter spec.*, the main colonizer of *Hydra vulgaris* (AEP). This observation may explain the reciprocal spatial distribution of NDA-1 and *Curvibacter spec.* with a peak of NDA-1 expression in head and basal disc where *Curvibacter spec.* abundance is the lowest.

Taken together, we show that neuropeptides have to be considered as important players in determining the microbial community members and their spatial localization.

**Keywords:** host-microbe interactions, antimicrobial peptides, neuro-immune interaction

PP-MS-07

**Volatile organic compounds of microbial symbionts - chemical ecology of fungus-farming ship-timber beetles**

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Ambrosia beetles farm their own fungal food within tunnels in wood - typically in social societies with division of labour. An exception are the ship-timber beetles (*Lymexyloidea*), which larvae live solitarily in their tunnels, where they farm yeast-like symbionts (*Saccharomycetales*) on their own. Compared to the social beetle farmers in the Scolytinae, ship-timber beetles are poorly known and studied.

**Objectives:** Here we give a first insight in the bacterial and fungal symbiosis of the ship-timber beetle *Elateroides dermestoides*, its chemical ecology and the putative role of microbial volatile organic compounds (MVOCs) in host-tree finding.

**Methods:** Bacterial and fungal symbiont communities of *E. dermestoides* nests, eggs and larvae were characterized using culturing and next-generation-sequencing. *In vitro* MVOCs of the primary symbionts were determined using GC-MS and compared to the *in vivo* volatiles of attractive host-trees. GS-MS in combination with EAD allowed us to identify the volatiles that induce a response in adult female antennae.

**Results:** Symbiont communities of *E. dermestoides* are dominated by different species of yeast-like fungi. Host trees emit a range VOCs and many of the behaviorally active compounds were found to be of microbial origin and produced by some of the bacterial and fungal symbionts. Highly attractive are MVOCs of the primary fungal mutualist *Ascoidea hylecoeti*.

**Conclusions:** Host-tree finding for egg-laying of adult female *E. dermestoides* barely depends on plant specific volatiles and is primarily directed by MVOCs produced by the beetles' symbionts. Though larvae live solitarily within their tunnels, this species breeds in groups and apparently uses their symbionts' volatiles for aggregation.

**Keywords:** Symbiosis, Volatile organic compounds, Animal fungiculture

PP-MS-08

**Host-microbe recognition in the sponge holobiont**

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Marine sponges host complex and species specific microbial communities, while feeding at the same time on microbes from the surrounding seawater. The mechanisms for the maintenance of this symbiotic association remain unknown. We aim to characterize sponge recognition of symbionts and identify the molecular basis with particular focus on host innate immunity. The two Mediterranean sponge species *Aplysina aerophoba* (high microbial abundance) and *Dysidea avara* (low microbial abundance) were selected. First, we assessed the sponges' microbial uptake of either bacterioplankton or sponge symbionts by flow cytometry. Both sponge species were feeding on the bacterioplankton, significantly affecting the concentration of bacterial cells over time ( $p$ -value < 0.01). When symbionts of *A. aerophoba* were added to the seawater, significant uptake was only detected in aquaria with *D. avara* ( $p$ -value < 0.05) but not in aquaria with *A. aerophoba* ( $p$ -value > 0.05). We hereby confirmed that sponges can distinguish between food bacteria and their own bacterial symbionts. Secondly, we collected tissue samples for RNA-seq analysis from sponges exposed to sterile filtered artificial seawater (SFASW) or to microbial elicitors (1 mg/mL in SFASW), in order to identify genes with a potential role in host's immune response. A total of 35 poly(A)-enriched RNA samples from control and treatment conditions for both species was generated, and Illumina HiSeq and MiSeq reads are currently being assembled. Our experimental approach will help to identify genes involved in the host's response to microbes.

**Keywords:** symbiosis, aquaria, immunity

**PP-MS-09**

**Volatiles from mutualist microbes benefit insects by disrupting fungal chemical defence**

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Protection from pathogens and parasites is a wide-spread means by which microbial mutualists benefit animals. In insects, defence against noxious bacteria or fungi often involves close association with specific microbes producing chemically complex antibiotics. Here we test whether yeasts, transiently associated with *Drosophila melanogaster* fruit flies, provide in addition to nutritional benefits protection from habitat invasion by insecticidal mould fungi. Moulds are a particularly relevant cause of mortality when *Drosophila* larvae develop on decaying fruits. We show that mould colonies exposed to common yeast volatiles lose their insecticidal properties and insects are better at keeping mould growth in check. This volatile-mediated shift in the outcome of this fungus-animal interaction is accompanied by the mould's inability to activate candidate insecticidal defence genes and a decline in fungal secondary metabolites. Yeast volatiles and invertebrate damage probably is an effective combination of chemical and behavioural factors that prevent insect habitat invasion by noxious moulds. Thus, without the need to form close symbioses and complex antibiotics transient mutualistic associations with microbes can provide efficient protection from otherwise noxious antagonists.

**Keywords:** defensive mutualism, insects, chemical defence