

# Abstracts

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## Content

### Abstracts sorted by Topics

Keynote Lectures	5-16
Behavioural Biology	17-68
Developmental Biology	69-76
Ecology	77-98
Evolutionary Biology	99-156
Morphology	157-204
Neurobiology	205-242
Physiology	243-268
Zoological Systematics	269-280

Index	281-289
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Imprint	290
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- B** Behaviour
- D** Developmental Biology
- EC** Ecology
- E** Evolutionary Biology
- M** Morphology
- N** Neurobiology
- P** Physiology
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**The evolution of insects: A phylogenomic approach**

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**Die Chemie muss stimmen - sexuelle Kommunikation bei parasitischen Wespen**

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Die Nutzung chemischer Reize und Signale ist für Insekten unabdingbar, um Nahrung und Paarungspartner zu finden oder natürlichen Feinden zu entkommen. Zur Kommunikation mit Artgenossen nutzen Insekten so genannte Pheromone. Sexualpheromone dienen der Anlockung von Paarungspartnern, deren Erkennung im Nahbereich oder der Auslösung von Paarungsbereitschaft. Damit die Kommunikation der Paarungspartner verlässlich funktioniert, müssen diese chemischen Signale artspezifisch sein. Das bedeutet, dass Artbildungsprozesse oft mit einer Diversifizierung chemischer Signale einhergehen. Wie die Evolution von chemischen Signalen abläuft, steht zunehmend im Fokus der Pheromonforschung. Hierbei sind drei Fragen von besonderem Interesse: (1) Was sind die Voraussetzungen dafür, dass bestimmte Naturstoffe im Laufe der Evolution informativ werden und als Pheromone fungieren? (2) Warum und wie verändern sich etablierte Pheromonsignale? (3) Was sind die zugrunde liegenden genetischen und biochemischen Mechanismen?

Parasitische Wespen haben sich in den vergangenen Jahren als hervorragende Modellorganismen erwiesen, um solche Fragen zu untersuchen. Hierbei handelt es sich um meist winzige Insekten aus der Ordnung der Hautflügler (Hymenoptera), die sich in anderen Arthropoden entwickeln und den Wirtorganismus am Ende ihrer Entwicklung töten. Sie spielen als natürliche Gegenspieler eine enorm wichtige Rolle für das Funktionieren von terrestrischen Ökosystemen und werden zur biologischen Schädlingsbekämpfung eingesetzt.

Anhand verschiedener Modellsysteme wird vorgestellt, wie Naturstoffe, die primär dem Verdunstungsschutz oder der Verteidigung dienen, im Laufe der Evolution zu Sexualpheromonen parasitischer Wespen wurden. An der Gattung *Nasonia* wird zudem detailliert gezeigt, wie durch enzymatische Modifizierung einer bereits vorhandenen Pheromonkomponente ein neues chemisches Signal entstehen kann, welches dazu beiträgt, Fehlpaarungen zwischen nahe verwandten Arten zu vermeiden.

### The neurobiology of individuality

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Individuals often display conspicuously different patterns of behavior, even when they are very closely related genetically. These differences give rise to our sense of individuality, but what is their molecular and neurobiological basis? Individuals that are nominally genetically identical differ at various molecular and neurobiological levels: cell-to-cell variation in somatic genomes, cell-to-cell variation in expression patterns, individual-to-individual variation in neuronal morphology and physiology, and individual-to-individual variation in patterns of brain activity. It is unknown which of these levels is fundamentally causal of behavioral differences. To investigate this problem, we use the fruit fly *Drosophila melanogaster*, whose genetic toolkit allows the manipulation of each of these mechanistic levels, and whose rapid lifecycle and small size allows for high-throughput automation of behavioral assays. This latter point is crucial; identifying inter-individual behavioral differences requires high sample sizes both within and across individual animals. Automated behavioral characterization is at the heart of our research strategy. In every behavior examined, individual flies have individual behavioral preferences, and we have begun to identify both neural genes and circuits that control the degree of behavioral variability between individuals. Our recent efforts focus on three questions: 1) what computation is performed by circuits that regulate behavioral variability, 2) can we identify "loci of individuality," morphological or physiological correlates of individual behavioral biases, and 3) does behavioral variability reflect developmental stochasticity/decanalization, or a regulated, adaptive bet-hedging strategy to thrive in variable environments?

### Courtship duets in the wild: electrocommunication at the limits of sensation

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Sensory systems evolve in the ecological niches each species is occupying. Accordingly, the tuning of sensory neurons is expected to match the statistics of natural stimuli. For an unbiased quantification of sensory scenes we tracked natural communication behavior of the weakly electric fish *Apteronotus rostratus* in their Neotropical rainforest habitat with high spatio-temporal resolution over several days. In the context of courtship and aggression we observed large quantities of electrocommunication signals. Echo responses and acknowledgment signals clearly demonstrated the behavioral relevance of these signals. Despite their relevance these signals are non-optimally represented in the sensory periphery. Frequencies of courtship signals are far outside of the neurons' best tuning range and signals occurring in assessment and attack behaviors drive sensory neurons just above threshold. Our results emphasize the importance of quantifying sensory scenes derived from freely behaving animals in their natural habitats for understanding the evolution and function of neural systems.

**Proximate and ultimate causes of developmental plasticity**

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The environment experienced early in life can shape phenotypes for life, sometimes inducing major phenotypic changes of key life history traits or behavioural strategies. Such lasting effects of developmental plasticity impacts Darwinian fitness and should be subject to selection. Nevertheless, the adaptive value of developmental plasticity is still subject to ongoing debate. One key problem hampering our understanding of developmental plasticity is that its mechanisms and function are mostly studied in simple laboratory environments testing for the effects of only a single environmental factor during a single ontogenetic period. However, natural environments are multivariate and complex, and environmental influences can affect development at multiple ontogenetic stages. I will present evidence how adding natural complexity to developmental experiments can promote our understanding of developmental plasticity. In order to understand the function of developmental plasticity we have to know (1) when during a life time environmental information influencing development should be obtained, and when this information is beneficial, and (2) how information obtained during multiple life stages or from multiple environmental parameters is integrated during phenotypic development. (3) Finally, to understand the evolution of developmental plasticity, we do not only have to understand its fitness consequences, but we also need to identify the traits that are actually evolving. This requires an in-depth understanding of the underlying mechanisms responsible for plastic responses. I will illustrate the above points by examples from recent studies mostly using cichlid fish as model organisms.

**Multiple mating, dispersal and (facultative) sex: can bet-hedging explain them all?**

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Bet-hedging has been called a ‘seductive’ explanation in evolutionary biology. This is because the rationale is easily captured in idioms such as “do not put all your eggs in the same basket” or “a bird in the hand is worth two in the bush”. But how much is evolution really guided by avoidance of the risk of remaining completely empty-handed (i.e. no surviving offspring), as opposed to simply maximizing the arithmetic mean of offspring production (which may be maximized if accepting some probability for the ‘no surviving offspring’ event)? I will review the theory of bet-hedging and (re)consider some published putative examples that interpret multiple mating females as hedging their bets. I will then ask if dispersal and sex, two traits that are less often discussed using bet-hedging terminology, might benefit from being viewed from this angle.

**The causes and consequences of selection at the gametic level in animal**

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An inescapable consequence of sex in eukaryotes is the evolution of a biphasic life cycle with alternating diploid and haploid phases. The occurrence of selection during the haploid phase can have far reaching consequences for fundamental evolutionary processes including the rate of adaptation, the extent of inbreeding depression and the load of deleterious mutations, as well as for applied research into fertilisation technology. While haploid selection is well established in plants, a current dogma assumes that in animals, all fertile sperm within a single ejaculate are equivalent at siring viable offspring. We examined the importance of haploid selection in the zebrafish *Danio rerio* and found strong fitness consequences of selection at the gametic level. Genomic data supports the idea that these effects may well be the consequence of selection at the haploid gametic level.

**Macroevolution meets macroecology: diversity in space and time**

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Macroecology has traditionally studied mostly spatial patterns of diversity and species' traits, e.g. the large-scale variation in species richness across continents. These patterns and their relationships with present-day climate, topography and other abiotic factors are comparatively well-known for many taxa today, but their dynamics back in time are rarely studied. In recent years, the integration of molecular phylogenies with macroecological patterns has boomed, and fans claim that the added historical or temporal information increases our understanding of underlying mechanistic processes. However, if biogeographic history, macroevolutionary processes or past environmental dynamics are considered in macroecological studies, they are usually reduced to a "footprint measure" that sums up accumulated change prior to today, e.g. the amount of evolutionary history represented by a phylogenetic lineage. Even with such simplified approaches, combining macroecology and macroevolution can increase our understanding of how diversity is generated and maintained. Going further, I argue that next-generation biogeography and macroecology should go beyond such approaches, because recent advances would allow explicit consideration of both space and time in combined analyses. I draw on two examples to illustrate these ideas. Firstly, citizen science can provide enormous temporally explicit datasets of species' occurrences today. These offer great opportunities in measuring seasonal or short-term temporal dynamics of species' ranges and diversity patterns, as I will show for bird assemblages in Australia. Secondly, paleontological databases are rapidly growing and often provide a detailed deep-time history of taxa and environments. I use the mammalian fossil record over the last 23 million years to illustrate deep-time dynamics of species richness and body size evolution, pointing out directions how these could illuminate the processes underlying present-day diversity patterns.

**Confidence in rats, humans and mathematics**

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**Ecological stoichiometry - a framework to understand trophic interactions and species coexistence**

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Ecological stoichiometry describes the growth and interaction of species based on their demand for multiple resources and the relative availability thereof. Since it makes predictions from subcellular to ecosystem levels, it has become a pervasive concept in the ecology of plants, animals and microbes. Starting with some basic information on the history of this concept, I will focus on three major questions that dominate the current debate on ES: How does the stoichiometry of available resources alter coexistence? How strongly do species (and individuals within species) differ in their resource use stoichiometry – and what regulates this difference? How do these stoichiometric constraints integrate at the level of food webs? I will shed light on these questions using empirical and modelling studies derived from a variety of systems (terrestrial to marine), organisms, and organizational levels. Whereas plant coexistence has long been interpreted in the form of resource ratios, this is less common for animals, despite potentially similar mechanisms being at work. These stoichiometric constraints on coexistence are based on inter- and intraspecific variation in nutrient incorporation, which are strongly related to growth conditions, food intake and competitive surrounding. Consequently, consumers respond to the presence of resource diversity and quality simultaneously, affecting their biomass production and nutrient regeneration. Summarizing this information, I will end the presentation with an outlook of how ES could be used to explain differences in food web organization between ecosystems.

**Understanding animals through sensory evolution and robotics**

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Work comparing the range of electrosensory systems to underwater visual systems led us to a new theory about why animals came up on to land 400 million years ago. Initial evidence for the theory is compelling, including a previously unappreciated tripling of eye size and change to a crocodylian ecotype just prior to full emergence on to land. Combined with evidence for a cornucopia of invertebrate prey on land at that time, our data strongly suggest that the increase in sensory range afforded by air over water allowed our aquatic vertebrate ancestors to sense prey on land and aided selection of limbs to better exploit this resource. This line of work was enabled by the detailed, quantitative understanding of electrosensory systems that has been its hallmark for decades, along with newer work in which robotic models of both the sensory and locomotion systems of electric fish have made our understanding more precise. What does this work on sensory evolution and robotics tell us about the super powers of animals, and where we should focus our empirical and theoretical work in the future? I will make some suggestions inspired by the negative spaces of those super powers: where it is that animals fail miserably.

BEH-S-01

### Sexual selection and life-history trade-offs mediate animal personality differences

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The presence of consistent behavioural differences among individuals of the same population is ubiquitous across the animal kingdom. In recent debates, critiques claim that research on such animal personality differences is mainly descriptive and that the function of such differences has rarely been tested. Here, I will show that personality differences are adaptive in very different systems and contexts. I will present a series of experiments in which we demonstrated that sexual selection and life-history trade-offs can generate and maintain personality differences. Our results from mate choice and breeding experiments in gregarious zebra finches, *Taeniopygia guttata*, and territorial African cichlids, *Pelvicachromis pulcher*, demonstrate, for instance, that individuals benefit from considering their own and their potential partners' personality during mate choice for raising offspring. In another example, I show that under strong life-history trade-offs it pays for pea aphids, *Acyrtosiphon pisum*, to commit to a consistent lifestyle, including consistent risk-taking behaviour towards a predator. Results from these studies advance our understanding of the existence of behavioural variation.

BEH-S-02

### Active inbreeding in a cichlid fish: functions and mechanisms

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Inbreeding, i.e. mating between genetically related individuals, is commonly considered as maladaptive because of inbreeding depression. This view, however, ignores the theoretical predictions that inbreeding can increase individual (inclusive) fitness, facilitate social evolution and drive ornament evolution and diversification. Here, I will present evidence for adaptive inbreeding in *Pelvicachromis taeniatus*, a West African fish of the speciose cichlid family. The species shows intense biparental brood care, colorful ornamentation in both sexes and mutual mate choice. In mate choice experiments, males and female showed mating preferences for close kin. These laboratory findings were supported by genetic data of the wild population from Cameroon. Ultimately, inbreeding individuals may increase their inclusive fitness and the reduced sexual conflict due to kin-selection within sibling pairs may result in better brood care. At the proximate level, our results indicate that kin recognition in *P. taeniatus* is based on phenotype-matching and that olfactory cues are involved. I will introduce promising fields for future research including experiments on how inbreeding preferences can be maintained and discuss further evolutionary implications of inbreeding.

BEH-O-01

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

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Recognising close relatives, i.e. kin, is crucial to avoid inbreeding. Many vertebrate species, including the zebra finch, use olfactory cues to recognize kin, even without prior association. This indicates 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.

The experiment consisted of two different conditions, consisting of two females and three unfamiliar males, each. The first condition contained one female and her unfamiliar genetic brother. The second condition contained one female, which hatched from a cross-fostered egg and was therefore exposed to another family odour after hatching, her genetic brother and a foster brother, i.e. male offspring of the foster parents.

We predict that if females recognise kin based on self-referent phenotype matching, females should 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.

Within 3 replicates, we determined mate choice decisions by using observations of pair bonding in combination with genetic parentage analysis and we evaluated breeding related parameters, e.g. reproductive success. Our data revealed that zebra finches suffer from inbreeding depression by a decreased growth rate of offspring. Furthermore, we show that the mechanism underlying kin recognition is rather self- than family referred phenotype matching.

BEH-O-02

**Unpredictable life history in an unpredictable habitat?**

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Life history traits and their plasticity play a key role in determining population demography and population dynamics as variations in life history traits (e.g. size at birth, growth, age at maturity, number, size and sex ratio of offspring) are directly linked to individual fitness. Disentangling these effects is often complicated as traits are bound together by numerous trade-offs including those between current reproduction and survival, current and future reproduction, and between number, size and sex of offspring. Moreover, the already complex interplay is further complicated by environmental perturbation. This study provides first estimates of life history traits and trade-offs of a tropical apex predator in an environmentally unpredictable habitat. We use 13 years of life history data of Galapagos sea lions (*Zalophus wollebaeki*) collected on a small islet in the Galapagos archipelago. We thereby offer insight into the effects of age, body conditions and environmental changes on the life history and in particular the Galapagos sea lion females' reproductive and survival rate.

BEH-O-03

**Babbling bats – how pups of the sac-winged bat, *Saccopteryx bilineata*, acquire their vocal repertoire**

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Human infant babbling is composed of different developmental stages and is considered to be a crucial step for language acquisition. So far, the description of babbling in non-human species has been limited to songbirds and one primate, the pygmy marmoset. A promising species to study vocal development is the highly social bat species, *Saccopteryx bilineata* which possesses a complex vocal repertoire. Pups learn at least one song type, the territorial song, by imitating tutor songs during ontogeny. Vocal imitation is achieved by conspicuous vocal practice in the form of babbling bouts, which bear a certain resemblance to the canonical babbling of human infants. The babbling bouts are composed of adult-like-syllable types and mostly graded transitions from one syllable type to the next; those transitions are not part of the adult vocal repertoire. We recorded and analyzed babbling bouts of 10 pups belonging to five different colonies to investigate the ontogeny of the vocal repertoire (10-12 weeks from birth until weaning). Preliminary results indicate that babbling bouts were dominated by repetitions of the same syllable type and bouts were mainly composed of transition syllable types (63% transition syllable types vs. 37% adult-like syllable types). With increasing pup age, the vocal bouts contained a greater diversity of syllable types per bout and duration of babbling bouts increased as well. Interestingly, aggressive adult-like syllable types appeared earlier in ontogeny than affiliative ones. Furthermore, transition probabilities among adult-like syllable types were not random, indicating that babbling bout sequences follow some basic phonological syntax rules. Taken together, our study on babbling behavior of *S. bilineata* pups offers new insights into a rare mammalian trait which is important for vocal repertoire acquisition.

BEH-O-04

**Effects of early cortisol elevation on personality in wild cavies**

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The study of consistent individual differences in behaviour, termed animal personality, has flourished over the last two decades because it has been recognised as a major contributor to differences in survival and fitness among individuals. The mechanisms by which personality is shaped are still poorly understood, although the connection between personality traits and hormones such as cortisol, has been demonstrated in a number of species. From the area of stress-research it is known that elevated cortisol levels during development can have profound long-term effects upon physiology and behaviour. Here I experimentally manipulate cortisol during early life to investigate effects on personality traits, cortisol and testosterone later in life. I predict that the cortisol treatment will not only change mean-levels of behaviour and hormones but also trait variances, thereby affecting trait repeatability and correlations among traits.

Cortisol was via food for three weeks starting shortly after weaning. Stress-coping, boldness, exploration and social behaviour were then tested three times after sexual maturation. In addition, repeated blood samples were taken to analyse cortisol and testosterone levels. In comparison to a control group, cortisol elevation led to a more passive coping with stress and more defensive behaviour in social situations later in life. In addition to these differences in mean-level behaviour, repeatability of stress-coping traits were enhanced in the treatment group. Likewise, the treatment group showed a higher trait repeatability in both hormones. Furthermore, the treatment affected the correlation structure among cortisol and stress-coping traits as well as between exploration and boldness. These results indicate strong organisational effects of hormones on different aspects of animal personality.

BEH-O-05

**Born to be aggressive, curious or fearless? – Heritability of 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 as well as the functions and consequences of different personality types are still difficult to explain. Heritability, the transmission of the phenotypic variability within a population from generation to generation, is a key genetic parameter regarding whether natural selection is able to generate evolution on a trait or not.

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. We calculated the heritabilities of the three selection line personality traits using parent-offspring regression, where the slope of the regression between mid-parent and mid-offspring personality trait scores gives an estimate of (narrow-sense) heritability. Preliminary analyses indicated that personality traits in zebra finches are partly heritable with heritability estimates between 0.12 and 0.44 after three generations of selection.

BEH-O-06

**The bat-moth arms race goes on: Barbastelle bats lead through the combination of low-intensity echolocation and intensity compensation**

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Ears evolved in several insect taxa due to the selection pressure of bats. Eared moths perform evasive flight manoeuvres when they hear attacking bats, thereby decreasing risk of predation. Yet, barbastelle bats, *Barbastella barbastellus*, capture eared moths in large quantities. We hypothesized that barbastelles lower the intensity of their low-intensity calls while closing in on prey, such that the level at the moth's ear remains below its hearing threshold and the moth fails to elicit its evasive manoeuvre. Yet, in many vertebrates, background noise causes an increase in vocalisation amplitude. Thus, we further hypothesized that noise alters the interaction between barbastelles and moths.

We tested these hypotheses in both the wild and captivity by offering tethered moths to barbastelles under silence and noise conditions. We reconstructed the bats' three-dimensional flight paths based on time-of-arrival differences of the echolocation calls at four microphones, measured the received sound levels at the moth's position with an additional miniature microphone, and calculated call source levels.

We show that barbastelles continuously reduced call intensity upon detecting a moth, thereby remaining below the moth's hearing threshold and rendering the bat's approach undetected by its prey until shortly before capture. Background noise altered call intensity differentially depending on noise frequency range and attack phase.

Barbastelles have combined intensity compensation with low-intensity echolocation to counter moth hearing during an attack. This novel strategy might have given them exclusive access to a formerly unavailable food source, thereby probably altering competition between sympatric bat species. In turn, selection pressure for eared moths might have increased, potentially fostering new anti-bat traits to evolve. Yet, increased source levels in noisy environments could foil the bat's stealth strategy if the moth's hearing threshold remains the same.

BEH-O-07

### The ontogeny of intentional signalling in chimpanzees of two communities in the wild

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The intentional nature of human communication has been emphasized as a cornerstone distinguishing language from other signalling systems. In recent comparative research, intentional usage of animal signals has been operationalized via a specific set of behavioural criteria. However, despite the well-documented influence of developmental experiences on socio-cognitive abilities in apes, ontogenetic effects on intentional signalling are poorly understood. In this study, we tested whether three established criteria for first-order intentionality are influenced by age and social factors in two chimpanzee subspecies (*Pan troglodytes verus*/*schweinfurthii*) living in communities in the wild. Using video recordings and focal scans, we observed twelve infants aged 9 to 78 months during 1190 hours over two consecutive three-month field periods. Our results suggest a strong impact of age, social context and interaction partner on the employment of intentionality markers in communicative interactions. Throughout the examined age range, chimpanzee infants increasingly demonstrated audience checking, sensitivity to the recipient's visual state, and persistence to the goal. Our study provides the first evidence for comparable developmental trajectories of popular behavioural criteria used to infer intentional signal use. We conclude that both age and social exposure profoundly contribute to the communicative complexity observed in primate species, and advocate considering both factors more explicitly in comparative research.

BEH-O-08

### Too small to be picky - Size-assortative mating in *Rana temporaria* is influenced by temporal migration pattern and male mating tactic

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In sexually reproducing species pairs are more likely to be formed if phenotypic traits are similar. This type of assortative mating can be found in a wide variety of taxa, but the behavioral mechanisms behind are scarcely investigated. We aim to understand the mechanisms leading to size-assortative mating in a widely distributed amphibian species, the European common frog (*Rana temporaria*). Therefore, we use field data from pairs collected over several years at two different breeding sites in Germany and show a consistent pattern of size-assortative mating in natural populations. Subsequently, we ask if size-assortment results from temporal migration patterns of differently sized individuals; and we conducted experiments to test for adaptive mechanisms like fertilization success of different size-matched pairs and mating speed between males. In our analyses we observed a migration pattern where larger individuals arrived earlier at the breeding sites, thus causing differences in mate availability and supporting size-assortment during migration. We detected an indiscriminate mate choice behavior of small males, which could result from large male advantage in scramble competition. By being less picky in choosing a mate, small males could increase the chance to get access to a female. The size-assortment of pairs does not influence fertilization success, but males could maximize the number of their offspring by preferring large females for mating since female fecundity correlates with body size. We show that mate finding in anurans seems to be a multicausal process and more complex than formerly expected.

BEH-O-09

### Reproductive behaviours in a risky world: are mothers trading-off offspring safety for future fitness?

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Predation risk is a major determinant of behavioural variation. However, individuals do not only have to eat without been eaten, they also have to balance the risk of mortality with their investment into both current and future reproduction. We studied this allocation trade-offs in rodents, that are highly depredated, have flexible mating systems (i.e. can mate singly or multiply), and can potentially simultaneously invest into nestling litters (current investment) and pregnancy (future investment). This produces a conflict between caring for the current offspring, and leaving the offspring temporally behind for mating in order to be able to invest into future offspring. We experimentally manipulated predation risk for the mothers and/or infanticide risk for the offspring, and reproductive investment (litter size or litter age) in a series of experiments on lactating but not pregnant rodent mothers in different temporal and spatial scales, in large scale field enclosures and in the laboratory. We monitored time allocation, physiological responses, space use and nest guarding of females. We expect mothers to adjust time allocation at the next to infanticide risk, and reduce mating effort if predation risk is high, and if the current investment was large.

We will compare responses of females to infanticide risk on different spatial scales, and may present preliminary result on our ongoing experiment on the conflict between mothers mating interest, her own predation risk and the size of the investment into different litter sizes.

BEH-O-10

### First comparative study on male bushcricket genitalia reveals a species-specific functioning of titillators

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The males of some bushcricket species have sclerotized genitalia, which are moved rhythmically during copulations. These spiny “titillators” vary greatly in their shape depending on the species, suggesting that they are under sexual selection. Bushcricket titillators were thought to function as stimulators for the females or to be used as anchors, which support the mating position. To date, titillator function has only been investigated in very few species.

In this study, the effect of titillator manipulations was tested in mating experiments in four different bushcricket species, with a gradual phylogenetic relationship. One Phaneropteridae species with a single titillator (*Letana inflata*) and three Tettigoniidae species with paired titillators (*M. roeselii*; *Tettigonia viridissima*, *Pholidoptera littoralis*) were used for that purpose.

After the spines of one titillator of *M. roeselii* males were removed, one third of the females showed resistance behaviour (Chi-square(1)=8.039,  $p=0.005$ ). In *L. inflata* females reacted likewise: two third of the females walked during matings with manipulated males (Chi-square(1)=19.200,  $p<0.001$ ), which led to a significant number of failed ampullae transfer (Chi-square(1)=6.348,  $p=0.012$ ). The titillators in these two species stimulate the females to ensure the acceptance of the mating and the male’s sperm.

However, in *Ph. littoralis* and *T. viridissima* the females did not respond to manipulated males, suggesting that their titillators do not function as stimulators. In *Ph. littoralis*, the removal of one or both titillators resulted in males slipping out of the mating position (Chi-square(2)=9.294,  $p=0.010$ ). Consequently, the titillators of *Ph. littoralis* secure the mating position by pulling both mating partners closer together.

We conclude that bushcricket titillators have species specific functioning; which calls a single hypothesis for insect genitalia functioning into question.

BEH-O-11

B

### Getting insight into the evolutionary roots of vocal greeting: the importance of mother-infant reunions

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In humans and mammals with complex and cohesive social systems ritualized vocal greetings play an important role during everyday's social interactions. Greeting rituals emerged first in parent-infant interactions after temporarily separation of care-giver and infant. To investigate whether vocal greetings occur also in a solitary foraging primate, we recorded vocal exchanges between mother and infants during reunions in the grey mouse lemur. This primate is an ideal model due to its infant-parking system, where separations of mother and infant occur regularly. Further, we proofed vocal signatures of greeting calls to shed light on the function during mother-infant reunion.

We audio- and video- monitored 11 families in the Hannover mouse lemur breeding facility (24 hours/d for the first month after birth). We analyzed the occurrence of mother and infant vocalizations when infants were 10/11 days old for the Reunion (=mother returned to the infant at sleeping sites) and the Together condition (=mother and infants were together at sleeping site). Vocal signatures of mother and infant calls were investigated using a multi-parametric sound analysis.

During Reunion both, mothers (trill call) and infants, produced calls significantly more often in the Reunion compared to the Together condition. However, mothers started to call significantly earlier and initiated more vocal interaction suggesting that mothers vocally greet their infants upon return to the nest. Mother trill calls and infant calls contained individual acoustic signatures suggested to function for mother-infant recognition. Thereby, infants produce vocal streams, which might be a pre-step of mother trill calls suggesting that infants practice the production of the adult-like greeting call during interactions with the mother. Thus, vocal exchanges between mother and infants in an infant-parking primate may represent a first crucial step for the evolution of vocal greetings in primates.

BEH-O-12

B

### Mate availability does not influence male complicity in sexual cannibalism in the spider *Argiope bruennichi*

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Mating strategies such as the investment in the current mate should crucially depend on mating chances. In the sexually cannibalistic spider *Argiope bruennichi*, males experience two copulations at most, but often die after the first one. Death occurs because females stereotypically attack males during mating and cannibalize them. However, males can avert this fate if they jump off the female at the right moment. Surviving males have the option to either stay with their first mating partner, or to mate with a second female. That chance critically depends on the density of females. Thus, males should be adapted to evaluate further mating chances, and they should adjust their mating strategies accordingly. As a low risk strategy, males could sacrifice their life during the first copulation. Alternatively, males could try to escape cannibalism and accept the associated risk of dying before copulating a second time. We hypothesize that *A. bruennichi* males are more likely to use the low risk strategy if alternative mating opportunities are rare. To test this hypothesis, we used mate choice test arenas, in which males perceived chemical cues from either one or four virgin females during mate searching. Contrary to predictions, we found no influence of female density on male sacrifice. Therefore, we conclude that mating chances can be less important in determining mating strategies than mate quality, which is known to influence mating strategy decisions in *A. bruennichi*.

BEH-O-13

B

**Extreme allomaternal care by unmated females in a cooperatively breeding spider**

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Division of reproductive behaviour and alloparental care are key aspects of many animal societies. In cooperatively breeding species, the interplay between ecological constraints and mating opportunities determines whether individuals become reproducers or non-reproducing helpers. However, the extent to which the reproductive state of an individual affects the tasks performed during offspring care remains poorly understood. In the social spider *Stegodyphus dumicola*, approximately 40% of females reproduce, and show extended maternal care including egg sac tending, regurgitation feeding, and matriphagy, in which they are consumed by the offspring. We asked whether and to what extent virgin females participate in extreme maternal care and if they differ from reproducing females in foraging activity. We show that virgin females contribute to all aspects of extended brood care, including regurgitation feeding and matriphagy. This suggests a physiological adaptation in virgin females to cooperative breeding, since in the subsocial *Stegodyphus lineatus* only mated females provide extended maternal care. Although virgin females and mothers are behaviourally totipotent, virgins engaged less in brood care and more in prey attack compared to mothers. High relatedness among nest mates and low probability of future reproduction in virgin helpers suggests alignment of reproductive interests between mothers and allomothers. Therefore, extreme allomaternal care of virgin helpers can be considered an adaptation to cooperative breeding in social spiders.

BEH-O-14

B

**Evolution of sex roles: the significance of sex-biased social environments**

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Sex roles in mating and parenting are widespread in nature and represent a fundamental component of sexual selection and population biology. Recent studies suggest that a major – yet not fully understood – predictor of sex roles is sex-bias in the social environment, as indicated by the adult sex ratio. But at which point in life history do sex-biases emerge? Here we evaluate the origins of sex biases and their consequences on sex role evolution using a detailed demographic analysis of six intensively studied wild populations of *Charadrius plovers* comprising over 6000 individually marked birds. Both among and within species, we found surprising variation in both sex roles and adult sex ratios. Sex role variation reflected biases in the adult sex ratio: parental cooperation was prominent in unbiased populations, whereas sex-biased populations exhibited high rates of parental desertion. Notably, in all populations, sex-biased apparent survival of juveniles, rather than adults, contributed most to adult sex ratio bias. Taken together, our study provides a major insight into the early life origins of sex-biases in the social environment, and their knock-on consequences for shaping sex-specific parental strategies later in life.

BEH-O-15

### Sheep in wolves' clothing and in wolves' smell: anatomical and chemical mimicry in army ant-associated staphylinids

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A diverse assembly of arthropods seeks close contact to army ant colonies. Successful infiltration of these societies offers easy access to high quality food and protection from own predators. However, seeking close contact to a top predator of tropical rainforests holds the risk of being detected and killed by the ants themselves. To avoid the latter, army ant guests often possess protective morphologies and behavioral adaptations. One of the most striking adaptations is the close anatomical resemblance of certain staphylinid beetles to their host ants. These myrmecoids are among the best integrated ant guests behaving as if they were members of the ant societies. We tested whether morphological adaptations in three myrmecoid species, associates of the Neotropical army ant *Eciton burchellii*, are accompanied by chemical integration strategies. Analyses of cuticular hydrocarbons (CHCs) revealed close similarity in CHC composition and CHC concentration between myrmecoids and host ants indicating chemical host deception. Compared to myrmecoids, ant guests of the genus *Tetradonia*, beetles with a typical staphylinid body shape, were behaviorally less well integrated and showed a lower level of chemical host resemblance in terms of CHC composition and CHC concentration. Our results support the proposition that accuracy in chemical mimicry plays an important role for social integration into ant societies. However, exploitation mechanisms of ant guests are multifaceted and future studies face the problem of considering various adaptations to the life with ants including morphological, behavioral, acoustical, and various chemical exploitation strategies.

BEH-O-16

### Sticklebacks become bolder in the presence of parasite manipulated conspecifics

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Many parasites alter the behaviour of their hosts to facilitate their transmission to a next host. If the next host is a predator, infected specimen often exhibit higher risk taking behaviour. Although such phenomena are well documented on the individual level, their possible effects on behaviours of uninfected conspecifics have received far less attention. We hypothesised that individuals engaged in groups, such as shoaling fish, are susceptible to the abundance of behaviourally altered conspecifics. To test this, we used the tapeworm *Schistocephalus solidus* which changes the behaviour of its three-spined stickleback host (*Gasterosteus aculeatus*), to make it more prone to predation by its final host, a fish-eating bird. We performed an experiment with groups of 6 sticklebacks and experimentally infected 0, 2, 4 or all 6 individuals with the tapeworm. On each treatment group, we simulated a bird attack and monitored the behaviour of each individual pre- and post-attack with seven replicates. We found that prior to an attack, there were no differences comparing individuals from all infected groups and all uninfected groups. However, after the bird attack, individuals from all uninfected groups were more likely to escape into cover and spend less time in the dangerous open water than individuals from all infected groups, confirming earlier studies of increased risk taking following *S. solidus* infection. More importantly, we found that the behaviour of the infected individuals was not dependent on the infection status of their group members. In sharp contrast, uninfected individuals responded to the infection status of their group members: the higher the number of infected individuals, the more risk taking uninfected individuals became. Our results are among the first to show that parasite infection not only increases risk taking of the infected individual, but also of uninfected, group members, shedding new light on social dynamics in host-parasite interactions.

BEH-O-17

**Interaction of two distance memories in desert ants**Harald Wolf<sup>1</sup>; Sarah Pfeffer; Matthias Wittlinger<sup>2</sup>; Lucian Kaack

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Estimation of distance covered during locomotion is an important component of navigation behaviour in animals. In North African desert ants, genus *Cataglyphis*, it has been shown that these animals possess indeed two odometer mechanisms, namely, stride and optic flow integration (Pfeffer & Wittlinger (2016) Optic flow odometry operates independently of stride integration in carried ants. *Science* 353, 1155; further references in there).

Although both mechanisms are well established, their mode of interaction remains enigmatic. We tackle this problem by selectively covering the ventral eye parts in *Cataglyphis fortis* foragers, the eye regions responsible for optic flow input in odometry. This was done during different sections of outbound and inbound travel, demonstrating that there are two odometer memories – one for stride integration, one for optic flow integration – that appear to be charged and discharged independently and assume different relative weights according to context.

This demonstrates that different navigation cues do not only interact, such as sun and polarization compasses in the sky, but that they are indeed independent to the stage of (distance) memory formation. An understanding of the interaction of different odometer mechanisms appears valuable not just for animal navigation research but may inform discussions on sensor fusion in both behavioural contexts and potential technical applications.

BEH-O-18

**Touchscreen-based visual object-location paired-associates learning: A first comparative approach in humans and a non-human primate.**Daniel Schmidtke<sup>1</sup>; Sandra Ammersdörfer<sup>1</sup>; Marine Joly<sup>2</sup>; Elke Zimmermann<sup>1</sup>

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Touchscreen-based assays on visual object-location paired-associates learning (PAL) are valuable tools to investigate the formation and retrieval of visual object-location memory across species. A recent study suggests that one particular task, the dPAL assay, allows an effective translation from animal models to humans. Here, we provide first evidence for the successful comparative application of the task to humans and a non-human primate (NHP), the grey mouse lemur (*Microcebus murinus*).

Young human adults reach the learning criterion after considerably less sessions (one order of magnitude) than young, adult NHPs, which is likely due to faster and voluntary rejection of ineffective learning strategies in humans. At criterion, however, all human subjects solved the task by either applying a visuo-spatial rule or, more rarely, by memorizing all possible stimulus combinations and responding correctly based on global visual information. An error-profile analysis in humans and NHPs suggests that successful learning in NHPs is comparably based either on the formation of visuo-spatial associative links or on more reflexive, visually-guided stimulus-response learning. The classification in the NHPs is further supported by an analysis of the individual response latencies, which are considerably higher in NHPs classified as spatial learners.

Our results, therefore, support the high translational potential of the standardized, touchscreen-based dPAL assay by providing first empirical and comparable evidence for two different cognitive processes underlying visual object-location paired-associates learning in humans and non-human primates. This study is part of a project which has received funding from the European Community's 7th Framework Programme (FP7/2007–2013) under grant agreement nu 278486 acronym "DEVELAGE" (<http://www.develage.eu/index.html>).

BEH-O-19

**Environmental acoustic cues guide the biosonar attention of a highly specialised echolocator**

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Sensory systems experience a trade-off between maximizing the detail and amount of sampled information. This trade-off is particularly pronounced in sensory systems that are highly specialized for one task and thus experience limitations in other tasks. We hypothesised that combining sensory information from multiple systems may resolve this trade-off and improve detection and sensing reliability. Specifically, we predicted that the limitations caused by specialization can be compensated for by phylogenetically older and less specialized systems. We tested this hypothesis in greater horseshoe bats, which possess morphological and neural specialisations allowing them to identify fluttering prey in dense vegetation using echolocation only. At the same time, their echolocation system is both spatially and temporally severely limited. We hypothesised that these limitations favour the opportunistic use of additional information for environmental perception. We show that bats detect and localise prey-generated and other environmental sounds by passive hearing, and then direct their sonar beam towards these sounds for further investigation with echolocation. These specialised echolocators thus supplement echo-acoustic information with environmental acoustic cues, enlarging perceived space beyond their biosonar range. This suggests that even specialised echolocators exploit a wider range of environmental information than previously believed, and that phylogenetically older sensory systems can support the evolution of sensory specialisations by compensating for their limitations.

BEH-P-01

**Deterministic or random search: How should I find my route again?**

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In many behavioural situations it is necessary to search efficiently for relevant places, the location of which being not exactly known. Although much research has been focused on optimal searching strategies to find locations dispersed sporadically in the environment, such as unvisited ower patches and preys, little is known about how an agent can find a previously learned route connecting at least two relevant locations.

In fact, most navigating animals (including humans) optimize their navigation in environments by learning and following routes. However, their journey along a learned route may be disrupted. The disruption may, for example, a consequence of the animal being required to avoid an impending danger (such as a predator), of navigational errors, or of wind that may displace a light-weight animal. We assess systematically by simulations of a variety of bio-inspired search strategies how well an animal is able to find its route back within a given time after been displaced by a given distance away from the route. We found that a unique best search strategy does not exist. Rather, the best strategy depends on the displacement of the agent from its route, the distance travelled that the agent can invest searching, and obviously the level of computational complexity the agent can achieve. Our simulation, moreover, highlight the importance to quickly detect any disruption of an agent's journey, as searching dramatically decreases the agent efficiency to navigate.

BEH-P-02

**High, low, or familiar? Laying hens' nest site preferences**

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Red jungle fowl are the ancestor of modern layers and ground breeding animals. Modern laying hens, however, are selected for increased egg yields and are provided in their housing with facilities for egg laying at given locations. Whether preference for breeding at the ground is still preserved in layer strains has virtually not been explored. Thus, we here aim to examine which nest heights are preferred in absence of their familiar nest locations and whether the preferred nest heights are more attractive than a familiar location. We used in total 108 hens of four different layer strains in two experiments. First hens were given for one-week free choice between nests at four different heights (0 cm, 39 cm, 78 cm, 117 cm above ground). Hens of the four strains differed in their nest height preferences ( $P = 0.0013$ ). While hens of three strains preferred ground level (all  $P < 0.007$ ), hens of the fourth line showed an equal preference for the ground level and level three, the latter level corresponding to the height of the nests in their home compartments. Secondly, we tested other hens of the four strains by giving the choice between ground level nests and nests at a familiar location, i.e. at the same location as in their home compartment. Here, hens of all strains preferred the familiar nest location ( $P = 0.002$ ) and preferences did not differ between strains ( $P = 0.77$ ). Thus, there still is a preference of laying hens for nests at ground level in the absence of a familiar nest. However, if possible hens continue to use a familiar nest location instead of a ground nest location. Our results are discussed with respect to a potential primary preference that may be modifiable by experience, which may have implications for commercial housing systems.

BEH-P-03

**Impact of kinship on allopreening behaviour in adolescent Bengalese finches.**

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Allopreening behaviour is defined as the act of cleaning those areas of conspecifics that cannot be cleaned by the other individual itself, such as the face or the neck. This behaviour is particularly common in social birds and is comparable to allogrooming observed in social mammals. While there is robust evidence showing that the degree of kinship influences allogrooming behaviour in mammals, less is known about the impact of kinship on allopreening behaviour in birds. This proposed project aims to disentangle the effect of familiarity, i.e. association and kinship on allopreening behaviour in Bengalese finches (*Lonchura striata domestica*). Using a classical cross-fostering design this project investigates the impact of familiarity and kinship on allopreening behaviour during adolescence in the Bengalese finch. Half of the eggs of each clutch will be cross-fostered into another nest to create broods that consist of unrelated and related nest mates. After reaching nutritional independence, "Teenie-groups" will be formed that contain at least two different cross-fostered broods. This way each "Teeni-group" consists of unfamiliar but close related individuals (same parents - raised in different nests) and familiar but unrelated individuals (different parents - raised in same nest). Daily observations should reveal whether and to what extent familiarity or kinship has an impact on allopreening behaviour.

BEH-P-04

### Bioluminescence in flashlight fishes. Diversity in blink frequencies and light organ function

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Bioluminescence is a widespread phenomenon in nature and especially common in the oceanic environment. The closely related flashlight fishes *Anomalops katoptron* and *Photoblepharon steinitzi* can be found in the shallow waters of coral reefs in the Indo-Pacific region. Both have been shaped light organs settled with luminous bacteria and produce striking blink patterns. We investigated the bioluminescence and blink behaviour of *A. katoptron* and *P. steinitzi* with infrared recordings in the lab and in the field. *A. katoptron* occur during dark nights in schools of up to 200 specimens near the water surface. *A. katoptron* display high blink frequencies of approximately 90 blinks/min and equal on/off times during the night. When planktonic prey was detected in the experimental tank, the open time increased compared to open times in the absence of prey and the frequency decreased to 20%. Furthermore, only luminescent specimens were able to detect prey. Thus, we provide evidence that *A. katoptron* use bioluminescent illumination to detect planktonic prey. In contrast, *P. steinitzi* live in pairs or small groups in caves and can be seen at the cave entrance. They show a territorial behaviour. *P. steinitzi* display a nearly constant glow during the night interrupted by approximately 8 blinks/min in the absence of stimulatory luminescent cues e.g. an intruder or a glowing fish dummy. In the presence of cues *P. steinitzi* increase the blink frequency up to approximately 72 blinks/min in correlation with aggression behavior. Thus, we provide evidence that territorial behaviour in *P. steinitzi* is correlated with blinking behaviour and aggression is encoded in high blink frequencies.

BEH-P-05

### Good vibrations: Are they involved in the courtship display of colourful birds?

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The ability to convey and assess the quality of a potential mate is central for sexual selection. Therefore, increasing signaling efficacy, for instance through multimodal courtship display, is likely to be beneficial to both sexes. In birds, studies typically focused on auditory and visual components. However, other communication modes, such as substrate-borne vibrational signals, may also be used by courting birds to enhance signaling efficacy.

In this study, we examined the courtship display of the polymorphic Gouldian finch (*Erythrura gouldiae*) in captivity, focusing on substrate-borne vibrational signals. More specifically, we aimed to assess potential informational content of vibrations, and compare vibration characteristics between individual birds and between colour morphs.

During staged encounters of male and female finches, we measured vibrations produced on perches where birds were sitting using a laser-doppler vibrometer. We then analyzed these vibrations in terms of temporal patterns, amplitude and frequency.

Determining the potential informational content and interindividual differences in substrate vibrations will pave the way for future studies investigating, whether these signals are used as an additional information channel in Gouldian finches.

BEH-P-06

**Variations in vibrational signals of *Karoophasma biedouwense***Simon Küpper<sup>1</sup>; Mike Picker<sup>2</sup>; Monika J.B. Eberhard<sup>3</sup>

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Vibrational communication is extremely widespread in insects and often used for mate attraction. In Mantophasmatodea, both males and females produce substrate-borne vibrational signals, enabling them to identify and locate conspecific mating partners. As in other animals, the signals might vary in their temporal characteristic and/or frequency, depending on the condition of the communicating individual. Additionally, environmental effects such as temperature will likely impact vibratory signals of the ectothermic animals.

This study aims to reveal the effect of food availability, mating status, age, and temperature on vibrational signals of male *Karoophasma biedouwense* (Austrophasmatidae). Males were collected near Clanwilliam, Western Cape, South Africa, in August and September 2016, and separated in different experimental groups. Recordings and analysis of vibratory signals were conducted with a portable Laser-Doppler-Vibrometer, using the software Vibsoft 5.2 (Polytec GmbH, Waldbronn, Germany). The results of these experiments allow us to identify differences in vibratory calls and whether any of the biotic or abiotic factors influence a male's biotremology performance.

BEH-P-07

**The Influence of Training on Dynamic Weighting of Multisensory Inputs in the Weakly Electric Fish *Gnathonemus petersii***

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An animal's perception of the environment is a prerequisite for reacting quickly to environmental changes. Many species obtain sensory information through multiple sensory channels. The model organism of this study, the African weakly electric fish *Gnathonemus petersii*, possesses multiple sensory systems and can detect objects with at least two different senses: the active electric sense and vision. To integrate multisensory information efficiently, sensory inputs are weighted dynamically depending on the sensory reliability of the different senses. This raised the question whether dynamic weighting of sensory inputs is shaped by experience or whether it is an innate property of the sensory system. In previous experiments, fish were trained to discriminate between two different objects placed at a short distance. The electric sense dominated at short distances, while the visual sense took over at longer distances.

In this study, fish were trained to discriminate between two objects of different shapes or sizes. During training, objects were placed either at short or at longer distances from the fish. Both senses, vision and the electric sense, were available. After reaching a learning criterion, the discrimination performance of the fish were tested at different distances. In additional tests, conflicting object information of both senses were presented to determine how sensory inputs are weighted. Fish could use either both senses simultaneously, only vision or only the electric sense. When trained at short distances, electric sense dominated vision, leading to an inability/decreased ability to discriminate between objects visually at short distances. In contrast fish, that were trained at longer distances also used visual information, even though they were also able to discriminate between the objects with only their electric sense available. Our results indicate that sensory experience during training can influence the dynamic weighting of multisensory inputs.

BEH-P-08

### Group dynamics, electric behaviour and motor-interactions of the weakly electric fish *Mormyrus rume* in natural and mixed groups

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The weakly electric fish *Mormyrus rume* emits brief, pulse-type electric organ discharges (EODs), which are used for both active electrolocation and electrocommunication. The temporal variations of inter-discharge intervals (IDI) of EODs play a pivotal role in communication and can be related to behavioural contexts and social reactions.

This study aimed to reveal patterns of electrocommunication and motor behaviours of *M. rume* in freely swimming groups of 3 fish and in mixed groups consisting of 2 fish and an EOD-emitting dummy. Our goal was to test, which role electrocommunication plays in group formation and coherence.

To quantify group, social and electric behaviour, we divided an experimental tank into a sheltered and an open-field area. The swimming trajectories and electric discharge of 3 fish swimming together from the shelter to the open area were recorded. In mixed groups one fish got replaced by a moving dummy. It emitted EODs recorded from the ahead swimming fish in the corresponding natural group. The behaviour of fish in mixed and natural groups was compared.

In both group constellations, the fish followed each other and showed similar swimming trajectories when swimming together into the open area. The dummy initiated following behaviour more successfully and at shorter distances compared to a real fish in natural groups. In all groups, alternating, pairwise synchronisations of EOD-activity occurred between all possible fish pairs. Fish also synchronised their EOD-activity with the signals of the dummy. Double pulses were produced at higher amounts in mixed groups, while discharge pauses occurred in natural groups only.

Altogether, the members of natural groups of *M. rume* showed strong group coherence possibly initiated by electric signalling. Similar results were obtained when one fish was replaced by an EOD-emitting dummy, which initiated even stronger following behaviour. Electric behaviour, however, differed to some extent in mixed and natural groups.

BEH-P-09

### Adaptive behavioural shaping during adolescence in male zebra finches (*Taeniopygia guttata*)

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Although the social rearing environment during adolescence can strongly influence the adult sexual behaviour of males, very little is known about the consequences for reproductive success. Previous work revealed that male zebra finches (*Taeniopygia guttata*) reared in mixed-sex juvenile pairs, mixed-sex juvenile groups and mixed-sex mixed-age groups during adolescence differ in their frequency of courtship and aggressive behaviour and the adjustment of aggressive behaviour towards different interaction partners. This variation in courtship and aggression is likely to affect the attractiveness and competitiveness of males, which might significantly influence their reproductive success. In order to verify this idea we investigated the effects of different social rearing conditions on the reproductive success of males competing over a limited number of females in a mate restricted breeding experiment. More group-reared males obtained paternity than pair-reared males and group males sired a larger number of offspring in a larger number of nests. Group males also obtained paternities in several nests, suggesting the occurrence of extra-pair paternities. Males reared in groups with and without adults did not differ in any measures. These results provide evidence that environmental conditions during adolescence can adaptively shape the behavioural phenotype for the predicted future environment.

BEH-P-10

### Do temperate bats keep their detection distances constant by adjusting call parameters to daily weather fluctuations?

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Bats rely on ultrasonic echolocation to detect and catch small insects in the dark of the night. Ultrasound is strongly attenuated in air, making echolocation a short-range sense that can detect prey only over distances of a few to few tens of meters, depending on call frequency. In addition to call frequency, sound attenuation depends on weather conditions, particularly ambient temperature and relative humidity. Fluctuating weather conditions over night and season cause changes in sound attenuation and thus the maximum prey detection distance. We hypothesized that bats adjust call frequency and/or call source level to weather conditions to maintain their maximum prey detection distance. Secondly, we hypothesized to find species-specific differences depending on each species' foraging ecology, with stronger effects on open-space bats that rely on long detection distances for finding prey. Using call recordings from a four-microphone array, we reconstructed the flight trajectory of multiple bat species and measured their call frequency and source level as a function of local weather conditions. We currently analyze the recordings to test our predictions of species- and ecology-specific differences in the reaction to changes in weather conditions. These results will also shed light on the question whether and how different species of bats might cope with altered atmospheric attenuation due to global warming.

BEH-P-11

### The influence of husbandry conditions to physical attributes and behaviour in zebra finch (*Taeniopygia guttata*)

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The influence of husbandry conditions to the animal welfare, health and behaviour is well examined in many groups of animals like farm animals, laboratory animals or pets. Alike an influence of early life conditions and experiences to the behaviour and health in adult life is repeatedly demonstrated. Such as in the model organism zebra finch (*Taeniopygia guttata*). Husbandry condition as a factor of influence on the outcome and comparability of experiments is less attended in zebra finch research. This study will do some steps to change this. In a first experiment we focused on the influence of differences of cage sizes. One part of the experiment was the detection of physical well-being, indicated by the weight, status of plumage and amount of visible subcutaneous fat, and the second part was the performance in an exploration and an association-learning task as behavioural components. Because studies detect strong genetic differences between breeding lines of different laboratories and personal experiences gives the impression of different behaviour in the breeding lines of the University Bielefeld this was added as additional factor. Related to the behaviour it seems there is no influence if birds were transferred from aviaries whether to small or medium cages. There seem to be small differences referred to the physical factors. Whereas the comparison of the breeding lines show bigger differences. In further experiments the influence of stronger variations in cage size will be studied and the number of physical attributes will be extended by measuring the flight ability.

BEH-P-12

**The behavioural dynamics during antagonistic encounters of *Mormyrus rume*: motor patterns and electrocommunication in fish-fish and fish-dummy interactions**

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Evaluation of the opponent plays a central role in antagonistic encounters. Communication during assessment can be studied in contest experiments, but so far no studies specifically tested contests in *Mormyrus rume*. By emitting pulse-type electric organ discharges (EOD), these weakly electric fish can communicate with each other. Different temporal patterns of EOD result in highly variable inter-discharge intervals (IDI) and offer clues about the sender's current behavioural state. Former studies let us to hypothesize that double-pulse patterns (alternating short and long IDI) might function as a threat signal. We therefore aimed to investigate not only the communication behaviour of *M. rume* during contests but also double pulses in particular by subsequently designed playback experiments.

Contests over a single shelter between size-matched pairs of *M. rume* were staged and tested for motor elements and IDI patterns. For each fish a "winner" or "loser" state was determined. Since the amount of double pulses differed significantly between later winners and losers, in subsequent fish-dummy interactions the fish were confronted with either a double-pulse playback or a control sequence.

According to sequential assessment, the *M. rume* of this study showed discharge and motor behaviours of varying intensity and changing frequencies over the course of the contests. Lateral displays, double-pulses and regularized discharges decreased while headbutts, chasing and the occurrence of discharge pauses increased. Overall a higher amount of double-pulses predicted later winners, which supports the idea that this IDI pattern functions as an assessment signal. However, in fish-dummy interactions the behavioural responses elicited did not differ between double-pulse and control sequences. Both treatments triggered a uniformly high production of double-pulses and aggressive attacks (ceiling-effect), which may be due to a lack of interactive discharge and motor patterns of the dummy.

BEH-P-13

**The more the merrier: Dynamics of behavioural interactions and electrocommunication behaviour in differently sized groups of *Mormyrus rume***

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In various animal species group formation and social interactions play an important role. Here we used the weakly electric pulse-type fish, *Mormyrus rume*, to study group behaviour and communication. Nocturnally active mormyrids emit and perceive weak electric signals (EOD) to orientate in their environment and to communicate with each other. During electro communication, temporal patterns of EODs result in specific inter-discharge intervals (IDI), which carry information. Little is known about group dynamics in *M. rume*, but prior observations suggest that these fish tend to show less aggressive behaviour with increasing group size. We investigated groups of three or four individuals to analyse group behaviour and to identify electric communication patterns during social interactions.

In groups of three, specific motor actions and IDI patterns were observed and a hierarchy was determined to analyse the electric behaviour of differently ranked fish. For a comparative approach, the total amount of behavioural interactions in groups of four was determined.

In the course of an interaction period, *M. rume* showed decreasing lateral displays, discharge synchronization and fixed order signalling, while chasing, probing and discharge pauses were increasing over time. Regarding the hierarchical structure, alpha fish tended to produce more double pulses and besides a higher amount of lateral displays, chasing and head-butts also motor activities such as backwards approach and probing were higher than in subordinate individuals. A comparison of motor actions revealed a lower amount of aggressive behaviour in groups of four compared to three individuals.

These findings support the idea that distinct motor actions together with specific IDI patterns are used to assess opponents at the beginning of an encounter followed by aggressive interactions, which finally lead to a hierarchical structure of the group. Overall, bigger sized groups tend to be more peaceful than smaller groups.

BEH-P-14

**Intra- and interspecific information transfer in foraging insectivorous bats**

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Animals can gain important information by attending to signals and cues of other animals in their environment. The echolocation call sequences of bats contain diverse information about identity and behaviour of the calling individual, which is perceptible to close-by individuals. Increasing evidence supports the communicative function of echolocation within species, yet data about its role for interspecific information transfer is scarce. In two playback experiments, we asked whether bats are attracted to conspecific and heterospecific foraging call sequences, whether attraction is based on similarity in call structure or foraging ecology, and whether attraction increases with increasing simulated foraging patch profitability (i.e., capture rate = feeding buzz density).

We first conducted a lab experiment with wild individuals of *Myotis capaccinii*. We broadcast 12 feeding buzzes per minute from either conspecifics or one of four heterospecifics in one of two flight room compartments, and analysed the proportion of total flight time that individuals spent in the playback compartment. *M. capaccinii* only approached call sequences of conspecifics and the heterospecific *M. daubentonii* that has similar acoustic call structure and foraging ecology. This confirms information transfer across species boundaries, yet suggests that only very similar species elicit positive phonotaxis at a feeding buzz rate of 12 buzzes per minute. Since our results suggest that bats selectively react to feeding buzzes of certain species but not of others, we secondly tested whether attraction to con- and heterospecific calls depends on simulated profitability. In the field, we again presented 1-min long playbacks of five bat species to free-ranging foraging bats. We varied, however, the feeding buzz rate between 0 to 96 buzzes per minute, simulating very poor to rich foraging grounds. We currently measure bat activity as a function of playback species and simulated capture rate.

BEH-P-15

**Behavioural variability as anti-predator adaptation? Reaction to ultrasound stimuli in eared moths**

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How to not end up as a predator's meal? This question is crucial for animals of prey; and therefore a multitude of adaptations for escaping predators evolved. One of the widespread adaptations is erratic and therefore unpredictable movement. Echolocating bats and eared moths are ideal to study this kind of behaviour. Upon detecting a bat many eared moths engage in evasive flight manoeuvres to escape the attacker. Previous studies revealed that moths' escape flight consists of two stages, directional and erratic flight. Surprisingly however, erratic flight seems to show some degree of stereotypy. As successful escape behaviour is mainly based on unpredictability, an open research question is how such stereotypical behaviour can be effective for avoiding predators. We hypothesize that interspecific variation in evasive flight exists across moth species, causing a masking effect of stereotypy of any single moth species. We recorded evasive flight behaviour of multiple European and North-American moth species using two different approaches. (A) Using an automated force-transducer, we recorded behavioural audiograms of stationary flying moths. Pure tone stimuli from 5-90 kHz were presented in randomized order and with increasing intensity of 20-90 dB SPL to flying moths. (B) To observe natural flight behaviour, we recorded 3D trajectories of free flying moths in an anechoic acoustic chamber in response to pure tone pulses of 30 kHz at 50, 65 or 80 dB SPL. Analysing behavioural thresholds (A) and the onset and three-dimensional shape of escape trajectories (B) will enable us for the first time to systematically compare moth escape flight across species, to compare behaviour to the underlying neuronal audiograms, and to study additional factors like moth size on escape behaviour. In sum, this will shed light on the specialised adaptations that evolved in prey species in response to the threat posed by their highly specialized predators, nocturnal flying echolocating bats.

BEH-P-16

### Dynamics of the Social Structure of Captive *Sapajus flavius* at Parque Estadual de Dois Irmãos, Recife, PE.

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The species *Sapajus flavius* is considered endangered by the Brazilian official lists and the IUCN. In order to disseminate knowledge about the species, this study aimed to (1) assess the welfare of the individuals who were part of the group pre and post enrichment by the degree of affiliation, (2) to analyze the interaction between individuals and the establishment of hierarchical positions during the formation of the new composition of the colony and (3) describe and determine the behavioral profiles of seven captive blonde capuchin monkeys. This research was developed at Dois Irmãos zoo from August to November 2015. The results showed that the colony was still in formation until the end of this study. The individuals in the group, in general, fed more during the morning and showed a predominance of affiliative behaviors in the afternoon. In all individuals were observed affiliative behaviors, but the male Urso was the main recipient of these, so was considered the dominant. Few agonistic behaviors were identified during the observation period. The results concerning the stereotype indicated that four of the seven individuals of the colony exhibited behaviors considered as artifacts of captive management procedures.

BEH-P-17

### The role of body condition and social environment during escalated singing contests in the bushcricket *Poecilimon ampliatus*.

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Many insects use acoustic signals to attract mates. During song contests, the asymmetry between rivals presenting different quality or different resource holding potential (RHP) may determine who will be the winner. An individual can decide to persist or give up the fight, using signals to assess the RHP of his opponent in comparison to its own.

In Orthoptera, males can modify their signaling depending on acoustic cues of the neighbors as honest indicators of body condition. Longer, louder and with higher rate calls are preferred by females, which mate mostly with larger and heavier males. This choice give females a direct benefit since heavier males provide a bigger nuptial gift during mating. We recorded the singing activity of the bushcricket *Poecilimon ampliatus* during acoustic contests in the laboratory. Competing couples of heavy and light males were placed at four inter - male distances to simulate different competition strength. We assessed the effect of body condition (body mass) and competition level (rival distance) to signal production by measuring the temporal song features. Both factors significantly affected the signaling of *P. ampliatus* males. Heavy competitors sang with longer verses and higher duty cycles than light ones. Additionally, heavier males incremented their song production with the increase of the contest's escalation, reaching the maximum level at the shortest inter-male distance, singing with longest verses and highest duty cycle. Our results show that males adjust their signaling accordingly to the strength of the fight. The males' response to the rival's presence indicate a mutual assessment strategy with lighter males, heaving a lower RHP, only slightly increase their signaling effort when a stronger and closer rival is present.

BEH-P-18

### Reduced sensor movement sequences for a partitioning of search area and a selection of discrete EEV contour-ring fragments in active electrolocation

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Weakly electric fish use active electrolocation to detect objects in their nearby environment. The major prerequisite is the possibility to generate and sense electric fields. In addition, fish perform scanning movements to obtain additional parameters of detected objects. Inspired by this example, an application for active electrolocation is shown based on reduced sensor movement sequences as a precursor for search area partitioning. A minimal set of scanning movements (Wolf-Homeyer et al., *Bioinsp. & Biomim.* (2016), 11(5):055002) is conducted with a transducer rig consisting of an emitter-dipole and an orthogonally arranged pair of sensor electrodes. Sensor measurements are used to look up contour-rings (Solberg et al., *Int. J. of Robotics Res.* (2008), 27(5), pp. 529-548) in EEVs (Ensemble of Electrosensory Viewpoints) which can be calculated online based on the simplified, mathematical formulation by Rasnow (*J. Comp. Physiol. A* (1996) 178, pp. 397-411). In combination with a marching squares algorithm, independently of FEM-simulations, two-dimensional discrete EEV-contour-rings of desired accuracy are extracted. The fixed scanning strategy allows to exclude polygons of the search area which leads to a fragmentation of the selected contour-rings. This in turn, implicitly reduces the number of ambiguous object positions. In a final step, the nearness of each combination of contour-ring fragments is calculated and used differently in dependence of the chosen scanning strategy. In the basic scanning approach (original EEV, rotation by 45°, linear shift) a simple nearness metric is defined and used to detect an object position. In the second strategy the basic approach is used three times with different linear shifts. The nearness of contour-ring fragments is used in a majority voting approach to extract the most likely object position. In the future, an application-oriented sensor-system will be set up and the corresponding physically experiments will be conducted.

BEH-P-19

### Do blowflies shape their walking style to detect camouflaged objects in three-dimensional environments?

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While walking animals explore their environment, they use visual cues to obtain spatial information about the layout of their surroundings. The motion of objects on the retina, known as optic flow, generated by translational movement can be used to estimate distance and to separate even texturally camouflaged objects from the background. Walking *Drosophila*, for instance, use motion cues to estimate distance, which is reflected in a preference for closer objects (Schuster et al. 2002). While flying blowflies segregate their flight into straight segments and quick turns, known as saccadic flight and gaze strategy, thereby maximizing the time of translational movement and, thus, facilitating the extraction of spatial information from the resulting optic flow (Egelhaaf et al. 2012), little is known about active behavioral strategies employed by walking blowflies in the context of spatial vision.

To address this issue, we allowed walking blowflies to explore a cylindrical arena where they could repeatedly choose between three unreachable targets placed at different distances. Objects were either defined by static image contrast (solid black or white objects) or texturally matching the background (i.e. camouflaged for a non-moving animal). We found no preference for objects based on distance unless the objects were camouflaged. However, in this case the preference can be explained as a consequence of a decreasing discriminability of the object with decreasing distance between object and the background. We further analyzed how walking blowflies approached camouflaged objects compared to more conspicuous objects. We found that all the parameters characterizing the walking style tested did not change when the objects were camouflaged. By analyzing the optic flow generated by the walking animal, however, we discovered that the walking style of blowflies inherently generates translational optic flow which could potentially be used to detect and approach the object.

BEH-P-20

**The problem of home choice in skyline-based homing**

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Navigation in cluttered environments is an important challenge for animals and robots alike and has been the subject of many studies trying to explain and mimic the navigational abilities of animals. However, the question of selecting an appropriate home location has, so far, received only little attention. This is surprising, since the proper choice of a home location might greatly influence an animal's navigation performance.

To address the question of home choice in cluttered environments, a systematic analysis of homing trajectories was performed in computer simulations using a skyline-based local homing method. Our analysis reveals that homing performance strongly depends on the location of the home in the environment. Furthermore, it appears that by assessing homing success in the immediate vicinity of the home, an animal might be able to predict its overall success in returning to it from within a much larger area, indicating a possible mechanism to optimise homing performance via home choice.

BEH-P-21

**Motion cues increase stimulus-directed behaviour and focused attention towards purely visual prey stimuli in a nocturnal primate**

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Visual information is of pivotal ecological importance to monkeys, apes, and humans. The role of visual information processing for the life of more basal, nocturnal primates is less clear as their visual systems lack many of the adaptations found in monkeys and apes. Therefore, we explored if purely visual information is sufficient to affect the behavioural state of a nocturnal primate (the grey mouse lemur, *Microcebus murinus*) and to evoke stimulus-directed responses. Abstract (shape), photographic (shape+detail), or video (shape+detail+motion) representations of arthropod prey (*Zophobas morio*) were presented to the subjects in a highly controlled, touchscreen-based environment. Stimulus-directed behaviours were assessed automatically (as touch-interactions with the stimulus) and videographically (as duration of focused visual attention towards the stimulus).

We found that all three representations of *Z. morio* significantly changed the behaviour of the mouse lemurs when compared to sessions without stimulus presentation. Both focussed attention towards and touch-interactions with the stimulus increased highly significantly from abstract and photographic to video representations. Touch-interactions additionally increased significantly from abstract to photographic representations.

Our results demonstrate for the first time that purely visual information is of specific importance for focussed attention and evaluation in a nocturnal primate, suggesting that vision may be of higher importance for nocturnal primate ecology than previously assumed. They emphasize the need for further vision-based experiments to gain deeper insight into the evolution of visual information processing and cognition in primates.

This study is part of a project which has received funding from the European Community's 7th Framework Programme (FP7/2007–2013) under grant agreement nu 278486 acronym "DEVELAGE" (<http://www.develage.eu/index.html>).

BEH-P-22

### How do scorpions walk? Locomotion and walking parameters of the scorpion *Mesobuthus eupeus*

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Not much is known about the mechanisms of eight-legged arthropod walking, and only few studies have examined the locomotion of scorpions. We analysed the walking behaviour of *Mesobuthus eupeus* via highspeed video recordings over a speed range from 216 to 3352 mm/s, corresponding to 5 to 81 body lengths/s. With increasing walking speed, stride frequency (from 1,70 to 63,88 Hz) and stride length (from 3,22 to 275,47 mm) increased, while swing phase duration (from 0,03 to 0,27 s), stance phase duration (from 0,02 to 0,43 s), and cycle period (from 0,06 to 0,59 s) decreased. Indicators of accuracy, like the order of successive leg lifts (up to 104 step sequence variants considering eight legs) as well as tetrapod coordination strength (TCS) for swing (from -0,43 to 0,43) and stance (from -0,41 to 0,60), showed broad variation, but were independent of walking speed.

There was only one walking gait identified for the entire speed range, the “alternating tetrapod”, again with high variance. Ideal step sequences were 4-3-2-1 for the tetrapod groups R4 L3 R2 L1 and L4 R3 L2 R1, and 4-2-3-1 or 3-1-4-2 for the left and right legs L4 L2 L3 L1 and R4 R2 R3 R1. The scorpions often deviated from these ideal combinations, contralaterally more often than in ipsilateral coordination. This indicates a high flexibility of scorpions interleg coordination. Formerly considered as a walker with strong repetitive leg movement pattern and a strict order of lift-off and touch-down events, further physiological and neurobiological studies on scorpion locomotion appear necessary in view of the unexpected flexibility observed here.

BEH-P-23

### Go with the flow? Contribution of visual and electrical parallax to depth perception in weakly electric fish.

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Weakly electric fish are known to recruit and integrate various sensory modalities for a broad amount of perceptual and behavioural tasks (Schumacher et al., 2016). It is known for example that they rely mainly on their advanced electrosensory system during shelter tracking, but visual information is consulted when electrosensory reliability is reduced (Sutton et al., 2016).

During this behaviour, electric fish maintain their position in the perceptual center of the moving shelter by keeping available sensory flow constant. Optic flow and motion parallax could serve as visual sensory flow cues. Moreover, a recent study suggests that comparable parallax cues are also perceived by the electric sense (Pedraja et al., 2016). This offers the chance to investigate how parallax originating from vision and electroreception are combined behaviourally.

In this study, we independently manipulated visual and electric information of sensory flow cues – reducing stimulation to one sense only. We equipped a shelter of two narrow vertical plates either with an electric grating that was visually covered by uniform cloth or a visual grating of the same spatial frequency without any electric information.

We currently test shelter-tracking in *Gnathonemus petersii* to establish the relative contribution of both sensory modalities to the behaviour. In the following we will modify the reliability of both modalities to address how vision and electroreception are integrated. We expect our findings to give further insight into the processing of sensory flow cues, and the recruitment of different sensory modalities by addressing them in a conflicting manner or actively altering their reliabilities.

BEH-P-24

B

### Population structure in the Antarctic fur seal: recolonization by a recovering population

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Hunting and other human pressures have reduced many wild animal populations. Understanding how populations respond to these (and other) pressures is a central question in conservation biology. The Antarctic fur seal (*Arctocephalus gazella*), a marine mammal that breeds on islands all around Antarctica, provides an interesting case study. This species was driven to the brink of extinction by 19th Century sealers, yet has recovered to over three million individuals globally. To investigate whether this recovery was facilitated by extensive migration among colonies, we genotyped over 1000 individuals from seven breeding locations at 40 microsatellite loci. Unexpectedly, in our preliminary analyses we found evidence for strong population structure, indicating that most colonies were re-founded by local individuals. This would suggest that local populations may be surprisingly resilient to human pressures and that extensive migration may not be required for population recovery.

BEH-P-25

B

### Road to recovery: tracing global population expansion of Antarctic fur seals via color polymorphism.

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Numerous species have declined due to human impact. For example, many seal species have experienced severe population bottlenecks after being hunted to near-extinction during the eighteenth and nineteenth centuries. However, the mechanisms behind many of these populations' recoveries are not yet known. In Antarctic fur seals (*Arctocephalus gazella*), a rare, non-synonymous mutation in the melanocortin 1 receptor (MC1R) gene, which results in the alteration of fur color from brown to blonde, has been identified. In order to provide insight into how *A. gazella* may have recolonized the Antarctic, we sequenced this mutation in over one thousand pups from seven geographically distinct populations worldwide. We found that the frequency of the mutation declined significantly with geographic distance from the main breeding grounds at South Georgia. This suggests that migrants from South Georgia may have played a limited role in the recovery of nearby populations.

BEH-P-26

**What's for dinner: olfactory food choice in oribatid mites**

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Animals need to consume food to maintain their metabolism and generate energy for growth and reproduction. Hence, various ways for the detection, foraging and processing of food evolved to exploit a wide range of resources. In above-ground systems, olfactory traits play an important role for many heterophic organisms to find and identify their food. In soil ecosystems, however, olfactory food selection has only been fragmentarily explored and it remains to be uncovered whether olfactory signals play a role in finding suitable food sources for mainly decomposing microarthropods (e.g., oribatid mites and springtails) in the highly structured soil microsphere. Hence, more data is needed for an understanding of the soil food web structure. We used two phylogenetically distinct oribatid mite species [*Archezogetes longisetosus* (parthenogenetic, opportunistic feeder) and *Scheloribates* sp. (sexual, myco-/phytophagous feeder)] in 780 laboratory food-choice bioassays (= 7800 individuals) to access two basal questions. Do oribatid mites use olfactory cues for food selection and if so, can they discriminate between different food sources. We further asked whether oribatid mites are habituated to odors of food they know. Additionally we chemically characterized volatiles and nutrients of the food sources (litter, lichen, fungi, bacteria). We found that oribatid mites use olfactory signals to find food and also differentiate among resources. Mites did not prefer well known resources over their generally preferred food. While *A. longisetosus* preferred a fatty acid rich bacterial diet, *Scheloribates* sp. mainly fed on fungal-based food sources (fungi and lichen). We also presented synthetic amino/fatty acid mixtures and glucose; again *A. longisetosus* preferred fatty acids, while *Scheloribates* showed no preferences. However, when we added the fungal volatile 3-octen-1-ol to glucose, *Scheloribates* sp. subsequently started to favour the modified glucose.

BEH-P-27

**Daphnia's swimming behaviour: Behavioural adaptations in a dangerous world**Sina Becker<sup>1</sup>; Linda C. Weiss<sup>1</sup>; Mikael Ekvall<sup>2</sup>; Giuseppe Bianco<sup>2</sup>; Lars-Anders Hansson<sup>2</sup>; Ralph Tollrian<sup>1</sup>

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Ecological communities are networks of interacting species. Such interactions ultimately affect and thereby shape ecosystems. Especially, the behaviour of organisms affects community structures. This has been well demonstrated in larger aquatic animals such as crustaceans, fish and sharks. In the case of plankton however studies on behavioural adaptations are scarce. Here, only the study on diel vertical migration represents one well-studied example. Nevertheless, a lot of these organisms play a pivotal role in aquatic ecosystems. For example, small crustaceans of the genus *Daphnia* belong to the most important species in lakes, transferring energy from the primary producers to the higher trophic levels and have been one focus of ecological research. Foremost, *Daphnia* is known for its remarkable ability to respond highly plastic to changing environmental conditions including temperature changes or the occurrence of predators. Unfortunately, up to now it was very difficult to observe the exact individual swimming behaviour of these animals because of missing techniques for adequate movement analysis. Here, three dimensional tracking most often failed because of the small body size and the low contrast between the transparent animals and their environment. Some studies only used two-dimensional monitoring approaches, but these animals move variably within all three dimensions. Therefore, we used a three-dimensional observation method and tagged the animals with fluorescent nanoparticles. We compared the general swimming behaviour of different *Daphnia* species as well as their behavioural defence strategies in the presence of predator cues: We defined the swimming type and motion patterns of the daphniids and analysed the swimming speed, the preferred swimming depth as well as the swarm formation behaviour. In this study, we observed species-dependent differences and showed that daphniids change their swimming behaviour in the presence of predator cues.

BEH-P-28

### Mouth-brooding within the Neotropical Cichlids genus *Apistogramma* (Regan, 1913)

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In 2008 the description of the first mouth-brooding species of the Neotropical cichlid genus *Apistogramma* (REGAN, 1913), *Apistogramma barlowi*, was published. As to that date only shelter brooding species were known among this group of “dwarf” cichlids, bi-parental mouth-brooding of that species was thought to be an extreme exception. Actual research has led to identification of another mouth-brooding species of the genus. Here we present results of ethological research, which led to the description of *A. megastoma*, indicating, that there might be more species in the Peruvian, Ecuadorian, and Colombian Amazonia exhibiting such brood care behavior. *A. megastoma* was not identified scientifically for several years for its striking overall phenotypic similarity and lumped with *A. barlowi*. Comparative ethological observation as well as genetic and close morphologic investigation brought this “cryptic species” to light. Other than its congener *A. megastoma* is a maternal mouth-brooder. During recent field collections in south-east Colombian tributaries of the Amazon two more yet undescribed mouth-brooding species of *Apistogramma* have been collected. One of these shows some overall similarities to the two species already known and has turned out to be a maternal mouth-brooder. This species eggs are comparable in size and number to all non-mouth-brooding *Apistogramma*-species, whilst those of *A. barlowi* are nearly 1.5 times larger and about 50 % reduced in number. Compared to these species, the size of eggs in *A. megastoma* is intermediate and their number not reduced. Present observations indicate, that in this species group bi-parental mouth-brooding may have evolved via maternal mouth-brooding from ancestral shelter brooding species. This case once more indicates, that multidisciplinary research activities can significantly contribute to  $\alpha$ -taxonomy. Our future activities will focus on additional field sampling, behavioral observation and genetic investigation of this group.

BEH-P-29

### Do maternal hormones in eggs correlate with offspring fitness?

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The yolk of eggs of birds contains considerable amounts of androgens like testosterone. These maternally derived hormones can influence the behaviour and growth of the chicks hatching from these eggs. Hence, maternal yolk androgens have been hypothesized to adaptively shape the offspring’s phenotype, particularly in relation to the rearing environment. However, the present evidence for this idea is mixed. We collected an unusually large data set in wild blue tits (*Cyanistes caeruleus*; >150 broods) to test three premises underlying the hypothesis of adaptive prenatal shaping of offspring phenotype. We investigated (1) whether there was substantial between-clutch variation in yolk testosterone levels; (2) whether such variation related to characteristics of the female or her environment; and (3) whether yolk testosterone levels related to offspring fitness. Importantly, in order to disentangle maternal hormone-related and environment-related variation in offspring fitness, we carried out a large-scale cross-fostering experiment. We found substantial between-clutch variation in yolk testosterone, which was partly explained by the female’s age and lay date, but not related to offspring growth or survival, providing only limited support for the presumed adaptive significance of maternal yolk androgens.

BEH-P-30

**B** **Innate social predispositions for animate motion and their neural correlates in newly-hatched chicks (*Gallus gallus*)**Orsola Rosa-Salva<sup>1</sup>; Uwe Mayer<sup>1</sup>; Mikolaj Hernik<sup>2</sup>; Elena Lorenzi<sup>1</sup>; Giorgio Vallortigara<sup>1</sup>

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Identifying animate creatures early in life is important for species as distant as birds and primates. Notoriously, naïve chicks preferentially approach a stimulus resembling a conspecific (a stuffed fowl) over a less naturalistic one. Chicks' preferences are elicited by features typical of animate agents, such as face-like patterns, self-initiated or semi-rigid motion (determined by the skeletal structure of legged vertebrates). Here we demonstrate that naive chicks are attracted by other elementary motion properties that reveal an internal energy source to the moving object (self propulsion) and elicit the perception of animacy in human observers. E.g., newly-hatched chicks preferentially approached a stimulus that spontaneously accelerates and then decelerates over another that moved constantly at the same average speed. Control experiments revealed that increasing the complexity of movement of the control stimulus did not alter chicks' preference, which was abolished only by occluding the speed-change events. Chicks also have a preference for objects keeping their body axis aligned to their trajectory (a feature typical of the motion of bilateria, due to the constraints posed by their body-plan). This property is also associated with a stronger perception of animacy in human observers.

We also investigated whether areas of the network that control social behaviour in adult vertebrates already respond to the first exposure to visual cues associated with animate motion. A series of experiments were run using the immediate early gene product c-Fos as a neuronal activity marker. Differential activation was found in septum, preoptic area and in amygdaloid nuclei of visually naive chicks exposed to the naturalistic motion of a conspecific or to a simple object changing its motion speed (as opposed to a rigidly rotating taxidermised chick or to an object traveling at constant speed).

**B**

DEV-O-01

**Cellular activity levels and cytoskeletal reorganization during diapause in *Daphnia***

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Diapause is a form of dormancy, predetermined by the genotype allowing animals to overcome harsh environmental conditions. It can occur during ontogeny, where development proceeds to a certain phase and is then brought to a halt. During the phase of apparent death, development, growth and metabolic activity is depressed until distinctive environmental cues signal favorable conditions. Resurrection of this apparent death is then induced via the perception of environmental cues. This strategy is known from various taxa in the animal kingdom ranging from mammals, fishes, insects, and crustaceans. Ontogenetic interruption is challenging for cell viability, as metabolic activity is paused. For that, cells must have mechanisms that prepare them for periods without metabolic resources. We investigated this using the freshwater crustacean *Daphnia*. Under favorable environmental conditions, *Daphnia* reproduce parthenogenetically. When conditions become harsh, they shift to sexual reproduction and breed haploid eggs. After fertilization, encapsulated embryos sink to the lake bottom, typically they enter diapause for months up to many years until being resurrected by exogenous stimuli.

We investigated mitotic activity, cellular activity, and cytoskeletal parameters before and during dormancy, and after resurrection using immunocytochemistry. Whereas mitotic activity comes to a halt during diapause, cellular activity does not fully arrest on the transcriptional level and rRNA processing. This indicates that cells are not fully dormant. Morphologically, cytoskeletal filaments (microtubules and actin-filaments) are reduced to a minimum, rendering the cells compact and condensed. On the one hand, this saves energy resources during diapause and on the other hand ensures that the cytoskeleton is quickly synthesized from a template upon resurrection. We here provide first insights into the cellular processes of diapause in the freshwater crustacean *Daphnia*.

DEV-O-02

**The development of neuronal and neuroglial elements in the sedentary annelid *Malacoceros fuliginosus* (Annelida, Spionidae)**

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Comparative investigations dealing with the ontogeny of larval nervous system characters shed light on conserved developmental mechanisms across various taxa. In Lophotrochozoa, one of the main groups of protostome invertebrates, most data are available for annelids and mollusks. Although thorough data exist on neural patterning, the question of where the first neurons differentiate and where the axonal scaffold of the central nervous system originates is still discussed and mainly based on immunohistochemical data. Both the anterior as well as the anterior and posterior onset of neurogenesis are described from several species, but respective gene expression data are scarce. Moreover, the developmental origin of neuroglia is largely unknown. Using a combined approach including immunohistochemistry with subsequent confocal laser scanning microscopy (clsm) and whole mount in situ hybridization (WMISH), we analyze the early neurogenesis of the spionid annelid *Malacoceros fuliginosus* (Claparède, 1870). With special focus on the origin and ontogeny of the larval nervous system, our study reveals first somata in an apical position and at the posterior larval end. The formation of the first neurites preforming the larval nervous system starts simultaneously from anterior and posterior. In line with this, a distinct anterior and posterior expression of genes indicating formation of neural precursors and neural differentiation can be observed. Notably, apical radial glia-like cells are detectable in direct vicinity to early neuronal precursors. Thus, the early neural development of *Malacoceros* reveals important insights into the formation of larval neuroarchitecture within Annelida. Consequently, our data represent an important basis for further comparative investigations to unravel ancestral patterns of the spiralian neural development.

DEV-O-03

**A morphological novelty based on a modified wing gene regulatory network**

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Insects have evolved an astonishing diversity of morphological adaptations while retaining a rather constant gene complement. An example for a morphological novelty are the gin traps, which are defensive structures found on abdominal segments of pupae in some beetle taxa. When knocking down one gene essential for wing development the gin traps are lost. This led to the suggestion that gin traps are serial homologous to wings.

We wanted to know in detail, how many genes of the wing gene network were re-used to form the gin traps. In addition, we asked how many non-wing genes were integrated. To this end, we first scored genes known from the *Drosophila* wing network for their involvement in gin trap formation. We found that a portion of these genes are involved. Secondly, we made use of the iBeetle RNAi screen to identify novel genes involved in the process. We found genes required for gin trap but not wing development.

I will discuss the relative contributions of re-deployment of the wing regulatory network versus the co-option of novel genes into the network responsible for this morphological novelty.

DEV-O-04

**First insights into the gene network underlying adult neurogenesis in procambarid crayfish**Georg Brenneis<sup>1</sup>; Martin Schwentner<sup>2</sup>; Prof.'in Barbara S. Beltz<sup>1</sup>

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Two decades after the discovery of life-long neurogenesis in the brain of decapod crustaceans, their adult neurogenic system has emerged as one of the best understood models for this phenomenon in invertebrates. The system in crayfish has proved particularly suitable for experimental approaches due to its accessibility on the brain's surface, anatomical simplicity, and the spatial separation of neural precursors as they divide and migrate. As a result, studies on *Procambarus clarkii* have recently provided evidence for the lack of bona fide neural stem cells in the adult niche, suggesting instead the replenishment of its neural precursor pool via hemocytes generated by the innate immune system. Aiming to better understand and characterize the processes and cell types involved in this adult system, we started to interrogate it at the molecular level. After generating transcriptomic data for *P. clarkii* and *P. fallax f. virginalis*, we identified members of genes/gene families that play key roles in arthropod neurogenesis and neural differentiation and subsequently performed *in situ* hybridization on embryos and adult brains, the latter coupled to *in vivo* cell proliferation experiments. Our embryonic data verify target gene expression in the expected neurogenic regions. Further, we show that most – but not all – of the genes are also active in the adult system, including SoxB transcription factors (TFs) in the majority of neurogenic niche cells, Achaete-Scute-homolog and Snail TFs in some niche cells and migrating neural precursors, and Elav in more advanced neural precursors and differentiated neurons. We demonstrate the suitability of our approach to identify and characterize prospective neural cells along their differentiation pathway, which is a crucial prerequisite towards unraveling the gene network governing the neural differentiation of hemocytes in the procambarid brain, when combined with future adoptive transfer experiments.

DEV-P-01

### Identification and characterization of novel genes involved in quinone synthesis in the odoriferous defensive stink glands of the red flour beetle, *Tribolium castaneum*

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The red flour beetle, *Tribolium castaneum*, uses defensive stink glands to produce antimicrobial p-benzoquinones and 1-alkenes. In the past, the morphology of stink gland has been studied in detail in tenebrionid beetles. However, very little is known about the genes that are involved in the safe production of toxic gland secretion. In this study, we identified a subset of genes that are essential for the benzoquinone production in red flour beetle. In the first phase, we selected 74 potential candidate genes from a genome-wide RNAi knockdown screen called "iBeetle". All these 74 candidate genes had indicated morphological phenotypes after RNAi-mediated gene knockdown. In gas chromatography-mass spectrometry (GC-MS) analysis of secretion volatiles in the respective RNAi knockdown glands, 33 of them showed altered phenotypes in stink gland content. Seven candidate genes were noted to display strongly altered glands, both in terms of secretion color as well as chemical composition, indicating their key role in biosynthesis of gland secretion. A complete lack of benzoquinones was observed in the knockdown of the sulfatase-modifying factor enzyme 1 and a member of the sulfate transporter family. Based on stink gland transcriptome data, I analyzed the function of the sulfatase-modifying factor enzyme 1 and the respective sulfate transporter via RNAi-mediated gene knockdowns, GC-MS, in situ hybridization, and enzymatic activity assays. In situ hybridization showed that these two genes are expressed around the vesicle of a certain subgroup of secretory stink gland cells. Enzymatic activity assays on stink gland tissue showed that these genes are involved in p-benzoquinone biosynthesis. These results suggest that sulfatase-modifying factor enzyme 1 and sulfate transporter family play a specific role in benzoquinone biosynthesis in red flour beetle.

Keywords— Red Flour Beetle, Defensive stink gland, Benzoquinones, Sulfate transporter, Sulfatase-modifying factor enzyme 1.

DEV-P-02

### Conserved versus derived patterns of controlled cell death during the embryonic development of two species of *Onychophora* (velvet worms)

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Apoptosis, a specific type of controlled cell death, is involved in various developmental processes of multicellular organisms, including cell migration and the formation and shaping of a variety of tissues and organs. Some of these processes are conserved across metazoans, while others are specific to particular taxa. Although the patterns of apoptosis have been investigated in different arthropods, no corresponding data are available from one of their closest relatives, the *Onychophora* (velvet worms). We analyzed the patterns of apoptosis in embryos of two onychophoran representatives, the lecithotrophic/matrotrophic viviparous peripatopsid *Euperipatoides rowelli*, and the placentotrophic viviparous peripatid *Principapillatus hitoyensis*. To detect apoptotic cells, we used terminal deoxynucleotidyl transferase-mediated dUTP nick end labeling (TUNEL) in combination with an antibody directed against the activated form of caspase-3. Our data show that apoptosis occurs early in development and might be responsible for the degeneration of extra-embryonic tissues. Moreover, apoptosis might be involved in the morphogenesis of the ventral and pre-ventral organs in both species and occurs additionally in the placental stalk of *P. hitoyensis*. Despite the divergent developmental modes in the two onychophoran species studied (yolkly versus yolkless eggs/embryos), our data revealed similar patterns of apoptosis suggesting that these are conserved among onychophorans. While apoptosis in the dorsal extra-embryonic tissue might contribute to dorsal closure – a process also known from arthropods – the involvement of apoptosis in ventral closure might be unique to onychophorans. Apoptosis in the placental stalk of *P. hitoyensis* is most likely a derived feature of the placentotrophic onychophorans.

DEV-P-03

### The genetically encoded voltage sensor ArcLight is a useful tool for investigating bioelectric phenomena during *Drosophila* oogenesis

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Bioelectric phenomena, such as gradients of membrane potential ( $V_{mem}$ ) and intracellular pH ( $pHi$ ), are known to exert influence on several developmental and regenerative processes. *Drosophila* ovarian follicles provide a suitable model system for studying the potential relations between electrochemical gradients, tissue polarity and cytoskeletal organization during the course of development.

Using the potentiometric dye DiBAC4(3) and the fluorescent pH-indicator 5-CFDA,AM, we found stage-specific electrochemical patterns within the follicular epithelium: Dorsoventral, anteroposterior and apicobasal gradients of  $V_{mem}$  and  $pHi$  as well as differences between specialized follicle-cell populations were observed.

In order to confirm the bioelectric patterns revealed by the fluorescent dyes, we used the genetically encoded fluorescent  $V_{mem}$  indicator ArcLight and a genetically encoded  $pHi$  sensor. ArcLight, which consists of a voltage-sensing domain and a pHluorin GFP variant, was activated by the Gal4-UAS-system in the follicular epithelium. While depolarization results in an increase in fluorescence of DiBAC4(3), it results in a decrease in ArcLight fluorescence.

Both methods lead to comparable results: In the follicular epithelium, a dorsoventral gradient appeared during mid-oogenesis (stage S10B), which was especially prominent with ArcLight. Moreover, an apicobasal gradient in the follicle cells was observed. Such stage-specific gradients of  $V_{mem}$  and  $pHi$  in the follicular epithelium could serve as physiological means to control tissue polarity as well as cytoskeletal organization. Since  $V_{mem}$ , as indicated by DiBAC4(3) fluorescence, can be hyperpolarized using various inhibitors of ion transport mechanisms, e.g. amiloride, glibenclamide and verapamil, we are currently analyzing comparable effects on ArcLight fluorescence. Our results show that genetically encoded bioelectric sensors provide useful tools for identifying bioelectric phenomena also in non-neural tissues.

DEV-P-05

### Development of morphological asymmetries in owls

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Evolution generally favors symmetry. Asymmetry is only found as adaptation to specific function. One case of asymmetry is found in owls (Strigiformes) where the ears are asymmetrically arranged in the head. The function of this asymmetry is to improve sound-localization capability in these birds, especially in the elevational direction. So far, ear asymmetry has only been described in adult birds. To our best knowledge, nothing is known about the embryonic development of ear asymmetry. This is interesting, because it may help to understand the evolutionary origin of ear asymmetry in owls. Therefore, we set up a systematic study to examine ear development in owls.

Here we describe the embryonal head development of the American barn owl (*Tyto furcata pratincola*). We describe the developmental stages according to a modified Hamburger-Hamilton scheme. The outer ear appeared first at stage 29. At this stage, the ear openings are symmetrically arranged in the head. Soon after, a dorsal movement of both ear openings could be detected. This movement was symmetrical for a short time. At stage 36, the left ear opening was located slightly more dorsal than its counterpart on the right. The ear asymmetry increased rapidly until stage 39 when the maximum difference was reached. This asymmetry continues to exist during the final embryonic days (stage 41). Since an asymmetry is found in adult birds, we assume that the asymmetry is present also after hatching and during post-hatching development.

Dorsal movement of the external ear is not restricted to owls, but is also found in other birds and even in humans. One interesting further question is whether symmetry or asymmetry is the default state for the order of owls or not. Ongoing research on other owl species will enable us to draw conclusions from the ontogeny of differently adapted species on the phylogeny and evolution of owl ear asymmetry. Genetic studies may uncover the molecular background of this asymmetrical development.

ECO-S-01

### Soil biodiversity beyond animals, bacteria and fungi: A consensus on the highly diverse and functionally important Protists (Protozoa)

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EC

Protists are tiny eukaryotes that have formerly been exclusively considered to be heterotrophic predators of bacteria in soils. Together with nematodes these “Protozoa” were therefore treated as microfauna. Soil protozoa were defined based on morphological features, grouped into flagellates, amoebae and ciliates. However, based on e.g. phylogenetics we now know that soil protists are far more diverse both in taxonomy and functioning; protists are (1) not microfauna but microorganisms like bacteria and fungi; (2) phylogenetically diverse, with amoebae and flagellates placed in many different eukaryotic supergroups, composing by far the vast majority of all eukaryotes; (3) functionally diverse as many feed not only on bacteria but depend on fungi, other protists and even larger nematodes as prey, are phototrophic or mixotrophic and are parasites of plants as well as animals.

In this presentation I will give an overview of the current state of knowledge on the taxonomic and functional diversity of protists and how to better study them in the near future. During the presentation I hope to clarify the functional importance of protists in soil food webs but also to increase plant performance. Protists might even be promising agents of potential and biofertilization- some companies now even start to include protists in their products to promote plant performance!

However, I will also try to bridge the knowledge on protists to other players in the soil food web, by focusing on nematodes.

Only the integrated knowledge on interacting biota in soils can lead to a cumulative understanding of the major players in soils and the functional importance of soil biodiversity. With novel techniques including high-throughput sequencing and network analyses we now have the methodological tool box to disentangle this black box. If we then share knowledge and collaborate we can make huge steps in the next future and I hope to provide some ideas where promising links can be made!

ECO-S-02

### Ecological divergence and context-dependent reproductive decisions along a salinity gradient

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Many animal parents put a tremendous amount of effort not only in gamete production but also into the well-being of their offspring. However, reproductive decisions are often shaped by underlying trade-offs and depending on the environmental context, parental effort may vary. Especially building and maintaining nests and the intensity and duration of paternal care can vary greatly depending the environmental context. Thus, many parents at the same time as caring regularly consume some or even all of their offspring. This behaviour is known as filial cannibalism and is particularly common in fish exhibiting paternal care. While eating one’s own young might seem odd at first sight, it is generally assumed to be an adaptive strategy maximising the cannibal’s lifetime reproductive success. In a combination of field studies at several sites across the Baltic Sea along a steep salinity gradient and controlled laboratory experiments, we investigated variation in nest availability and male’s reproductive prospects and tactics in the common goby (*Pomatoschistus microps*) and manipulated developmental stage, infection history and paternity of eggs in individual males’ nests. While males made no distinction between own and foreign eggs, they preferentially consumed many more infected than healthy eggs, a situation more prevalent under low salinity conditions. On the other hand, males originating from low salinity sites also suffered from a shortage of nesting resources and hence prospects for mating. Nevertheless, those males invested much more in accessory glands that may serve as an antimicrobial aid during nest preparation. We discuss insights and implications on spatial dynamics of sexual selection interacting with the natural ecological context in relation to paternal care and alternative reproductive tactics and its implications for population divergence.

ECO-O-01

**Aphid feeding can increase nutritional value of the phloem**

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The aphid species *Macrosiphoniella tanacetaria* and *Uroleucon tanaceti* are specialists for their host plant *Tanacetum vulgare*. In the field, *M. tanacetaria* is mainly found on the upper plant stems, whereas *U. tanaceti* is found on old leaves. In addition, feeding of *U. tanaceti* leads to leaf senescence which may be mirrored in changes of the phloem sap composition. To test whether the performance of aphids differs when feeding on different plant parts and whether aphid feeding can affect phloem chemistry, we fixed aphids to stems close to the inflorescences, young and old leaves, respectively, and collected and analysed phloem exudates of these plant parts. Aphids of *M. tanacetaria* survived equally well on all plant parts and produced most offspring on stems, whereas *U. tanaceti* showed the highest survival and reproduction on old leaves. Thus, *M. tanacetaria* appears to realise a broader niche than *U. tanaceti*. The phloem exudates differed in the composition of sugars, organic acids and amino acids between plant parts. In control plants, stem exudates had high amino acid concentrations and low sucrose to amino acid ratios, which are thought to improve aphid performance and might explain the high reproduction of *M. tanacetaria* on the stems. However, aphid feeding led to changes in the phloem chemistry, which were specific with regard to the aphid species, plant part and metabolite group. In summary, we show that aphid species are able to increase the nutritional value of the plant tissue, potentially matching or improving their niches on the plants.

ECO-O-02

**Understanding honey bee pathogen dynamics through high-throughput qPCR analysis**

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Honey bees are under increased pressure from the intensified agriculture and the introduced parasitic mite *Varroa destructor*, resulting in more frequent colony losses mediated by a number of viral, bacterial and eukaryotic pathogens. Colonies normally suffer from multiple infections before their final decline, yet little is known about the dynamics of inapparent infections.

We hypothesize that many infections are multifactorial, synergistic processes and that co-occurrence of some pathogens may be predictive markers for colony decline. Testing this hypothesis requires quantitative measurements of all relevant pathogens over extended time periods in many colonies. Some of these will eventually develop diseases, and pathogen dynamics before the outbreaks can be analyzed for synergistic interactions. To date, simultaneous quantitative analysis of many pathogenic organisms has been expensive and time consuming, and was therefore rarely applied.

We deploy high-throughput qPCR analysis to quantify honey bee pathogens, intestinal bacteria and the expression of selected immune and control genes in a large number of samples. Forty-eight qPCR assays were newly developed or adapted from published studies, and are evaluated with reference material. In a pilot study we survey twenty-four colonies in six apiaries kept under different operational modes, with a monthly sampling scheme during the warm season. Single forager bees are analyzed to assess pathogen abundance on individual and colony level. As first results, bees from healthy colonies show absence or low titers of pathogens whereas colonies e.g. diseased with dysentery showed high titers of viral and bacterial pathogens and intestinal parasites. By this approach we will gain substantially new insights into the complex pathogen dynamics and interactions within honey bees. The developed method may serve as valuable approach for future research projects.

ECO-O-03

**Factors affecting dispersal propensity and flight performance in a butterfly:  
When willingness and ability do not equate**

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Dispersal, defined as any movements potentially leading to gene flow, is a complex process comprising an important aspect of a species' capacity to respond to global change phenomena such as rising temperatures, habitat loss and fragmentation. However, the multi-causality of dispersal makes it difficult to capture all relevant factors. We therefore employed a multifaceted approach here to disentangle the relative importance of morphology, physiology, behaviour, and environment on movements in the temperate-zone butterfly *Lycaena tityrus*. To this end, we used an experimental platform dedicated to study dispersal, the Metatron, to observe dispersal propensity in two-patch metapopulations under different environmental conditions. Subsequently, individuals were subjected to a flight performance test and several morphological and physiological measures. We could demonstrate that sexes differed substantially in morphological traits arguably related to flight performance (e.g. wing loading, thorax-abdomen ratio), and that males showed a better flight performance than females. Nevertheless, the above traits did not influence dispersal propensity, which was higher in females than in males. Additionally, environmental conditions affected condition, flight performance, and dispersal propensity. Poor habitat quality such as shade and a lack of resources increased dispersal propensity. In summary, our results suggest that dispersal is not random in *L. tityrus*, but an active process triggered by habitat quality and internal motivation. However, traits indicative of flight performance were only marginally associated with increased dispersal propensity. Our results may have important implications for trying to forecast future species distributions, as deteriorating habitat conditions are likely to increase dispersal.

ECO-O-04

**Food habits of Galapagos Owls: a preliminary study**

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There are two species of owls in the Galapagos, *Tyto alba punctatissima* (Barn Owl) and *Asio flammeus galapagoensis* (Short-eared Owl). The Barn Owl occurs on the largest islands, whereas Short-eared Owl is present in all major islands. Information about the behavioral ecology of both owl species has received little attention recently. The last study on diet was done more than 30 years ago. Since then much has changed on the Galapagos Islands, mainly on the most populated island, Santa Cruz, but also on different islands like Isabela and Santa Fe. Thus, the question arises, whether the owls have adapted their diet to the changed environment. This study aims at providing more information about actual owl food habits in the Galapagos assessing diet by pellets analysis. During March 2016 and 2017 we collected pellets that owls had cast on roost and breeding sites, mainly from Santa Cruz Island. A few further pellets were also obtained from other islands, specifically Isabela and Santa Fe Islands. In this way we have several hundred pellets for analysis, mainly from the Barn Owl.

The analysis of the pellets showed that barn Owls prey largely on rodents (93%), insects (7%). We very rarely (3 of 580 pellets) found bird bones in Barn-Owl pellets. By contrast, the few pellets (n= 45) from Short-eared Owls showed that these birds feed more on birds (56%), but also on rodents (44%). These data are similar to the results reported earlier, indicating that diet of the owls has not changed in the last 30 years. Interestingly, about a quarter of the Barn Owl pellets containing not only rodent remains but also insect remains. This observation shows that owls combine mammals and insects as diet. In the future, we plan to carry out a more detailed analysis breaking down our sample into different categories (time of the year, location). We also plan to collect data on food availability in order to be able to assess how the owls use the prey available in the hunting areas.

ECO-O-05

**pCO<sub>2</sub> dependent effects on freshwater zooplankton**

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Fossil fuel combustion results in rising atmospheric carbon dioxide. Since the industrialization era, atmospheric levels of CO<sub>2</sub> have already increased by 40%. If unstopped this is expected to double by the end of the century. At present 50% of the atmospheric CO<sub>2</sub> is taken up by the oceans changing their hydrogeochemistry resulting in ocean acidification. Together with increased water temperatures, this has detrimental effects on marine ecosystems. Not only ocean ecosystems are prone to acidification, also freshwater ecosystems are suggested to be affected. However, up to now surprisingly little is known about the potential consequences of elevated atmospheric pCO<sub>2</sub> on freshwater ecosystems and studies on pCO<sub>2</sub> effects on freshwater species are scarce. Latest discussions suggest that the rapid increase of atmospheric CO<sub>2</sub> impact pCO<sub>2</sub> levels of freshwaters. This is expected to affect freshwater biota and cause shifts in phytoplankton species composition. However, an effect of pCO<sub>2</sub> dependent acidification on zooplankton species remained undetermined. We tested this using the keystone freshwater crustacean *Daphnia* that forms the trophic link between primary producers and higher trophic levels. We continuously exposed *Daphnia* to elevated levels of pCO<sub>2</sub> in a flow-through system and analysed their responses. This allowed the documentation of the pCO<sub>2</sub> effect on *Daphnia pulex* over three successive generations. We conclude, that increased levels of pCO<sub>2</sub> can have strong effects on this keystone species making it more prone to environmental challenges and reducing fertility. This may have cascading effects for freshwater ecosystems and their biodiversity.

ECO-O-06

**Beating the competition: Filter-feeding isopods conquer a habitat devoid of life on the underside of the Antarctic shelf ice**Christoph Held<sup>1</sup>; Dominik Nachtsheim<sup>2</sup>; Nils Owsianowski<sup>1</sup>; Claudio Richter<sup>1</sup>; Richard Steinmetz<sup>1</sup>; Horst Bornemann<sup>1</sup>

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The colonization of a new habitat affords an important advantage to the successful pioneer species because competitors, predators and parasites are likely to be out of step. Here, we report the first retrieval and molecular characterization of a cryo-benthic community of isopod crustaceans that live at depths of 80-150m on the underside of a floating shelf-ice tongue at the Drescher Inlet (Riser-Larsen Ice Shelf), Eastern Weddell Sea. The specimens were retrieved with a sampler mounted on a remotely operated vehicle (ROV) when video transects were carried out.

The molecular analysis of mitochondrial and nuclear genes of four specimens spanning the size range of individuals collected confirmed that (1) all belonged to a single species and that (2) this species has previously been identified in benthic communities in the Eastern Weddell Sea as *Antarcturus* cf. *spinacoronatus*. The molecular phylogeny shows that the cryo-benthic *A.* cf. *spinacoronatus* are deeply nested in a family of isopods characterized by increasing complexity of morphological and behavioural adaptations to the acquisition of detrital and planktonic food particles. This demonstrates that the floating shelf-ice was likely colonized from the seafloor and not vice versa and that the filter-feeding life style of *A.* cf. *spinacoronatus* formed a predisposition playing a key role in the colonization of the new habitat.

Density estimates of *A.* *spinacoronatus* under the floating shelf ice (25 adults and 190 juveniles per square meter) are significantly higher than on the seafloor, suggesting that the transition to the new habitat devoid of any macrofaunal competition or predation provides a major advantage to the species and thus may be a geographically more widespread phenomenon.

ECO-O-07

**Holistic defense - morphological and chemical traits combined in the ptychoid oribatid mite *Euphthiracarus reticulatus***

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Decomposing oribatid mites are among the primordial faunal elements and potential prey organisms in terrestrial food-webs. Thus, they have a long-lasting evolutionary defensive history. Many species evolved “holistic” defensive strategies by combining several morphological and chemical traits. We show the morphological and chemical base of predator defense in the ptychoid mite *Euphthiracarus reticulatus*. Functional morphology and biomechanics of ptychoidy were investigated based on SR- $\mu$ CT and high-speed life-radiography data. Oil-gland secretions were collected from 20,000 field-sampled adult mite specimens. The secretions comprised two components: the diterpene  $\beta$ -springene and a novel compound with a mass of 276 g/mol to which we assign the trivial name  $\delta$ -acaridial. Adaptive values of morphological and chemical defenses were tested in bioassays on mite specimens with and without defensive secretions against three predators: a similar-sized gamasid mite (0.8 mm, with slender, piercing chelicera), and two larger staphylinid beetles (*Stenus junco*, 7 mm, with sickle-shaped mandibles) and *Othius punctulatus* (14 mm, with basal biting mandibles). Upon predator attacks by *S. junco*, *E. reticulatus* reacted quickly: within 150ms from the first contact the encapsulation was almost completed – less time than the beetle needed to retract the labium to the mandibles. Chemically defended specimens of *E. reticulatus* effectively repelled all predators. After depletion of oil-gland reservoirs, however, *O. punctulatus* easily cracked the cuticle and fed on the mites while *S. junco* and *S. junco* were not able to overcome the morphological barrier of the strong cuticle and ptychoid body form. Hence, we conclude that, being faced to a high diversity of predator types in soil, a costly holistic defensive strategy including effective morphological and chemical traits enables life in an almost “enemy-free space”.

ECO-O-08

**A geographic mosaic of coevolution between mites and burying beetles**

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Most classic examples of coevolution are obligate symbioses with strong fitness effects. With the association of burying beetles and mites of the *Poecilochirus carabi* species complex, we studied a rather loose species interaction that appears to be heavily affected by abiotic ecological parameters. Both symbionts reproduce on vertebrate carcasses. Previous studies paint no clear picture of the nature of the interaction: Suggested fitness effects range from mutualistic to antagonistic, potentially depending on the environment. In multiple controlled laboratory experiments, we found a consistent antagonistic fitness interaction, which lead to a symbiont-species-specific specialisation by both mites and beetles. Mite development time exemplifies the specialisation. The trait varies genetically between populations and is adapted to both the host beetle brood care and the abiotic environment, with countergradient adaptation to temperature. In an artificial selection experiment, we show that there is enough standing genetic variation to allow for rapid adaptation, e.g. when beetles migrate to novel habitats or mites switch host species. We find intraspecific variation among populations in both symbionts to affect fitness outcomes of the interaction, conforming to a geographic mosaic of coevolution, with some populations being locally adapted to their symbionts, and varying effects of the abiotic environment. We are currently taking the mite-beetle system back to the field to get a better grip on further ecological variables involved in the interaction.

ECO-P-01

**Mucus – “How flatworms affect nematode prey fitness”**

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By constructing physical structures or modifying pre-existent habitat structure, organisms can affect biogeochemical gradients in a way that becomes beneficial for their own ecological success and also that of other species. Previous studies showed that, through excretion of sticky mucus, freshwater triclad flatworms can maintain the local availability of their prey by increasing the quantity of sediment getting trapped on the leaf surface. But the effects of mucus itself were not specifically examined. Therefore we exposed bacterivorous nematodes with short (*Caenorhabditis elegans*) and long (*Plectus acuminatus*) life cycles to flatworm (*Polycelis tenuis*) mucus. Growth, reproductive output, and the feeding preferences of nematodes were determined in different contexts. Additionally, the importance of mucus on intraspecific flatworm interactions was analyzed. The results suggested that mucus played a minor role in flatworm interplay, but had a major impact on prey fitness. Primary effects of mucus exposure resulted in reduced length and reproductive output for *C. elegans*, but secondary effects due to an introduction of protozoans and bacteria outperformed these. An introduced protozoan (*Tetrahymena pyriformis*) negatively affected reproductive output in both nematode species and length of *C. elegans*, while especially the fitness of *P. acuminatus* benefitted from bacteria growing on mucus. In summary, ecological engineering effects through excretion of mucus had an impact on prey fitness, although this mechanism was primarily mediated by an effect on non-prey microbes.

ECO-P-02

**Perspectives of coherent anti-Stokes Raman scattering microscopy (CARS) for assessing fatty acid content as an additional fitness trait of microscopic biological samples**

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Measuring fatty acid (FA) content of micro-invertebrates using mass spectrometry is challenging because of the need to accumulate signal from many individuals to detect a relevant signal. This chiefly precludes species-specific or intra-cellular investigations of FA distribution. Therefore, we applied the individual-based and label-free coherent anti-Stokes Raman scattering microscopy (CARS).

Raman scattering is based on inelastic scattering of light by molecular bonds with characteristic vibrational energies. By collecting all photons which are spontaneously scattered by molecular bonds in a sample, a spectrum of the distribution of bonds, i.e. its chemical composition, can be assessed. In rare cases, by receiving energy from a molecular bond in an excited vibrational state, the scattered photon is blue-shifted (anti-Stokes Raman scattering). This process can be amplified by coherently exciting and detecting all photons in a process called coherent anti-Stokes Raman scattering, which also enables imaging the distribution of these molecular bonds. CARS can detect the 2845 cm<sup>-1</sup> CH<sub>2</sub> vibration in aliphatic chains, which functions as a general FA biomarker and provides a detailed 3D picture of FA distribution in microscopic samples. CARS is non-destructive, chemically selective and sample preparations and optical measures are quick and relatively inexpensive.

Here we applied CARS microscopy to visualize and quantify stress induced changes of FA distribution in free-living nematodes like *Caenorhabditis elegans* and to use the detected amount of lipid stores as an additional fitness trait. Significant fat storage was only found for adult nematodes, and exposure to copper at EC20 reduced the number and size of FA droplets. CARS microscopy has the potential to reveal patterns of lipid metabolism without labelling in microscopic organisms at an unprecedented resolution.

ECO-P-03

### Molecular identification of nematodes across Germany with the ribosomal D3-D5 region

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Molecular barcoding aims at the identification of an (unknown) individual via a known short characteristic DNA segment (the so called barcode). In order to identify an individual to a high resolution and precision, a detailed, reliable, and accurate database has to be the fundament. Several projects aim to collect as many species as possible for curating biodiversity of this plant. As a part of the German Barcode Of Life (GBOL) project, nematodes were sampled at 150 locations across Germany from terrestrial and limnic habitats. The nematodes were taxonomically identified to species level via light microscopy and the ribosomal D3-D5 region (around 500 bp) as a part of the Large Ribosomal Subunit (LSU) was amplified for almost 600 nematodes belonging to 79 species. For most species in this study one distinct barcode was found, while some morpho-species exhibited more than one barcode. The intra-specific variability ranged from 0.09% to 7.9%. For a few closely related species identical barcodes were detected, concluding that for those species the resolution of the applied marker was not adequate. The barcodes were delivered to the BOLD (Barcode of Life) database and will help to shed light into the diversity of German nematode species.

ECO-P-04

### Mate recognition in *Muscidifurax raptorellus*

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Mate recognition is a key factor for the perpetuation of premating isolation. Species and sex specific cues and signals can be perceived via different sensory modalities (e.g. visually, acoustically, olfactorily). In insects, chemical information plays a dominant role in mate recognition. Usually, the male will initiate courtship behaviour after recognizing a potential mate, which is then followed by either acceptance or refusal to mate by the other individual. We studied mate recognition in the parasitoid wasp *Muscidifurax raptorellus* (Hymenoptera, Pteromalidae). In this species, courtship behaviour consists of wing fanning (high frequency wing beats while standing or walking), and, once the male has positioned himself on the female, stereotypical antennal movements followed by initiation of copulation itself. We investigated the chemical signals involved in mate recognition by evaluating the reaction of male *M. raptorellus* towards dummies treated with whole body extracts or extract fractions of conspecific males and females. Our results indicate that visual stimuli are important in addition to chemical ones. Also, despite species and sex specific cuticular hydrocarbon profiles, these compounds alone are not sufficient for mate recognition.

ECO-P-05

### Transcriptional responses to short-term versus long-term host plant adaptation and parasite load in an oligophagous beetle

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Oligophagous insects must adjust their enzymatic machinery when feeding on different host plant species. Adaptations should occur quite rapidly if a new host is approached, but may differ from long-term physiological adaptations to hosts that are experienced for many generations. We used an experimental evolutionary approach to study effects of long-term experience versus short-term plastic responses to different host plant species, *Brassica rapa*, *Nasturtium officinale* or *Sinapis alba* (Brassicaceae), in the oligophagous mustard leaf beetle *Phaedon cochleariae* (Coleoptera: Chrysomelidae). After 26 generations of exclusive feeding on one of the three host plant species, larvae of the next generation were kept on these plants or transferred to one of the other host plant species for ten days. Performing microarrays, global transcriptional signatures were investigated. In dependence of the long- versus short-term host plant experience, up to 16 % of all 25,227 putative genes were differentially expressed in comparison to the control line permanently kept on *B. rapa*. In particular, genes related to metabolism, digestion and general cellular processes were affected. Thus, transcriptional plasticity in these genes plays a key role in long- and short-term responses of herbivores to adjust to changing host plant conditions. Interestingly, all lines were infected by a gregarine parasite. The drastically differing gene expression regulation found in the larvae in relation to the gregarine infection presents a new layer of complexity in ecological studies of plant-insect interactions.

ECO-P-06

### Comparing skin microbiomes of wild and captive zebra finches

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An animals' skin is densely populated with bacteria and although investigations in this field are emerging, we are still lacking information on the composition, ecology and the influencing factors of these microbiotas.

Here we investigate whether the animals' environment, social interactions or the genotype represent the most influential factor. We therefore collected skin microbe samples from three different populations of zebra finches: A wild population from Australia and representatives from two populations of captive zebra finches in Germany. The captive birds were sampled before and after one population was introduced to the other captive population. To characterise the skin microbes and compare the bacterial composition, we used 16S rRNA gene sequencing.

As our study birds are all zebra finches, we expect the microbiomes of the populations to not differ significantly from another, if the skin microbiome is shaped primarily by the animals' genotype. If the environment plays a major role in shaping the skin microbial community, we anticipate a rather different microbiome in the three populations and wild zebra finches to be the most divergent. Furthermore, we expect members of the two captive populations to become more similar after they were housed together for two weeks.

ECO-P-07

### Thermoregulatory behaviour and high thermal preference buffer impact of climate change in a Namib Desert lizard

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Knowledge of the thermal ecology of a species can improve model predictions for temperature induced population collapse, which in the light of climate change is increasingly important for species with limited distributions. We use a multi-faceted approach to quantify and integrate thermal ecology, thermal habitat properties, and past and present distribution of the xeric-adapted

Namibian lizard *Pedioplanis husabensis* (Sauria: Lacertidae) to model its local extinction risk under future climate change. We asked whether climatic conditions in various regions of its range are so extreme that local extirpations of *P. husabensis* have already occurred, or whether this

endemic species is adapted to the extreme conditions and uses behaviour to mitigate environmental challenges. We collected thermoregulation and climate data on a micro-scale and combined it with micro- and macroclimate data across the species' range to model extinction risk. We found that *P. husabensis* has high thermal preferences. In cooler parts of its range individuals are capable of departing thermally favourable conditions unused during the day. Furthermore, during summer individuals regulate at body temperatures below its high thermal preference to avoid body temperature excursions near the critical thermal maximum (CT<sub>max</sub>). This resilience in the face of high environmental temperatures is supported by persistence of populations at the hottest localities within its geographic distribution. We found no evidence of range shifts since the 1970s despite a documented increase in air temperatures. Nevertheless, *P. husabensis* has a

small safety margin between the upper limit of its thermal preference and its CT<sub>max</sub>. Hence, we conclude that his species is projected to undergo range reductions under even the most moderate climate change scenarios.

ECO-P-08

### Mass, phylogeny and temperature are sufficient to explain differences in metabolic scaling across mammalian orders?

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Whether basal metabolic rate-body mass scaling relationships have a single exponent is highly discussed, and also the correct statistical model to establish relationships. Here, we aimed at 1) to identify statistically best scaling models for 17 mammalian orders, Marsupialia, Eutheria and all mammals, and 2) thereby to proof whether correcting for differences in species' body temperature and their shared evolutionary history improves models and their biological interpretability.

We used the large dataset from Sieg et al. (2009) providing species' body mass (BM), basal metabolic rate (BMR) and body temperature (T). We applied different statistical approaches to identify the best scaling model for each taxon: ordinary least squares regression analysis (OLS) and phylogenetically informed analysis (PGLS), both without and with controlling for T. Under each approach, we tested linear equations (log-log-transformed data) estimating scaling exponents and normalisation constants, and such with a variable normalisation constant and a fixed exponent of either  $\frac{2}{3}$  or  $\frac{3}{4}$ , and also a curvature. Only under temperature correction, an additional variable coefficient modelled the influence of T on BMR.

Except for Pholidata and Carnivora, in all taxa studied linear models were clearly supported over a curvature by AICc. They indicated no single exponent at the level of orders or at higher taxonomic levels. The majority of all best models corrected for phylogeny, whereas only halve of them included T. When correcting for T the mathematically expected correlation between the exponent (b) and the normalisation constant (a) in the standard scaling model  $y=a \times b$  was removed, but the normalisation constant and temperature coefficient still correlated strongly. In six taxa, T and BM correlated positively or negatively. All this hampers a disentangling of the effect of BM, T and other factors on BMR, and an interpretation of linear BMR-BM scaling relationships in the mammalian taxa studied.

ECO-P-09

**Gone with the wind: The passive dispersal of nematodes**

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The ability of dispersal is a crucial factor for organism's distribution, abundances and thus, for their community structure at different sites. While larger animals can cover distances on their own, small organisms (<2 mm) are passively dispersed. Common vectors for a passive dispersal are the transport by larger organisms (e.g., flying insects, birds or mammals) or by wind.

In general, it is assumed that mainly propagules which can survive unfavorable environmental conditions are blown away from dry surfaces. This trait qualifies wind drifted organisms as typical pioneers in new habitats. However, the number of individuals contained in the air decrease with increasing distance to source habitats.

Interestingly, there are only few investigations which mentions nematodes as components of the aerial plankton. Because nematodes are the most abundant metazoans in aquatic as well as in terrestrial systems and can colonize new habitats within days, it is very likely that they are blown with the wind.

In the framework of a one-year field experiment we documented the wind dispersal of nematodes, focusing the following questions: (i) Is there a long-range transport of different nematode species by wind? (ii) Are propagules or living individuals transported by wind? (iii) Is there a continuous dispersal of nematodes during the year? (iv) What are the decisive factors for the dispersal (environment and meteorological parameters)? For this purpose, we installed experimental vessels filled with formaldehyde (to examine the dispersal rate of nematodes) and with water (to examine their colonization) in a natural surrounding and on the roof of the Bielefeld University (eleventh floor). We collected up to 195 nematodes m<sup>-2</sup> in 14 days, belonging to 29 species. Our results clearly reveal, that only living nematodes are dispersed by wind, especially in natural environments during winter and early spring.

ECO-P-10

**Sublethal insecticide exposure affects the chemical phenotype and fitness of a leaf beetle**

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Agriculturally used areas and with this the use of pesticides are steadily increasing. Thereby, insecticides can accumulate in ecosystems and pose a risk also to non-target organisms when present in sublethal concentrations. We investigated the impacts of a sublethal pyrethroid exposure on cuticular hydrocarbon (CHC) profiles and reproductive traits of a leaf beetle (*Phaedon cochleariae*). Besides, we examined transgenerational effects of a parental insecticide exposure on growth and antennae symmetry of the unexposed offspring. Our results demonstrate that an insecticide exposure, even at doses 20 times lower than the LC<sub>50</sub>, altered the chemical phenotype (CHC profile) of adults, with distinct effects on males and females. The egg number produced by the adults and the hatching rate were decreased due to the insecticide exposure. Moreover, the development and antennae symmetry of the unexposed offspring were negatively influenced by the sublethal insecticide treatment of their parents, revealing transgenerational effects. The insecticide impacts on the CHC profiles of the parental generation may have been caused by alterations of CHC precursors, which possibly were induced by insecticide application on the insect's diet. A changed CHC pattern likely has implications for intra- as well as interspecific communication and thus, e.g., for mate choice or interactions with other arthropod species. The observed detrimental transgenerational impacts may be explainable by a reduced investment in the offspring, maternal transfer or epigenetic processes. An asymmetry of the antennae might lead to an impaired reception of chemical signals. Overall, the results reveal that, besides negative (transgenerational) impacts on fitness-related traits, an insecticide usage can alter the chemical communication between individuals, with effects on the sender (i.e., the chemical phenotype) and the receiver (i.e., caused by asymmetry of antennae).

ECO-P-11

**Patterns and dynamics of neutral lipid fatty acids in Formicidae – implications to study ant ecology**

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Trophic interactions are a fundamental aspect of ecosystem functioning, but often difficult to observe directly. Several indirect techniques were developed to assess these interactions, such as fatty acid analysis. Fatty acid profiles can indicate intra- and interspecific differences in diets, while biomarkers can point out specific interactions between organisms. Ants are among the most important terrestrial invertebrates, but little is known about their lipid metabolism, and no study so far used fatty acids to study their trophic ecology. We set up an 8-week feeding experiment to elucidate patterns and dynamics of neutral lipid fatty acids (NLFAs) assimilation in *Formica fusca* and *Myrmica rubra*. We asked whether dietary NLFAs are assimilated through direct trophic transfer, how diet influences NLFA profiles over time, and whether these processes are similar across species and life stages (larva/adult). Ants fed with a high-fat food quickly accumulated specific dietary NLFAs (C18:2n6, C18:3n3 and C18:3n6), compared to ants fed with a low-fat food. Diet did not affect amounts of total body fat or NLFAs extensively biosynthesized by animals (C16:0, C18:0, C18:1n9). NLFA profiles reflected dietary differences, which became more pronounced over time. Dynamics of specific dietary NLFAs was similar regardless of species or life stage, but these factors affected dynamics of profiles, other NLFAs and total body fat. We showed that ants accumulated dietary NLFAs via direct trophic transfer, and some dietary NLFAs are potential biomarkers. Ants were able to synthesize high amounts of NLFAs from a sugar-based, low-fat diet, but dietary composition had a stronger effect on metabolic dynamics and profiles of NLFAs. Therefore, fatty acids can be a useful tool to study trophic ecology of ants, but several factors should be taken into account in an ecological context, such as reproduction and life stage.

EVO-S-01

**genomics of ecological speciation across the Swiss Alpine whitefish radiation**

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Recent advancements in sequencing technology allow us to start addressing long-standing evolutionary questions on the genomic architecture underlying adaptation and speciation even in non-model organisms. The adaptive radiation of Swiss Alpine whitefish is a fantastic system that permits us to assess genomic divergence along various continua of geographic, genetic, and ecological differentiation. A systematic re-evaluation of its rich endemic species diversity, which is well depicted by ecological, morphological, and phylogeographic data, revealed loss of multiple species and of adaptive genetic differentiation between remaining species. I will present first genome-wide polymorphism data on whitefish from the neighbouring lakes Walen and Zurich, showing pronounced repeated genomic differentiation when comparing sympatric species distinct to allopatric populations comparisons. Repeated outlier loci suggestive for being shaped by selection are found to be not clustered but widely spread across the genome. Further, I will outline our effort to build comprehensive genomic resources to further aid our understanding of adaptive divergence in this system. Yet, genomic approaches in whitefish are challenged by a large and complex genome resulting from a recent whole genome duplication in the ancestors of trout-like fish (salmonidae). However, taking up this challenge will provide a powerful genomic perspective on a fascinating adaptive radiation.

EVO-S-02

**From conceptual to mechanistic analyses: Eco-evo-devo of social insect plasticity**

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Using the ant species *Cardiocondyla obscurior*, a versatile emerging model, we study the proximate factors involved with the expression of continuous (passive) and discontinuous (anticipatory) plasticity. At a basic level –taking advantage of its suitability for laboratory-based research- we aim to understand how pathways pertaining to sex differentiation and cell signaling are involved in producing discrete adult morphologies, and how the evolution of novel traits and kin selection feeds back into the evolution of the species. I am further interested in how genetic novelty via transposable elements, horizontal gene transfer and the bacterial symbiont *Candidatus Westeberhardia* affects development and enables adaptation to novel environments of this invasive species. I will show that this ant with two female castes (specialized for reproduction and helping) and two male morphs (specialized for outbreeding and inbreeding) with dramatically different life history strategies makes a good model to look beyond the fascinating world of social complexity alone.

EVO-O-01

### Heterotic effects of a sex-chromosome inversion on sperm characteristics and siring success in zebra finches

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Polymorphic inversions constitute an evolutionary puzzle because they often have negative effects on embryo viability in heterozygous carriers. Zebra finches (*Taeniopygia guttata*) are polymorphic for a large inversion on the sex chromosome Z that we have shown to slightly decrease embryo viability sired by heterozygous males. Despite this, the inverted haplotype has spread in wild Australian zebra finches to an allele frequency of around 40%. Using data on two captive populations of zebra finches, we show that this inversion has strong and robust heterotic effects on several sperm characteristics. Males that are heterozygous for the inversion have the sperm design that leads to the highest sperm velocity, resulting in the highest male fertility and the highest within-pair and extra-pair siring success. However, males which are homozygous for the derived allele show detrimental sperm characteristics and hence the lowest siring success, suggesting the mechanism by which this inversion polymorphism is maintained in the population at an intermediate allele frequency. The described genetic effect on sperm design is remarkable in terms of its effect size and it further explains how substantial genetic variation in sperm design can be maintained despite ongoing directional selection.

EVO-O-02

### Environmental versus genetic sources of variation in avian sperm dimensions – estimates from a natural songbird population

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Spermatozoa are the morphologically most diverse type of animal cells and show remarkable interspecific but also intraspecific variation in size and form. In birds, variation between species has recently received substantial attention, but causes and consequences of intraspecific variation in avian sperm traits remain poorly understood. Separating genetic from environmental sources of phenotypic variation is an important step for a better understanding of avian sperm trait diversity. Up to date, however, this has only been conducted under controlled laboratory conditions although trait heritabilities determining evolutionary trajectories in wild populations may be environment-dependent. Here we applied quantitative genetic methods to a pedigreed multigenerational data set of the Collared Flycatcher *Ficedula albicollis*, a long-distant migrant passerine bird with high levels of extra-pair paternity and, for the first time, separate environmental from genetic sources of phenotypic variation in sperm dimensions in a natural bird population. We found strong evidence for individual phenotypic plasticity in sperm size in response to the progressing breeding season and a significant heritability of sperm length, although substantially lower compared to estimates from laboratory populations. We discuss potential explanations for this discrepancy and its consequences for the evolution of avian sperm traits in the wild as well as potential adaptive versus non-adaptive explanations for seasonal sperm trait plasticity.

EVO-O-03

**Does inbreeding increase or decrease cooperative care?**David Wells<sup>1</sup>; Hazel Nichols<sup>2</sup>; Joseph Hoffman<sup>1</sup>1 Universität Bielefeld; 2 Liverpool John Moores University  
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Relatedness between group members can explain cooperative breeding where members of a social group provide care for the offspring of other members. Therefore, processes which increase relatedness can be important for the evolution of sociality for example monogamy has been implicated in the evolution of cooperation in invertebrates and vertebrates. In a similar fashion, inbreeding increases relatedness between individuals and is predicted to increase cooperation. However, empirical tests of this hypothesis are rare. Alternatively, inbred individuals may contribute less to cooperative care because inbreeding depression means they are less able to secure resources. As such is it unclear whether inbreeding encourages or impedes the evolution and maintenance of cooperative breeding.

The banded mongoose is a cooperative breeder and an ideal species in which to test this hypothesis because their social structure causes regular inbreeding. In contrast, species which inbreed as a result of recent population reduction are unlikely to have evolved in response to the selection pressures of inbreeding. Using over 15 years of observational data and a seven generation pedigree of a wild banded mongoose population we show that, as expected, inbred individuals are more related to their social group. In addition we investigate whether vary the amount of alloparental care they provide with their own inbreeding coefficient.

We find no evidence that inbred individuals are more likely to provide care or provide more care than outbred individuals. Instead, we find that inbred males are less likely to provide alloparental care and may provide less care. Therefore, it seems that the frequent inbreeding observed in this species does not contribute to the maintenance of their cooperative breeding system and may in fact reduce the benefits of group living.

EVO-O-04

**Does defense, not food, drive specialized associations between insects and plants?**Georg Petschenka<sup>1</sup>; Alice Exnerova<sup>2</sup>; Jürgen Deckert<sup>3</sup>; Rayko Halitschke<sup>4</sup>

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Competition for dietary resources is widely assumed to select for specialized interactions between insects and toxic host plants. In addition, if plant toxins are sequestered for defense, predators and parasitoids may also select for the use of toxic plant species. The milkweed bugs (Lygaeinae) likely radiated on cardiac glycoside-rich Apocynaceae, and both, resistance to cardiac glycosides and sequestration, are ancestral characters of this clade. Although milkweed bugs are associated with specific plants, many of them feed on a great variety of hosts. Given this feeding habit, it is unlikely that acquisition of dietary resources drove the use of particular toxic plant species. Here we studied three species of milkweed bugs specialized on cardiac glycoside producing plants outside of the Apocynaceae (Plantaginaceae, Ranunculaceae, and Asparagaceae) and found that they maintained sequestration of the toxins. We furthermore show that a fourth species is strictly associated with meadow saffron (*Colchicum autumnale*) and sequesters high amounts of the toxic alkaloid colchicine. Inclusion of these toxic plants into the generalist diets did not lead to better growth but sequestered toxins protected the bugs against predators. While preadaptation facilitated shifts to novel sources of cardiac glycosides, switching to a plant with non-related chemistry required evolution of a novel resistance trait. Our data suggest that the availability of toxins for sequestration, and not the acquisition of dietary resources, causes novel specialized insect-plant associations. We conclude that dietary generalists have specialized interactions selected for by the third trophic level which depend on the availability of toxins for sequestration and that these interactions depend on ancestral or novel resistance traits.

EVO-O-05

### Chemical Ecology and Pheromone Evolution in *Leptopilina*, a Parasitoid of *Drosophila*

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Information transfer in insects is mediated by a variety of sensory modalities, whereby the use of chemical compounds, i.e. pheromones, is a common phenomenon and intensely investigated. Nevertheless, the origin and evolution of olfactory communication remain often puzzling.

Recently, it was shown that females of the parasitic wasp *Leptopilina heterotoma* produce a defensive secretion consisting mainly of (–)-iridomyrmecin, which has evolved secondary functions as a chemical cue to avoid competition between females on host patches and as a major component of the female sex pheromone. This supports the so-called precursor hypothesis, which predicts that pheromones can evolve from already previously used non-communicative chemical compounds.

To reconstruct the evolution of pheromone communication in the genus *Leptopilina*, chemical, behavioral and ecological data of several *Leptopilina* species are compared in this study. All nine species of *Leptopilina* studied so far produce iridomyrmecin and other iridoid compounds. Our data show little variation in the use of the iridoid compounds for defence against predators and as chemical cue to avoid competition between female wasps on host patches. However, we find large differences between species in the composition of the female sex pheromone and the response of males towards the iridoid compounds. So far, *Leptopilina heterotoma* is the only species whose female sex pheromone consists solely of iridoid compounds. The sex pheromones of the other species consist either of a mixture of iridoid compounds and cuticular hydrocarbons (CHCs) or of CHCs only.

The phylogenetic relationship of the species correlates with the production of (–)-iridomyrmecin and its enantiomer (+)-iridomyrmecin, but the phylogeny fails to explain the strong divergence in the composition of the female sex pheromone in the genus. Therefore, other factors, like the mating system, might be relevant to understand the pheromone evolution in *Leptopilina*.

EVO-O-06

### The skin microbiomes of three different estrildid finch species reveal individual- and species- specific differences

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An animals' body is densely populated with bacteria. Although a large number of investigations on physiological microbial colonisation have emerged in recent years, our understanding of the composition, ecology and function of the microbiota remains incomplete.

Here, we investigated whether songbirds have an individual-specific skin microbiome that is similar across different body regions. We collected skin microbe samples from three different bird species (*Taeniopygia guttata*, *Lonchura striata domestica* and *Stagonopleura guttata*) at two body locations (neck region, preen gland area).

To characterise the skin microbes and compare the bacterial composition, we used high-throughput 16S rRNA amplicon sequencing. This method proved suitable for identifying the skin microbiome of birds, even though the bacterial load on the skin appeared to be relatively low. We found that across all species, the two evaluated skin areas of each individual harboured very similar microbial communities, indicative of an individual-specific skin microbiome. Despite experiencing the same environmental conditions and consuming the same diet, significant differences in the skin microbe composition were identified among the three species. The bird species differed both quantitatively and qualitatively regarding the observed bacterial taxa. Although each species harboured its own unique set of skin microbes, we identified a core skin microbiome among the studied species. As microbes are known to influence the host's body odour our findings of an individual-specific skin microbiome might suggest that the skin microbiome in birds is involved in the odour production and could encode information on the host's genotype.

EVO-O-07

**Sexual dimorphism of cuticular hydrocarbons in cuckoo wasps**Ruth Castillo<sup>1</sup>; Thomas Schmitt<sup>1</sup>; Oliver Niehuis<sup>2</sup>

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Sexual dimorphism is ubiquitous in the animal kingdom. Explaining the origin and evolution of widespread sex differences has been a common subject of study. Although few studies have shown that sexual dimorphism can arise due to natural selection on the female phenotype, its origin is commonly attributed to sexual selection on males, an idea that was strongly supported by Charles Darwin. Here, we show that natural selection has played an important role in the evolution of sexual dimorphism of chemical profiles of cuckoo wasps (Hymenoptera: Chrysididae). Cuticular hydrocarbons (CHC) are hydrophobic molecules in the outer layer of insect cuticles with a dual function: they are desiccation barriers and they play a role as signals in intra and interspecific communication. Using comparative phylogenetic analyses of CHC profiles of males and females of 56 species of cuckoo wasps, we explore the evolutionary changes that have originated chemical sexual dimorphism. Cuckoo wasps are solitary parasitoids and cleptoparasites of other solitary wasps and bees and represent a good example to study how natural selection has contributed to the origin of sexual dimorphism because several cuckoo wasps profit from chemical mimicry to remain undetected after oviposition into their host nests. According to our results, the mode by which CHC profiles evolved in cuckoo wasps differ strongly between both sexes, with males but not females exhibiting a strong correlation between chemical (Bray-Curtis dissimilarity of CHC profiles) and phylogenetic distances. Disparity through time plots and a comparison of the cuckoo wasps' phylochemospace suggest that females diverged significantly more than males and that this divergence was likely driven by natural selection on females for mimicking the CHC profiles of their hosts. We suggest that in cuckoo wasps, natural selection acting on females has played a more important role than sexual selection on males in generating sexual dimorphism.

EVO-O-08

**Elongases, key for cuticular hydrocarbon (CHC) diversity?**Victoria Moris<sup>1</sup>; Thomas Schmitt<sup>2</sup>; Oliver Niehuis<sup>1</sup>

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Elongases perform a key role in the biosynthesis of cuticular hydrocarbons (CHCs) by adding carbon atoms to fatty acyl-CoA chains. Since CHCs, acting as anti-desiccation agents for insects, are also exploited for intra- and inter-specific communication (e.g., as sex, territorial, pheromones, and for caste and species recognition), they likely play a role in speciation and contribute to the evolution of the extant insect diversity. To better understand how CHCs evolve, we need to identify the genes that are involved the biosynthesis of CHC. For this purpose, we exploited a CHC dimorphism that females of the spiny wasp, *Odynerus spinipes* (Insecta: Hymenoptera: Vespidae: Eumeninae) exhibit. Females with different CHC chemotype differ qualitatively in more than 70 CHCs, but do not seem to differ any other traits. Using differential gene expression analyses, we identified around 20 genes being differently expressed in females exhibiting different chemotypes and likely being involved in the biosynthesis of CHCs: desaturases, a fatty acyl synthase, a fatty acid binding protein, a fatty acyl-CoA reductase and elongases. Elongases seem to play a major role in the generation of the *Odynerus spinipes* CHC dimorphism: of the 21 elongases identified in an *O. spinipes* draft genome, nine differ in their expression between females exhibiting different chemotypes. Tracing the evolutionary history of elongases by analyzing transcriptoms of 166 species of Hymenoptera ([www.1KITE.org](http://www.1KITE.org)), we identified nine main clades of elongases in Hymenoptera, each of which included at least one elongase gene also present in the genome of *O. spinipes*. Intriguingly, all elongases differently expressed in *O. spinipes* females exhibiting different chemotypes belong to one of the above nine clades. We currently hypothesize that all elongases of this clade are involved in the biosynthesis of CHCs in Hymenoptera. To test this hypothesis, we are currently conducting RNAi experiments on various species of wasps.

EVO-O-09

**Exploring the power of 'genomic' quantitative genetics for understanding and predicting adaptation**Phillip Gienapp<sup>1</sup>; Frédéric Guillaume<sup>2</sup>; Katalin Csilléry<sup>3</sup>

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**E** Polygenic adaptation to environmental can be well understood and, to some extent, predicted by the traits' genetic (co)variances. Quantitative genetic analyses require information about relatedness among individuals to estimate these genetic (co)variances. This information can be obtained from breeding experiments or pedigrees, which, however, limits QG to certain taxa. Relatedness can also be estimated from molecular markers but early applications suffered from the limited numbers of available markers. Advancements in molecular genetic technology allow now cost-effective genotyping for hundreds to thousands of markers, in virtually any species. 'Genomic' quantitative genetics, based on relatedness estimates from high-density markers, is hence possible in theoretically any species and is also likely to give more accurate quantitative genetic estimates. Furthermore, it allows quantifying individual (inclusive) fitness by calculating an individuals' average relatedness to the population as fitness measure. We here demonstrate the applicability and usefulness of this approach using simulated and empirical data from a range of species. Consequently, 'genomic' quantitative genetics has the potential to substantially advance and widen our understanding of adaptation in natural populations.

EVO-O-10

**ddRAD sequencing resolves fine-scale population structure in a benthic invertebrate with implications for understanding phenotypic plasticity**

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**E** The field of molecular ecology is transitioning from the use of small panels of classical genetic markers such as microsatellites to much larger panels of SNPs generated by approaches like RAD sequencing. However, few empirical studies have directly compared the ability of these methods to resolve population structure. This could have implications for understanding phenotypic plasticity, as many previous studies of natural populations may have lacked the power to detect genetic differences, especially over micro-geographic scales. We therefore compared the ability of microsatellites and RAD sequencing to resolve fine-scale population structure in a commercially important benthic invertebrate by genotyping great scallops (*Pecten maximus*) from nine populations around Northern Ireland at 13 microsatellites and 10,539 SNPs. The shells were then subjected to morphometric and colour analysis in order to compare patterns of phenotypic and genetic variation. We found that RAD sequencing was superior at resolving population structure, yielding higher *F*<sub>st</sub> values and support for two distinct genetic clusters whereas only one cluster could be detected in a Bayesian analysis of the microsatellite dataset. Furthermore, appreciable phenotypic variation was observed in size-independent shell shape and colouration, including among localities that could not be distinguished from one another genetically, providing support for the notion that these traits are phenotypically plastic. Taken together, our results suggest that RAD sequencing is a powerful approach for studying both population structure and phenotypic plasticity in natural populations.

EVO-O-11

**Individual reproductive behaviour in a social context**

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Research on reproductive behaviour has predominantly focused on quantifying the fitness consequences of individual reproductive decisions. Recent scientific evidence indicates however that, to understand individual reproductive behavior, the reproductive decisions of other individuals in the social environment have to be taken into account. For the passerine bird the great tit (*Parus major*) it was shown that parents only paid survival costs of reproduction in social environments with a high competitive pressure. We investigated a potential mechanism to explain these effects: family size may negatively affect parental competitive ability and only under high competition this results in fitness costs of reproduction. Within a great tit population, we manipulated family size by reducing or enlarging broods, relative to a control group. Next, we measured parental competitive ability both in winter and in the following spring by experimentally increasing the level of competition for vital resources as winter food, winter roosting sites and breeding boxes. We found evidence that experimental family size negatively affected the probability of parents to win competitive interactions over food in winter and over high quality breeding boxes in spring. Such carry-over effects are important because they show that the selection pressures that shape individual reproductive behaviour depend on 1) the resource abundance and the level of competition an individual experiences later in life and 2) the reproductive investment of the competitors in the current breeding season.

EVO-O-12

**Measuring inbreeding in Antarctic fur seals**Emily Humble<sup>1</sup>; Jaume Forcada<sup>2</sup>; Joseph Hoffman<sup>1</sup>

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Inbreeding depression has been a major focus in ecology, evolution and conservation for decades. In an age where climate change and habitat destruction threaten to reduce the size of many natural populations, quantifying the extent and impact of inbreeding depression in the wild is of critical importance and yet has been hampered by the difficulty of precisely measuring individual inbreeding coefficients.

Antarctic fur seals (*Arctocephalus gazella*) provide an ideal opportunity to investigate the impacts of inbreeding in the wild. During the 1800s, fur seals were pushed to the edge of extinction due to years of persistent hunting for their pelts and consequently experienced a severe bottleneck. Despite this, when hunting ended, the species quickly recovered to reach numbers in the millions. However, environmental change has led to increased sea surface temperatures and reduced sea ice around the western Antarctic Peninsula. As a result, the quantity and quality of Antarctic krill, the seal's primary food supply, has declined. Over the last three decades, this has led to a reduction in pup birth weights, increased mortality of inbred pups, and consequently, the population is experiencing a severe decline yet again.

For many years, the gold standard for precisely measuring individual inbreeding was to use a multigenerational pedigree. However, recent simulation and empirical studies explicitly demonstrate how genomic inbreeding coefficients are even more precise than pedigree-derived measures. For the first time in a marine mammal we have used tens of thousands of genomic markers together with a reference genome to precisely measure individual inbreeding in multiple populations of Antarctic fur seals. I present evidence for inbreeding in our study population and consider the applications of my methods to other vulnerable species.

EVO-O-13

**A comparative genetic study on the demographic histories of Pinnipeds: The consequences of the big hunt for fur and blubber.**

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E

Large-scale commercial hunting in the 19th century brought many Pinniped species to the edge of extinction. Although most species recovered after immense conservation efforts and seal hunting bans, the genetic traces of severe reductions in population sizes are still visible. The exact extent of hunting can merely be guessed for most species based on a few and scattered historical reports. Although attempts have been made to estimate historical population sizes based on current genetic data, these approaches mostly have the disadvantage to rely on a single (and mostly unknown) mutation model for the underlying genetic marker. Here, we analysed current genetic data from 28 Pinniped species together with coalescent simulations in a bayesian framework to estimate the probabilities of past bottlenecks and the most likely lowest historical population sizes. We found a huge variation in current genetic variability across Pinnipeds, whereby more than a third of the species have likely undergone a dramatic reduction in population size. Furthermore, we determined the most likely microsatellite mutation model in Pinnipeds and explored the ecological factors which made some species more vulnerable towards hunting and a loss of genetic diversity than others. Our results have extensive implications for our understanding of the interplay of genetic variation, population size and ecological factors and hopefully lead to better conservation decisions for Pinnipeds in the future.

EVO-O-14

**Genetic and behavioral investigations into African weakly electric fish signal evolution**

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E

Understanding the evolution of animal signaling requires an examination of both the proximate and ultimate mechanisms driving signal diversification. This is of particular interest when signal diversification can be linked to species diversification, as seen in African weakly electric fish. These mormyrid fish have evolved an electric organ, which generates a species-specific electric organ discharge (EOD) for the purpose of electrocommunication and orientation. Across over 200 described species, the EOD waveform can vary notably in form, duration, phase polarity, and phase count. Furthermore, the temporal pattern with which these EODs are emitted can vary in a context dependent manner (sequence pulse interval, SPI), which potentially includes species-specific statistics. The potential genetic, ecological, and reproductive mechanisms underlying the diversification of these electric signals (EOD and SPI) and consequently the adaptive radiation of mormyrid fish are therefore of particular interest. Here, we have examined the expression of ion channel genes and identified a pattern of upregulation in voltage-gated potassium channels in species with an elongated, derived EOD waveform. Furthermore, we have conducted behavior experiments to determine the importance of the EOD in preventing hybridization among sympatric species. Our results indicate a male mediated species recognition system in at least two mormyrid *Campylomormyrus* species. Additional playback studies suggest that while both the EOD waveform and SPI statistics are species-specific, the cues necessary for species recognition may differ among species. For example, while the EOD and SPI were both necessary and sufficient for species recognition in *C. compressirostris* males, *C. tamandua* males apparently utilize other, non-electric modalities. Mapped onto a recent phylogeny, our results suggest that discrimination by electric cues alone may be an apomorphic trait evolved during a recent radiation in this taxon.

EVO-O-15

**Morphological adaptation in a clonal invasive aquatic snail**Gerlien Verhaegen<sup>1</sup>; Maurine Neiman<sup>2</sup>; Martin Haase<sup>1</sup>1 Ernst-Moritz-Arndt-Universität Greifswald; 2 The University of Iowa  
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Organisms featuring wide trait variability that occur in a wide range of habitats can serve as a model to study mechanisms of adaptation. The ovoviparous New Zealand mudsnail, *Potamopyrgus antipodarum*, is characterized by wide variability in shell size and shape, especially - but not only - in its native country, where diploid sexual and polyploid asexual lineages coexist in a wide range of aquatic habitats. *P. antipodarum* has successfully invaded many freshwater sites across the globe, though only the asexual lineages are found out of the snail's native range. We hypothesized that shell morphology is an adaptive trait with high potential for phenotypic plasticity that facilitated the *P. antipodarum* invasion. We addressed this hypothesis by collecting a total of 425 snails at 23 localities across Belgium, the Netherlands, and Germany and measured ten environmental parameters. We used mitochondrial Cytochrome b and 16S rRNA sequence data and 50 SNP markers to identify clonal lineages, and geometric morphometric analyses to analyze shell shape and size independently. These analyses revealed that only two clonal lineages were present across our sampling sites and that shape but not size was related to lineage. Shape and size also differed between river and lake populations, with river snails characterized by a shorter but wider shell with a relatively larger aperture and larger size than lake samples. These differences in size might be linked to selection favoring relatively larger feet in river populations with stronger currents. Among environmental parameters, water temperature and conductivity had an effect on both shell shape and size. The number of brooded embryos increased with size and water temperature but shape had no effect. In conclusion, variation in shell morphology among European clonal *P. antipodarum* has both genetic as well as phenotypically plastic components. Our study results suggest that at least the latter might be adaptive.

EVO-O-16

**Convergent evolution of raptorial appendages in arthropods: first steps towards a quantitative approach**

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Raptorial appendages represent a functional and morphological predatory specialization of the arthropod leg. Differently to chelipeds or other predatory limbs, raptorial appendages involve seizing the prey through the folding of different parts of the leg. This type of structure is notably found in a plethora of different not closely related insect groups, such as in Mantodea (praying mantises), Reduviidae (assassin bugs, Hemiptera) or Mantispidae (mantid lacewings, Neuroptera). Analogues to this structure, though, are also present in other arthropod groups, such as in Caprellidae (skeleton shrimps, Amphipoda, Eucrustacea) or Laniatores (armoured harvestmen, Opiliones, Eucelicerata). Although the functionality of these appendages is basically the same, the involved components may differ between the groups. This poses a potentially interesting case of convergent evolution within arthropods. For this reason, we review some groups with this specialization from a functional morphology perspective. In addition, we propose a quantitative approach to infer the presence and, subsequently, the degree of convergent evolution across these lineages. Our investigations involve measurements of the raptorial appendages as well as analyses on the presence of certain key characters. Furthermore, we also incorporate fossil data, mainly for Mantodea, to include a deep-time aspect into the evolutionary analysis. In addition to insights into the evolution of raptorial appendages within, as well as the convergent evolution between different arthropod groups, this approach could also be used to understand connections between morphology and ecology.

EVO-O-17

**Experimental evolution of *Spiroplasma* symbionts in *Drosophila***

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**E** Symbiosis between multicellular organisms and microbial symbionts is near universal, and it is now clear that many aspects of organismal biology cannot be understood without reference to interactions with microbes. In insects, this includes a diverse range of heritable symbionts, which pass from a female host to her progeny. These symbionts are highly adapted to their host, and encode important properties, such as defence against natural enemies. In contrast to classical adaptive phenotypes, symbiont traits generally arise through a host shift event – the movement of a microbe from into a novel host species. While horizontal symbiont transmissions are frequent in nature, we know from lab experiments that not all novel symbiont-host combinations are compatible. However, little is known about the mechanistic factors that contribute to a successful (or unsuccessful) match of microbe and host.

In this work, we use the *Spiroplasma*–*Drosophila* system to establish the genetic factors associated with a poor symbiont-host combination. To this end, a *Spiroplasma* symbiont was transferred from *Drosophila hydei* to *D. melanogaster*. This artificial host shift resulted in high pathogenicity in the novel host. Continued passage of *Spiroplasma* over 20 host generations however strongly diminishes this pathogenicity phenotype. We here aim at understanding the genomic adaptation of *Spiroplasma* that results in this phenotype shift by comparing genomes of the native and evolved lines of the symbiont.

EVO-O-18

**Two chromosomal regions govern local adaptation to high altitude in honey bees**Andreas Wallberg<sup>1</sup>; Caspar Schöning<sup>2</sup>; Matthew T. Webster<sup>1</sup>; Martin Hasselmann<sup>3</sup>

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**E** Understanding the genetic basis of local adaptation of organism is an important and challenging task in evolutionary biology. In East Africa, populations of the honey bee *Apis mellifera* live in the mountain forests and differ in behavior and morphology from those inhabiting the surrounding lowland savannahs, which likely reflects adaptation to these habitats. We performed whole genome sequencing on 39 samples of highland and lowland bees from two pairs of populations to determine their evolutionary affinities and identify the genetic basis of these putative adaptations. We find that levels of genetic differentiation between highland and lowland populations are very low, consistent with them being a single panmictic population. Interestingly, we identify two loci on chromosomes 7 and 9, each several hundred kilobases in length, which exhibit near fixation for different haplotypes between highland and lowland populations. The highland haplotypes at these loci are extremely rare in samples from the rest of the world. Patterns of segregation of genetic variants suggest that recombination between haplotypes at each locus is suppressed, indicating that they comprise independent structural variants. The haplotype on chromosome 7 harbors nearly all octopamine receptor genes in the honey bee genome. These have a role in learning and foraging behavior in honey bees and are strong candidates for adaptation to highland habitats. Molecular analysis of a putative breakpoint indicates that it may disrupt the coding sequence of one of these genes. Divergence between the highland and lowland haplotypes at both loci is extremely high suggesting that they are ancient balanced polymorphisms that greatly predate divergence between the extant honey bee subspecies.

EVO-O-19

**HSP90 as a capacitor for rapid evolution in the red flour beetle *Tribolium castaneum***

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Evolution can be astonishingly fast. The mobilization of 'cryptic genetic variation' (i.e. genetic variants that are invisible under normal conditions) is a particularly fascinating possibility for a population to quickly respond to environmental change. However, tests of this intriguing idea are rare. The molecular chaperone heat shock protein 90 (HSP90) has a crucial role in this process, since it normally stabilizes developmental pathways and thus allows for the accumulation of cryptic genetic variation, which can be released under stressful conditions when HSP90 becomes limited. We recently showed in the important model insect *Tribolium castaneum* that the down-regulation of HSP90 is mediated by social cues indicative of a stressful environment. We now tested whether HSP90 reduction indeed releases cryptic genetic variation in *T. castaneum*. As expected, reduction of HSP90 in the parental generation, either by RNA interference or with the specific chemical inhibitor 17-DMAG, revealed a very interesting 'reduced eye' phenotype. Interestingly, this morphological trait was inherited to the next generations, suggesting that this phenotype was based on a normally cryptic genetic variant and that it could be genetically assimilated. Our results provide further evidence that the environmentally regulated release of cryptic genetic variation might enhance rapid adaptive evolution.

EVO-O-20

**The t haplotype: A selfish genetic element that manipulates migration propensity in its carrier?**

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Selfish genetic elements (SGE) are genetic loci that drive, meaning that they are inherited by more than 50 percent of offspring. This comes at a cost to the alternative allele, and potentially to the rest of the genome and organism, resulting in conflict. This conflict creates selection on the rest of the genome to suppress the drive, which leads to counter-selection on the SGE to evade suppression. This conflict can be explored using an SGE in house mice, the t haplotype (t). In male carriers, the t is transmitted to 90% of offspring. Although in theory it should spread rapidly, it is less frequent in natural populations than predicted based on its drive because of homozygous lethality and extremely low sperm competitiveness. Thus, it is prone to extinction in small and large populations, due to drift and multiple mating, respectively. Nonetheless, it has survived for two million years and is widespread, which is puzzling. We hypothesized that, similar to manipulative parasites, the t modifies the behaviour of its carrier to increase its own fitness. For the t, placing more of its carriers in populations with few other t carriers and a low occurrence of multiple mating would be advantageous. This could be achieved by increasing the emigration propensity of the t's carrier. We tested this by analysing data on juveniles disappearing from and migrating within a long-term free-living house mouse population. We found that t-carriers were indeed more likely to emigrate from the population as juveniles, particularly when the juvenile population size was large. This is the first evidence that any driving element influences host migration. To further test this hypothesis, we are conducting experiments that test emigration behaviour and using agent-based models to simulate the evolution of migration propensity for t and wildtype.

EVO-O-21

**Parental effort and telomere dynamics - a longitudinal study in jackdaws**

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Reproductive success and lifespan are two key components affecting fitness in an interplay. Where resources are limited, life-history theory predicts that the allocation of resources towards reproduction comes at the expense of somatic maintenance. The evolutionary dynamics driving this link as well as the underlying mechanisms remain poorly understood. Telomeres, evolutionary conserved DNA structures at chromosome ends, function in genome stability and shorten with age. Telomere dynamics relate to ageing-associated diseases and survival in mammals and birds and present a candidate biomarker of ageing or somatic state. Previous investigations in our study population of free-living jackdaws (*Corvus monedula*) have shown that individuals with an experimentally increased reproductive effort suffered an increased mortality rate with age. Our aim was to test how brood size manipulation and increased mortality rate affect future reproductive success and if telomere dynamics mediate or reflect this trade-off between reproduction and lifespan. We applied a longitudinal brood size manipulation approach to increase or reduce brood size over life in jackdaws. Individual-based data on reproduction and blood samples for telomere analysis were collected during every breeding season since 2005. We find that parents with constantly enlarged broods showed accelerated senescence and increased their reproductive effort in subsequent breeding attempts. Telomere dynamics differed between experimental groups, but first results revealed opposite effects for the sexes. We discuss these results in a life-history theory context.

EVO-O-22

**Alternative reproductive tactics and a sexually antagonistic inversion**

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Chromosomal inversions often lead to dramatic changes in appearance and behaviour. An approximately 4.5 Mbp dominant autosomal inversion is responsible for discrete alternative reproductive tactics among male Ruffs *Philo-machus pugnax*. Males of this lekking shorebird belong to one of three mating morphs: 1) Independents, who compete aggressively for matings and represent the most frequent morph (84% of the males), 2) Satellites (15% of the males), who gain access to the lekking competition through submissive co-display with Independent territory holders, and, 3) Faeders, the rarest morph (1% of the males), who obtain matings as non-aggressive female mimicking sneakers. The inversion reduces the mating skew among males by enabling further males to reproduce using alternative reproductive tactics. The costs and benefits of the inversion for females are less well understood. Since the inversion is homozygous lethal and is associated with reduced size, it likely reduces fertility of females. Using data from captive and wild Ruff populations I investigate frequencies of inversion carriers in males and females during different life stages. Consistent with a sexual antagonism, inversion carriers were indeed rarer among females than among males. Given that the adult sex ratio is strongly female biased the inversion may only have a small overall negative impact on the fitness of Ruff populations. These results provide intriguing insights how the inversion changes the mating dynamics in this iconic model of sexual selection.

EVO-P-01

**Speciation in Space & Time**

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In continuous habitats without a physical barrier, reproductive isolation evolves as a by-product. Models therefore invoke adaptive selection along environmental gradients or sexual selection for the evolution of reproductive isolation in non-allopatry.

This project is the first attempt to discriminate and support the two subspecies of the Mediterranean bushcricket *Poecilimon veluchianus* genetically. Mainly we focus on populations of its partially reproductively isolated subspecies to investigate patterns of genetic variation and gene flow to evaluate different models of speciation. Based on AFLP-fingerprinting and the analysis of a nuclear marker (ITS) we conclude that diversification in allopatry with a secondary contact of the two subspecies is a likely scenario. A barrier to gene flow could be estimated, but no selective loci or a steep ecological gradient were found. On subspecies level, isolation by distance influences the genetic variation. Local ecological variation leads most likely to the observed genetic patterns on population level. Which ecological factors are important for differentiation however is still unclear.

Hybrids are low in abundance. Whether they are fertile or selection is acting against them we are going to further investigate.

EVO-P-02

**Do gut symbionts have an impact on the mate choice of Zebra Finches?**

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Vertebrates harbor a complex and diverse community of symbiotic microorganisms in their gut. In addition to its physiological functions, gut microbiota also influence a host's behavior and plays a potential role in kin recognition and mate choice. Although the exact mechanism of this interaction is not known, olfactory signals produced by gut microorganism are hypothesized to influence behavior. Hence, determining factors effecting gut microbial composition and understanding how these bacteria influence evolution of host behavior is crucially important.

We aim to identify the genetic pathways and environmental factors influencing gut microbiota in an avian model system. We will document the host-specific differences in composition of gut microbes using 16S rRNA gene sequencing and investigate internal (genetics and sex) and external (maternal seeding, food and nest mates) factors contributing these host-specific differences using a cross-fostering strategy.

The findings will enable us to expand our understanding regarding relative contributions of environmental conditions and genetic factors to variations in gut microbial composition and will open a new window to further explore how variations and alterations in the composition of gut microbiota affects host fitness, evolution of mate preferences and kin recognition.

EVO-P-03

**Immunolocalisation of opsins in tardigrades (water bears)**

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The ability to perceive light is widely distributed among animals, but the evolution of this complex sensory capacity is not fully understood. One particular gap in the knowledge concerns the visual system of tardigrades (water bears). Despite their key phylogenetic position as one of the closest arthropod relatives, insufficient data are available on photoreception in tardigrades. In particular, data on the expression of opsin genes, which have been identified recently in the eutardigrade *Hypsibius dujardini* Doyère, 1840, are completely missing, although these proteins play a key role in light reception and light-induced behaviour. Our goal is therefore to immunolocalise the key opsin proteins in *H. dujardini* using whole-mount preparations, including one r-opsin and three c-opsins. Based on transcriptomic and genomic data, we generated individual antisera against specific regions of these membrane proteins. The obtained results will provide insights into the function of opsin proteins and help to clarify which of these proteins are involved in vision. The new findings will shed light on the evolution of photoreception since the divergence of the three major panarthropod groups: Arthropoda, Onychophora, and Tardigrada.

EVO-P-04

**Untangling the diversification of malaria parasites: Insights from whole-genome sequencing of *Polychromophilus***

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Phylogenetic analyses of parasites provide the greatest potential to address fundamental questions regarding the processes of host switching that underlie numerous epidemic diseases. Haemosporidan parasites, which are one of the most diverse assemblages of protists, lack a well resolved phylogeny. Most previous analyses were limited to a small set of genes mostly of mitochondrial or apicoplast origin. This resulted in weakly supported hypotheses and wide discrepancies in the literature as to the evolutionary relationships among haemosporidians. In particular, the placements of the most likely exclusive bat-infecting genera remain enigmatic. The use of deep next-generation sequencing and genome-wide analyses makes a reliable reconstruction of the haemosporidan phylogeny tractable. While the number of sequenced genomes, almost exclusively of primate- and rodent-infecting *Plasmodium* species, has continued to increase, chiropteran haemosporidians have been largely neglected. Here, we present a first insight into the genomic data of the malaria-like blood parasite *Polychromophilus* sp. We performed a multi-step strategy to filter the sequences of the parasite from those of its host, *Myotis daubentonii*. Using this approach, we obtained genome sequences that are a solid basis to trace the phylogeny of Haemosporida. The genome data will further help to reveal new insight into evolutionary events of malarial adaptive traits.

EVO-P-05

### Agony of choice — The impact of assembly strategies on phylogenetic studies in Cladobranchia (Gastropoda, Mollusca)

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Despite the progress that next-generation sequencing techniques have made during the past decades, reference-free de novo assembly of transcriptomic sequences from non-model organisms still remains a challenge. This is at least in part due to the sheer number of software packages available for transcriptome assembly, each of which features different algorithmic approaches and a plethora of settings meant for customising the assembly process. However, taking into account all assemblers and all possible combinations of settings will inevitably result in an enormous number of assemblies when dealing with larger numbers of datasets, often rendering a completist approach impracticable where time, manpower or computing power are limiting factors.

There are only few publications that compare different software packages with regard to the quality of the assemblies. These could act as a guideline for choosing an assembly tool, but so far only a small number of organisms or a limited number of assembly tools have been investigated in those studies. Furthermore, it is currently unclear what impact the choice of the assembly tool can have on subsequent phylogenetic analyses.

We aim at shedding more light on this latter aspect of transcriptome assembly. To this end, we are assessing the performance of six commonly used assembly tools that were run with default settings to assemble the transcriptome sequences of 61 species of heterobranch sea slugs (56 members of Cladobranchia, three of Doridoidea and two of Pleurobrancoidea). For each species, we identified the best and the worst assembly using a variety of descriptive parameters. These assemblies were then searched for orthologous genes that are presumed to be single-copy in molluscs. The identified genes were used in a supermatrix approach to calculate two phylogenetic trees of Cladobranchia. Our results show what impact the selection of an assembly tool can have on phylogenetic analyses in cladobranchs.

EVO-P-06

### Stronger together: collective antimicrobial defence in *Drosophila* larvae

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Collective antimicrobial defence – often termed social immunity – is a widespread strategy among eusocial insects to keep pathogens in check. We show experimentally that saprophagous *Drosophila* larvae suppressed the spread of habitat invading toxic mould fungi at a higher per capita rate when they feed in larger groups. A group size-mediated collective action benefit rather than a mere numerical density-dependent advantage may thus contribute to pathogen control by a non-eusocial insect. Antimicrobial defences involving collective actions are therefore not restricted to eusocial insects. We hypothesise that antimicrobial defences in eusocial systems may have their evolutionary origin in comparatively primitive semisocial aggregation behaviours in non-eusocial insects.

EVO-P-07

**Prezygotic and postzygotic barriers between strains of the parasitic wasp  
*Lariophagus distinguendus***

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The mechanisms leading to the formation of new species have been the subject of research since the 19th century. Speciation depends on the formation of isolating barriers. Prezygotic isolating barriers prevent the fertilization of the egg and comprise for example different ecological niches and sexual isolation. Isolating mechanisms occurring after fertilization, such as hybrid sterility or cytoplasmic incompatibility (CI) caused by endosymbionts, are called postzygotic barriers. Our study focused on isolation barriers in *Lariophagus distinguendus* (Hymenoptera: Pteromalidae), a parasitoid of coleopteran larvae. *L. distinguendus* has been shown to consist of various strains that display different levels of isolation and can be grouped into two distinct lineages. One lineage is a specialist on the drugstore beetle *Stegobium paniceum* (Coleoptera: Anobiidae) (drugstore beetle lineage) whereas the second lineage uses several hosts such as the granary weevil *Sitophilus granarius* (Coleoptera: Dryophthoridae) (granary weevil lineage). Previous studies using strains of both lineages revealed both sexual isolation and CI as isolating barriers between the lineages. To investigate which of these barriers developed first, one strain of the drugstore beetle lineage and one strain of the granary weevil lineage were crossed to examine sexual isolation and CI. We could show that sexual isolation exists between the chosen strains. There was however no evidence for CI as a form of postzygotic isolation. Therefore, our results suggest that in *L. distinguendus* sexual isolation was established as a barrier prior to CI.

EVO-P-08

**Sex determination of larvae of a flea beetle with extremely skewed sex ratio**

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The flea beetle species *Altica lythri* has a complex genetic population structure of three different mtDNA haplotypes that co-occur with three different strains of *Wolbachia*. These bacteria as well as *Spiroplasma* and *Rickettsia*, which also infect *A. lythri* at high frequencies, are known reproduction distorters and often responsible for a strongly female biased sex ratio. Depending on the haplotype and possibly on the infection status of an individual *A. lythri* female, her adult offspring's sex ratio will show a strong excess of females. While the adult beetles' sex can easily be determined morphologically, larvae still lack any morphological sex dimorphism. Since all of the bacteria mentioned above might act as male killers it is essential to decide at which stage the female excess comes about. Based on a transcriptome of a male and a female *A. lythri*, we developed primers that make use of sex specific splice variants of the sex determination gene *doublesex* (*dsx*). Starting from RNA extractions, these primers can determine the sex of early instar larvae by simple length differences of RT-PCR products. Correlating offspring sex ratio, female haplotype and infection status, this approach will enable us to decide on the genetic mechanism underlying the strongly female biased sex ratio of *A. lythri*.

EVO-P-09

**Fertility and extra-pair paternity in a wild population of great tits**

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Socially monogamous birds commonly engage in extra-pair copulations (EPC); the benefits for males are clear, yet it is still poorly understood why females seek out EPCs. Females may engage in EPC in order to assure fertilisation of their eggs because their social mate may not be fertile (the 'fertility insurance hypothesis'). Females may also engage in EPC in order to mate with a higher-quality male than their social mate ('good genes hypothesis'). We investigated the importance of these hypotheses in explaining patterns of extra-pair paternity (EPP) in a wild population of great tits (*Parus major*). EPP levels were measured in breeding pairs in nest boxes, and sperm samples were obtained from each male. We measured sperm morphology and vitality, which are indicators of male fertility. Low levels of fertility would indicate a potential benefit to females of EPCs under the fertility insurance hypothesis. We related males' sperm quality to both their within-pair paternity (WPP) and their success in obtaining EPP. Male fertilization success may have been a direct consequence of their sperm quality or it may have been related to female choice for secondary sexual characteristics. We compared male fertilization success to the width of the black breast band, an important sexually selected visual ornament in this species. Our results are important for the understanding of post-copulatory sexual selection in the wild. In particular, the relationship between sperm quality and fertilisation success has, up to now, received little investigation in the wild.

EVO-P-10

**Resource allocation trade-offs can explain the allometry of sexually selected traits**

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Allometry is a method used to highlight sexual selection pressures when comparing the scaling of trait size with the body size of animals in a population. It is assumed that traits under strong directional selection scale disproportionately with body size and therefore exhibit positive allometry. This pattern is in particular observed for conspicuous traits like some ornaments or weapons, but it is far from universal for these traits. The current theoretical framework for allometry offers no clear explanation for this lack of a clear trend. One prominent criticism of classical allometry is that simplifying assumptions are used to explain the development of allometry: Often the exact fitness related costs and benefits for the development of the trait and possible interactions between related traits are omitted. Therefore we explored these criticisms in order to create a more precise model on the emergence of patterns of allometry with a trade-off model based on resource allocation. This model allowed considering a pre- and a postcopulatory trait, representing different, however connected episodes of selection in mating, under scenarios of different intensities of selection pressures. The model predicts a trade-off between the two traits depending on the intensity of the selection pressure: (i) Strong selection pressure on a given trait results in positive allometry for this trait, but only if there is negligible selection pressure on the other trait which then results in isometry for this trait, and (ii) if there are comparable intensities of selection pressures the allometric slopes of these traits are attenuated. Our model therefore predicts patterns of allometry found in nature and possibly explains the lack of a clear pattern of positive allometry in weapons traits as a result of a resource allocation based trade-off between two traits.

EVO-P-11

**Teasing apart environmental vs inherited components of a termite gut microbiome**

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Termites rely on a complex microbial symbiosis to digest plant material such as dead wood and grass. The core gut microbiota is thought to be transmitted vertically via dispersing alate reproductives from the parent colony to new colonies established with a mate from a different parent colony, as well as horizontally between nestmates. Previous work has defined the core microbiome in various ways: using a single colony to represent a species, including multiple colonies over a large distance, or comparing different species across locations. Here we synthesise these approaches, exploring differences between castes, colonies, species, and locations over time, to differentiate the core microbiome of a species, common but not essential gut community members, and environmentally acquired microbes. We find that the number of colonies and castes included in the analysis affects the size and composition of the resulting core. A limited set of vital partners simplifies the potential co-evolutionary interactions and reduces the potential for transmission failure during the colony establishment bottleneck. Microbes common to a location may be resident or transitory, perhaps assisting with the digestion of local foodstuffs by degrading inhibitory plant secondary compounds. Work over longer time scales will be necessary pinpoint the core community and detect seasonal influences.

EVO-P-12

**Identification and gene-knockdown of putative seminal fluid proteins in a simultaneously hermaphroditic flatworm**

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Seminal fluid proteins (Sfps) are thought to play a key role mediating post-mating sexual selection, by potentially modulating recipients' behavior and physiology in ways that influence reproduction, as well as in sexual conflict. Despite the importance of Sfps for the reproductive physiology and behaviour of the ejaculate recipient and the fertilizing ability of the donor, the identification and characterization of seminal fluid proteins has to date focused on just a few animal groups and mainly on species with separate sexes. Here we report a comprehensive screen for putative seminal fluid proteins in the simultaneously hermaphroditic flatworm *Macrostomum lignano* based on existing RNA-seq data. For 147 transcripts known to be a) predominantly expressed in the tail region of worms, where the seminal fluid-producing prostate gland cells are located and b) differentially expressed in social environments differing in sperm competition level, strongly implying they are a plastic aspect of male allocation, we performed whole mount in situ hybridization experiments. We identified 76 prostate-gland limited transcripts as expected for Sfps. Additionally we report RNAi knockdown experiments for 18 seminal fluid candidates to probe the function of this putative seminal fluid proteome, with diverse predicted roles impacting fertility and competitive fertilization success.

EVO-P-13

**The impact of ageing on male post-mating reproductive success**

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E Ageing is characterized by a progressive decline in bodily functions leading to an increased risk of death. This process is accompanied by a decline in reproduction. We here studied male reproductive ageing with a focus on post-mating processes. Prior studies mainly explained male reproductive ageing with a reduction in sperm quality with negative effects on offspring development and quality. However, alongside sperm males also transfer seminal fluid proteins (Sfps) at mating, which are important determinants of male reproductive success. Receipt of Sfps leads to female post-mating changes affecting for example ovulation rate and sperm competition dynamics. Using the fruit fly *Drosophila melanogaster* we studied whether the traits mediated by the non-sperm fraction of a male's ejaculate also show signs of change with increasing male age and tested the consequences for male reproductive success. We allowed males to age for up to 49 days and assayed their ability to elicit female post-mating responses after a single mating. We found that with increasing age males were less able to induce a number of these responses. We also measured expression for five of the genes across different male age groups. Taken together our findings indicate that with advancing age males transferred less effective ejaculates and that Sfp composition might change over a male's lifetime in quantity and/or quality, significantly reducing male reproductive success.

EVO-P-14

**Opportunistic males and female remating in a sex role reversed spider**Fedra Bollatti<sup>1</sup>; Alfredo Vicente Peretti<sup>2</sup>; Anita Aisenberg<sup>3</sup>

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E Sexual Selection is a powerful evolutive force which acts on the abilities of one sex to accessing potential pairs. In this scenario, conspecifics intrasexual opponents could find different solutions to reproductive competition, which will evolve in alternative reproductive tactics towards the same functional end. *Allocosa senex* is a nocturnal sand-dwelling spider which shows reversal in sex roles and sexual size dimorphism: conversely to what is typical in spiders, females are smaller than males and they are the mobile sex that searches for males and initiates courtship. According to previous studies, males construct long burrows and stay inside expecting female's visits. However, as males donate their burrows to females after mating, when they emerge during the night to feed they can potentially bump into mated females inside the burrows donated by previous males. Our objective was to test if males of *A. senex* can detect mated females inside other male's burrows and if they are accepted for mating by those females. Virgin males were placed in a terrarium 48 h before the trial to allow burrow construction. Each experience (n=7) begun when a virgin female was introduced into that terrarium and ended after the copulation was concluded. Once the trial was finished, the male was removed and the female was allowed to remain inside the donated burrow for 3-5 days. After that, a second male was introduced to the terrarium and courting and mating behaviours were recorded. Preliminary results show that second males can detect and court mated females staying in donated burrows in a high percentage (71%), while in 43% cases even they mate. These results suggest that males of *A. senex* can modulate their reproductive tactics adopting an opportunistic strategy using those burrows dug by others males, which allows them to mate with a mated female on an alien male's burrow avoiding the great investment that implies burrow digging.

EVO-P-15

### Sexual selection acting on male genitalia, copulation behaviour and spermatophore size in a bushcricket

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E Sexual selection by female choice seems to have a great impact in various animal species, including insects as driving force on genital evolution. Males of different tettigoniid bushcrickets (Orthoptera: Ensifera: Tettigoniidae) possess a pair of sclerotized genital structures (titillators). During copulation males move their titillators rhythmically inside the female's genital chamber. These structures seem to play a role in correct placement of the spermatophore, consisting of the sperm containing ampulla and a spermatophylax. Even more, titillators stimulate females during copulation and suppress female mate rejection behaviour. Therefore, titillators can be assumed to be under sexual selection due to female choice.

We studied the correlation of titillator length with male traits (body size and mass) as well as investment into the nuptial gift in the bushcricket *Metrioptera roeselii* (Hagenbach, 1822).

Larger males were absolute and relatively heavier and produced heavier spermatophores. They had also longer titillators and performed more titillator movements during copulation, in line with the hypothesis that titillators are under sexual selection. Sexual selection acts on variable individuals exhibiting traits to different extent, therefore, we analysed the amount of variance. We found great differences in the extent to which male traits varied. The two morphological characters, the male hind femur and the titillator, showed with <10% the lowest levels of variance. Intermediate levels ranging from 11 to 30 % are found for male body mass and spermatophore mass. Behavioural characters differed most, having variances between 23 and 160 percent for the approach duration, the time to reach the copula position, the number of copulatory movements and the copula duration. This shows that sexual behaviours are far more dynamic characters than body masses or body sizes.

EVO-P-16

### A distinctive violent courtship behavior does not influence paternity in the Siberian grasshopper *Gomphocerus sibiricus*

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E Since females are usually the choosy sex, mating success of males often depends on the quality of their courtship behavior. Even after a successful mating-attempt males cannot be sure to fertilize the eggs of the mated female. Cryptic female choice has the potential to strongly influence male mating success and several studies have shown that the quality of male courtship behavior can be the crucial factor for the fertilization success of a focal male when the female copulates also with other males. The species of our study – the Siberian grasshopper *Gomphocerus sibiricus* – shows a very interesting courtship behavior that may potentially be selected by cryptic female choice. As most other gomphocerine grasshoppers also *G. sibiricus* males show a courtship song but in addition to that they exercise a “dance” with their antennae and also an unique behavior: They hit the female's pronotum with their thickened foreleg-tibias during mounting.

We experimentally diminished the strength of these hits by attaching foam rubber 1. to the inner side of the male's tibia, 2. to the outer side of the male's tibia (control), 3. to both lateral sides of the female pronotum or 4. to the top of female pronotum (control). With these animals and additionally with non-treated animals we performed matings in different combinations. After these first matings we removed the foam rubber from all animals and the females were mated a second time with another male. We observed the courtship and mating behavior. All eggs laid after the second mating were collected for determining paternity (P2-values).

We found no treatment effects in mating latency or copulation duration but a significantly higher amount of hitting behavior in pairs were both animals were padded with foam rubber on the crucial body parts compared to all other treatments. The proportion of paternity (P2-value) seems uninfluenced by the treatment and more or less randomly distributed.

EVO-P-17

### Selfing delay and sex allocation in a natural population of a preferentially outcrossing, simultaneously hermaphroditic flatworm

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Self-fertilization (selfing) occurs in a variety of simultaneously hermaphroditic organisms as a form of reproductive assurance when outcrossing is not possible. In the case of preferential outcrossers, selfing usually comes at a cost, leading to inbreeding depression in the resulting progeny. To avoid that, some organisms have evolved a strategy called “delayed selfing”: they commence to self-fertilize only after a period of time (“waiting time”) during which they first wait for potential outcrossing opportunities to appear. One such organism is the marine flatworm *Macrostomum hystrix*; previous research on a laboratory population demonstrated that it significantly delays reproduction when forced to self-fertilize. In order to investigate this phenomenon further, we focused on a natural *M. hystrix* population, finding that field-collected worms forced to self, exhibit on average longer and more variable “waiting time” than worms maintained in the lab. Isolated worms from the two sources also differ widely in their sex allocation, which for simultaneous hermaphrodites refers to the optimal partitioning of the reproductive resource budget into the two sex functions. Field-collected worms, investing almost equal amount of resources into each sex function, appear to be on average less male-biased than the laboratory population. The present study, being the first to investigate selfing propensity in a natural *M. hystrix* population, highlights the key role ecological circumstances play in the evolution and maintenance of variation in important reproductive traits.

EVO-P-18

### Lineage specific gene duplication as driver for sex specific physiological changes in the honey bee *Apis mellifera*

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Gene duplication and its subsequent divergence of functional duplicates play an important part in the evolution of novel gene functions. Social insects have gained many novel morphological and behavioral traits relative to their solitary ancestors. Taxonomically restricted genes (TRG) may have played an important role in that evolutionary process. Within this context the enzyme farnesyl pyrophosphate synthase (fpps) was detected as a candidate gene affecting honey bee physiology. Compared with other diverse insect species fpps is tandemly duplicated in the honey bee. Fpps is involved in catalyzing long chain hydrocarbon molecules within the Mevalonat signaling pathway which in turn are the starting products for the juvenile hormone branch in insects.

We want to test the hypothesis that the regulatory signaling of the sex determination pathway affects the regulation of the Mevalonat signaling pathway. We further propose that fpps copies have evolved a new or modified gene function with linking genes associated to the Mevalonat signaling pathway that affect the synthesis of potentially cuticular substances. We expect differences for male and female honey bees.

By detailed molecular analysis we studied seven predicted paralogous copies of fpps. We reveal the evolutionary history of the gene complex by comparative analysis with other insect genomes. Further we quantified the expression levels during different developmental stages for males and females in the honey bee. Preliminary analyses of cuticular surface substances will potentially decipher key components that differ between male and female honey bees.

EVO-P-19

### Is cytoplasmic incompatibility (CI) acting as an isolation barrier between two strains of the parasitic wasp *Lariophagus distinguendus*?

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The evolution of new species has been object of research for over 150 years, however the mechanisms of speciation are not completely clarified. One essential step in the evolution of a new species is the development of isolation barriers between two populations. They can either appear prezygotic (e.g. different ecological niches) or postzygotic as in the case of cytoplasmic incompatibility (CI). CI is caused by endosymbionts and can act as a reproductive barrier by preventing a successful reproduction. Although there are studies dealing with CI as barrier in insects, it is still unclear whether it acts as initiator on the base of speciation or evolves later in the speciation process.

In this study, we investigated the role of CI in the parasitic wasp *Lariophagus distinguendus* (Hymenoptera: Pteromalidae)(Förster 1841). It is a suitable model organism for research on speciation mechanisms because of the short generation time, high offspring numbers, "sib-mating" and monandry. There are two lineages in *L. distinguendus*. While one is a generalist on beetle larvae and feeds for example on the granary weevil (*Sitophilus granarius* L.) (Coleoptera: Dryophthoridae), the other is specialized on the drugstore beetle (*Stegobium paniceum* L.)(Coleoptera: Anobiidae). Previous studies showed that there are pre- and postzygotic isolation barriers between two of our wasp strains, where one is from the *S. granarius* and one from the *S. paniceum* lineage. They also showed a significant decline of F1 hybrid females, both in the occurrence and in the number of females. We hypothesized that endosymbiont induced CI could be the reason for that. To test this, we performed mating and fecundity experiments with tetracycline treated strains.

Our results show that despite the treatment, neither the numbers nor the occurrence of F1 hybrid females had increased. This suggests that CI is not the major player in the speciation process but rather other factors like different numbers in chromosomes.

EVO-P-20

### Clonal variability of predation induced phenotypic plasticity in ciliates

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Predation is a major factor driving adaptation. Trait variation is a result of genetic diversity as well as phenotypic plasticity. Prey species have evolved defensive strategies that reduce predation risk. The stabilizing effect of predator induced phenotypic plasticity on population dynamics has been shown. Classically, prey species show adaptive behavioural traits, morphological features, or shifts of life history parameters. However, sometimes predators can counter prey plasticity, by being plastic themselves. This has been described for ciliate species. *Euplotes octocarinatus* is known to develop protective lateral "wings" in the presence of the predatory ciliate *Lembadion bullinum*. This defended morphotype exceeds the mouthparts of its predators, reducing or even preventing engulfment. Interestingly there is a reciprocal adaptation of the predator. *Lembadion bullinum* is able to gradually adjust its size to the size of its prey, facilitating prey ingestion. This kind of prey induced offence strategy is plastic and therefore reversed when prey species are undefended. Just as in inducible defences, inducible offences are only formed when they are needed and cost for offences are saved when they are not essential. This observation adds a high level of complexity to predator-prey interactions. This is further complicated when taking genetic trait variability into account.

In our project within the Dynatrait consortium, we will use this system to perform community experiments and to study eco-evolutionary effects of inducible defences and offences. We will present first results showing inter- and intraspecific distinctive morphological features with variable degrees of plasticity differing between *Euplotes* strains.

EVO-P-21

**Phenotypic plasticity and genetic adaptation in a rapidly range-expanding spider**

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Global climate change can result in poleward range expansions. A new and promising model species for rapid range expansion is the orb-weaving spider *Argiope bruennichi* that spread from the Mediterranean region into continental climates and up to Baltic countries within less than 100 years. Consequently, its current distribution covers very different climates and environments. We collected mated females from three populations each of the northern range limit (Estonia), the original range (Southern France), and from genetically distinct populations of the Azores Island São Miguel. After oviposition, the spiderlings overwinter in egg sacs that were allocated to a common garden treatment with simulated winter conditions from all regions.

We investigated effects of origin and winter conditions on survival probability, dispersal propensity, body weight, and temperature stress resistance of the spiderlings. By performing large scale ballooning tests, we particularly explored dispersal behavior as a prerequisite for rapid range expansion. Overall, we found large effects of origin and winter treatment on all traits investigated, highlighting the importance of the interplay between phenotypic plasticity and genetic adaptation for range expansion.

EVO-P-22

**Melting pots in the city: Novel contact zones emerge when hybrid swarms meet**

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Human mediated dispersal has facilitated the emergence of more than 100 populations of the common wall lizard of non-native origin in Germany, representing genetic lineages of the same species but native to other parts of Europe. We investigated cities, as hotspots of human transportation, within the native range of lizards in Germany. In a fine-scale and individual-based genetic sampling approach, we quantified the frequency of non-native lineages and determined population structure of lizards as well as the amount of admixture, or hybrids, between clusters. In a next step, we used individual-based Bayesian assignment methods of individuals to clusters of origin, to test the hypotheses of multiple founder effects, multiple independent introductions or high-levels of admixture shaping population genetic structure in cities. Despite some remaining clusters of single lineage origin, most clusters contained haplotypes of multiple lineages. Although founder effects and multiple independent introductions must have occurred previously, currently, the prevailing population genetic structure depicts high levels of recent admixture between lineages, resulting in multiple and genetically isolated clusters of hybrid swarms. More so, hybrids between clusters were most frequently hybrids between two hybrid swarms, leading to a novel contact zone when hybrid swarms meet. From an evolutionary point of view, this may be an interesting opportunity to observe the beginnings of homoploid hybrid speciation. At the same time, lizards encountered at this novel contact zone illustrate genetic displacement of the protected native lineage of the common wall lizard, raising conservation concerns.

EVO-P-23

**Avian malaria and sperm morphology in songbirds with extra-pair paternity**

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Females of most socially monogamous songbird species copulate with males other than their social partners resulting in broods with mixed paternity that contain both within-pair offspring and extra-pair offspring. It has recently been suggested that avian malaria prevalence is linked to individual variation in paternity loss in broods of blue tit *Cyanistes caeruleus* males: infected males had a higher probability of having extra-pair offspring in their broods when their social females were themselves not infected. Malaria infection may negatively affect sperm quality and thus compromise the competitive fertilisations success of infected males. Based on large sample sizes, we therefore tested the hypothesis that malaria prevalence affects sperm morphology in three socially monogamous songbird species that show high levels of extra-pair paternity: blue tits, great tits *Parus major*, and coal tits *Periparus ater*. Furthermore, we report species- and sex-specific patterns of malaria prevalence for sympatrically breeding populations of the three study species.

EVO-P-24

**Analysis of the Na,K-ATPase  $\alpha$  and  $\beta$ -subunits of the cardenolide-adapted large milkweed bug *Oncopeltus fasciatus***

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The transmembrane enzyme Na,K-ATPase is essential for the maintenance of membrane potentials and therefore responsible for cell functionality in all animal cells. It is composed of a catalytic  $\alpha$ -subunit associated with a  $\beta$ -subunit that is necessary for its maturation, targeting, stability and functional expression. The Na,K-ATPase can be inhibited by cardiac glycosides (CG) that bind at a special binding site located in the  $\alpha$ -subunit. Nevertheless, several insects are able to cope with these toxins. The large milkweed bug *Oncopeltus fasciatus* is even able to sequester CGs for its own defense. Its insensitivity is gained by specific amino acid substitutions in the binding site of the Na,K-ATPase. Three gene copies of the Na,K-ATPase  $\alpha$ -subunit (A, B, C) with differing number of substitutions and four copies of the  $\beta$ -subunit ( $\beta 1-3$  and  $\beta x$ ) can be found in *O. fasciatus*. Especially the inhibitory effect of the CG ouabain on invertebrate Na,K-ATPase is well studied. However, the commercially available ouabain does not occur in hostplants of *O. fasciatus*. The aim of this study is to compare the inhibitory effect of ouabain on different  $\alpha$ - $\beta$ -subunit combinations with that of calotropin, a CG purified from its hostplant *Asclepias curassavica*. Literature on the mammalian enzyme suggests that CGs with the steric conformation of calotropin have less inhibitory potency than those with the steric conformation of ouabain. In contrast, our enzyme assays show a much stronger effect of calotropin on the Na,K-ATPase of the milkweed bug. The identity of the  $\alpha$ - $\beta$  subunit combinations and the number of substitutions present in the  $\alpha$ -subunit strongly modulate the Na,K-ATPase's behavior. This indicates functional differentiation which we are currently elucidating by tissue specific characterization of the  $\alpha$ - $\beta$  subunit combinations present.

EVO-P-25

**Phylogeny of Forkhead transcription factors**

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Forkhead domain containing genes (FOX genes) are a largely expanded family of transcription factors which is present in all metazoans and even in unicellular animals, with many different roles in development, cell cycle control, metabolism, and signal transduction. Additionally, several FOX family members have been shown to be present in genetic clusters in many different bilaterian lineages, implicating a shared regulation of these genes.

Previous attempts to identify forkhead family members have often focused on the presence of these genes in a single lineage and the subsequent inference of phylogenetic relationships among closely related taxa. With the recent increase in the amount of sequenced genomes, it is now possible to attempt a more complete approach. Here we present the unbiased identification of FOX genes from 22 species, sampled from different clades of the animal system, and the phylogenetic relationships of these identified sequences. Furthermore, we analyzed the presence of genetic clusters of FOX genes in the sampled species and confirm the presence of close genomic associations of foxD-foxE and foxL1-foxC-foxF-foxQ1, respectively. Finally, we show how the shared functions of the single FOX family members correlates with the evolutionary novelties of the taxa in which these genes first evolved.

EVO-P-26

**Why do moths have sperm that cannot fertilize eggs?**

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Moths and butterflies are unusual in that they display a dichotomous spermatogenesis producing eupyrene (nucleate) and apyrene (anucleate) spermatozoa. Although both types of sperm are concomitantly transferred to the female genital tract during copulation, only eupyrene sperm fertilize the eggs. The function of apyrene sperm, however, remains unclear and represents one of the most perplexing questions for evolutionary biologists. Among the several hypotheses concerning the function of apyrene sperm, a prominent idea is that they play an important role in sperm competition for example by acting as cheap filling material to decrease female remating propensity. Up to date, however, no experimental approach has provided convincing evidence for this hypothesis, primarily because an efficient method for isolation and quantification of apyrene sperm was lacking.

To provide new insights about the evolution of dichotomous spermatogenesis, we here investigated whether apyrene sperm have a function in sperm competition using the lek-mating lesser wax moth *Achroia grisella*. In this species, males gather on leks to display ultrasonic courtship calls targeted by strong female pre-copulatory mate choice. Approximately 20% of females remate with another male and own previous results showed that males under elevated sperm competition risk transferred a higher proportion of available eupyrene (fertilising) sperm. In this follow-up study, we focus on apyrene (non-fertilising) sperm by applying a recently developed method to reliably quantify apyrene sperm expenditure of males experiencing elevated sperm competition risk as simulated by the presence of a competitor during early adult life. We predict that males will increase apyrene sperm expenditure under elevated sperm competition risk and expect to corroborate the idea that post-copulatory sexual selection represents a significant but as yet underappreciated evolutionary force shaping male reproductive traits in lek-mating systems.

EVO-P-27

**Indication for selfing in geographically separated populations of the pulmonate land snail *Cylindrus obtusus* (Pulmonata: Helicidae)**

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**E** *Cylindrus obtusus* is an endemic snail species of the Eastern Alps. Peculiar intraspecific differences have been observed in its genital tract: in the eastern populations the two mucus glands associated with the love dart sac are highly variable, while no variation was observed in the western populations. This raises the question whether the mode and success of reproduction of the populations are different. To find out whether these anatomical differences reflect genetic differentiation, we investigated a 650 bp fragment of the COI (280 individuals) and 9 microsatellite loci (487 individuals) from samples covering the whole distribution range of the species. The COI sequences show a geographic differentiation between eastern, central and western populations. The westernmost localities, which were covered under ice sheets during glacial periods, are characterized by extreme low variability. Overall genetic distances among all individuals are small (max. 1.7 %). The microsatellite analysis reveals a high differentiation between populations, implying restriction of gene flow. The most peculiar outcome of the study is the strong evidence for selfing in *C. obtusus* as indicated by the microsatellite data in the easternmost populations (Kruckenhauser et al 2017): All individuals from the eastern populations, are homozygous in all loci, although different alleles were found within populations. This finding is supported by the deformation of the mucus glands in the same populations. Since mucus glands play an important role in sexual reproduction, it is plausible that in selfing organisms these structures are reduced. The phylogeographic structure implies that the species has survived the ice ages within the Calcareous Alps.

Indication for selfing in geographically separated populations and evidence for Pleistocene survival within the Alps: the case of *Cylindrus obtusus* (Pulmonata: Helicidae) 2017 Kruckenhauser et al, BMC Evolutionary Biology DOI: 10.1186/s12862-017-0977-0

EVO-P-28

**And then there were four – hidden genetic diversity within the cyprinid freshwater fish *Garra barreimiae* from Oman**

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**E** The North of the Sultanate of Oman is characterized by the Al Hajar mountains, which consist of anticlinal folds of limestone and dolomites. It is a harsh and arid environment with high mountain peaks and many wadis, which occasionally dry out. Only some of the bigger ones carry water permanently. These water bodies are inhabited by the cyprinid *Garra barreimiae*, which is endemic to the northern Oman and the UAE. Within this species, three subspecies have been described: *G. b. barreimiae* Fowler & Steinitz (1956), *G. b. shawkahensis* Banister & Clarke (1977) and *G. b. gallagheri* Krupp (1988). The latter has been lifted to species status recently (Lyon et al., 2016).

In the present phylogeographic study, we investigated the species' genetic diversity using mitochondrial (CR, COI) and nuclear (microsatellite) markers. The analyses based on mt data display a high genetic diversity, resulting in four well defined clades. This is also supported by the microsatellite data, which highlights substructuring within the clades. These clades have different geographic distributions which are in accordance with the drainage systems of the Al Hajar mountains. Between these clades the genetic distances are high and in the range of those between *G. barreimiae* and the closely related *Garra rufa*. A recent study showed that these groups are morphologically variable and only few meristic characters separate the West clade from the others (Pichler et al., submitted). While the West clade comprises samples of both subspecies *G. b. barreimiae* as well as *G. b. shawkahensis*, the remaining three clades correspond to not yet described taxa.

Our results clearly show cryptic variability within *G. barreimiae* and will help to decipher the taxons' historic background. Consequently, as *G. barreimiae* is not monophyletic according to our results, this study depicts the necessity for a revision of this group from Oman, which should cover the three newly discovered clades and establish them as species.

EVO-P-29

**From genes to the environment and back**

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E How does environmental variation affect living organisms? The answer to this question is expected to deepen current understanding of the processes that underlie disease and adaptation. In this talk, I will explore the implications of some empirical observations which suggest that suboptimal external environmental conditions may promote changes in eukaryotic DNA. These changes, while generally potentially harmful, may in turn facilitate adaptation to those selfsame suboptimal conditions.

EVO-P-30

**Fruit flies conform in love**

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E Social information use is a major strategy of mate choice. It can be gathered by observing potential mates' sexual interactions. Mate-copying is a form of such socially learned mate choice in which the fact that an observer female witnesses conspecifics' sexual interactions influences its future mate choice. Mate-copying was found in many vertebrates, but only in one vertebrate (*Drosophila melanogaster*) using artificially colored males (green or pink). To study conformism in mate choice we developed the hexagon setup, where 6 observer females in a central compartment can watch 6 demonstrations simultaneously in 6 peripheral compartments. There were 9 treatments with varying proportions of demonstrator females copulating with green or pink males: majorities of 6/6 (100%), 5/6 (83%), 4/6 (67%) and 3/5 (60%) for each color, plus one control (3/6: 50%). Observer females were then given the choice between 2 males, one of each color and we recorded the color of the chosen male. As expected, control observer females did not build any mating preference, and situations where all 6 demonstrator females copulated with the same male color led to strong mate-copying. As long as one male color was more often chosen than the other in the demonstration (majorities of 100% to 60%) observer females learnt to prefer males of the most commonly chosen color. Furthermore, social learning was equally efficient in the 4 situations that showed a majority of one color. Thus, mate-copying followed a step function with females learning equally well to prefer the most commonly chosen male color whatever the level of majority. This step function reveals surprisingly strong conformism in mate-copying. Conformism constitutes a major process of repair by which a population preference for a given male phenotype can persist over many transmission steps in which formerly observer females become demonstrators for new observer females, and so on.

EVO-P-31

**Ecological speciation in African weakly electric fish (genus *Campylomormyrus*): The influence of gravel size on species-specific feeding behavior**

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Weakly electric fishes are characterized by their ability to generate weak electric organ discharges (EODs) from a specific organ called electric organ. These fishes use EODs mainly for navigation, electrolocation, and electrocommunication. Recent studies have shown that the divergence in the morphology and EODs of African weakly electric fish (genus *Campylomormyrus*) are the two main factors that promote its adaptive radiation. For instance, the snout morphology, as an ecological trait, is apparently under disruptive natural selection and may play a role for niche specialization. The divergence of EODs is presumably acting as prezygotic isolation mechanisms, but may be related to feeding behaviour as well.

Apart from EOD divergence, species exhibit morphological differences in their trophic apparatus - an elongated trunk-like snout used for grasp-suction feeding - which varies among the different species in length, thickness, and curvature. In this study, we hypothesize that the morphological diversity of weakly electric fish corresponds with different diets and feeding habits. Feeding behavior and stomach content analyses of two *Campylomormyrus* species will be used to verify this hypothesis. Currently, dichotomous choice feeding experiments are being conducted to show behavior differences among different substrates, including different gravel sizes and sand. Nocturnal video recordings and EOD trains are sampled, encoded, and further processed. Preliminary results show that at these two *Campylomormyrus* species with significantly different snout morphologies correspondingly associate with different substrates and gravel size. Though still preliminary, our study provides initial evidence that the diversification in the trophic apparatus found in the radiation of these electric fish may be an adaptation to feeding on different substrate.

EVO-P-32

**Developmental plasticity of seminal fluid protein gene expression in a simultaneously hermaphroditic snail species**

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On a per gamete basis, sperm are much cheaper than eggs, but the total investment in a male ejaculate - comprising many sperm and seminal fluid proteins (Sfps) - can be substantial. For example, the great pond snail *Lymnaea stagnalis* is a simultaneous hermaphrodite (i.e., being male and female at the same time), but they are most likely to copulate as male when they have fully replenished ejaculate components. Given the cost of producing ejaculate, males are expected to adjust the production of ejaculates depending on their social situation, e.g., the number of mates. Here we examined whether *L. stagnalis* alters the production of Sfps depending on mating group size. Sfps are transferred together with sperm to female acting partners, and they trigger changes of reproductive physiology, e.g., egg laying. We developed the protocol for quantifying relative expression levels of five Sfp genes in *L. stagnalis* using qPCR. Then, we exposed snails into three different mating group sizes: isolated, paired and grouped (N=5 per replicate). Paired and grouped snails experienced copulations, though only grouped ones are exposed to sperm competition. Therefore, we expected that grouped snails show higher expression level of Sfp genes than paired snails. In this presentation, we will discuss the outcome and implications for further understanding of post-copulatory sexual selection.

EVO-P-33

**The structure of protein-coding genes: a comparison of unreviewed automatically inferred and of manually curated annotations**Jeanne Wilbrandt<sup>1</sup>, Bernhard Misof<sup>1</sup>, Kristen Panfilio<sup>2</sup>, Oliver Niehuis<sup>3</sup>

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E Structural annotation (i.e., location and structure), of protein-coding genes within a genome is typically automated by prediction algorithms. The inferred predictions are not free of error. It is therefore frequently stated that manual curation and validation of gene models is mandatory in order to be able to draw solid conclusions when comparing protein-coding gene repertoires and the genes' structural properties across genomes. As this approach is limited by available work force, it is vital for comparative genomics to assess which research questions can be answered when relying on automatically generated gene models and which not, because they require manually curated gene models

MOR-S-01

**Evolution and functional morphology of the mammalian inner ear**

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The mammalian inner ear is located in the bony labyrinth of the petrosal bone and houses the hearing and the sense of balance. The bony labyrinth serves as a proxy for the soft tissue structures and therefore can be investigated in extant as well as fossil species by  $\mu$ CT to elucidate the evolution and functional morphology of the inner ear.

**M** The coiled cochlea is a key innovation of modern Theria (marsupials and placentals) and improves the range of hearing frequencies. However, monotremes show a less degree of cochlear coiling and a different pattern of internal osteological structures for the innervation of the inner ear. Based on recently described petrosals of non-mammaliaform cynodonts and Mesozoic Mammaliaformes a new insight into the evolution of the therian cochlea has been provided. The fossil record clearly demonstrates the stepwise coiling of the cochlear canal of the bony labyrinth including the timing and development of relevant internal structures as present in therian mammals. The results are discussed against the background of the embryogenesis of inner ear structures in extant mammals.

The semicircular canals (SC) of the inner ear are involved in the detection of angular motion of the head and therefore exhibit adaptive patterns for locomotor behavior. Generally, it is assumed that the SCs show low levels of intraspecific variation due to high functional constraints. A comprehensive morphometric analysis of the bony labyrinth in Xenarthra reveals high variation in shape, relative size, and angles of the SCs in sloths (*Bradypus*, *Choloepus*) which is in contrast to faster-moving xenarthran species. This unique pattern of variation in sloths reflects a release of constraints on their organ of balance and is coincident with their slow and infrequent locomotion. The morphometric analysis of the SCs in the fossil ground sloth *Megatherium americanum* supports convergent evolution of the peculiar suspensory locomotion in the two extant sloth genera.

MOR-S-02

**Morphology and evolution of sensory and processing systems in mandibulate arthropods**

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**M** In view of numerous hypotheses concerning arthropod phylogeny, independent data are needed to supplement knowledge based on traditional external morphology and modern molecular sequence information. One promising approach embraces the comparison of structure and development of the nervous system. Compared to hexapods and crustaceans, our knowledge on the architecture of the peripheral and central nervous system in myriapods and chelicerates is limited. Myriapods display conspicuous evolutionary novelties as well as characters considered plesiomorphic for Mandibulata. The organization of sensory organs (especially of ommatidia and antennal sensilla) as well as associated processing centers for visual, chemo- and mechanosensory information in the nervous system strongly gave support to the Mandibulata hypothesis and a sistergroup relationship of Myriapoda and Tetraconata or Pancrustacea. Another prominent example in arthropod comparative neuroanatomy is the morphology of serotonin-immunoreactive neurons in the ventral nerve cord that can be identified individually due to their low number, characteristic soma position and neurite morphology and thus allows establishing homologies on a single cell level. New data likewise support the taxon Mandibulata by the presence of anterior and posterior neurons with contralateral projecting neurites. In order to evaluate existing neuroanatomical data, identify apomorphic and plesiomorphic characters as well as presumptive evolutionary transformations across Metazoa in general and Arthropoda in particular, a morphological database was created to compile a standardized character matrix that contributes to our understanding of invertebrate phylogeny. The talk will give insights into the evolutionary morphology of selected sensory organs and processing centers in the central nervous system and will highlight the neurophylogenetic approach to unravel nervous system evolution in mandibulate arthropods.

MOR-O-01

**Exploring the third dimension of insects - A novel approach using focus stacking and photogrammetry**

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Visualizing the three-dimensional structure of animals is a major challenge in morphological research. Several biological disciplines rely on information that can be obtained from 3D-models, such as surface/volume ratios or geometric morphometry from landmarks. But also archiving biodiversity would benefit from easy, time- and cost-effective techniques to digitize collection material in 3D, store the data in databases and make it available to the scientific community.

We developed a novel 3D-scanner to image pinned insects of various body size (ca. 2-40 mm) with an extended depth of field and several hundreds of poses covering nearly all viewing angles. These images can be used to investigate the specimen from almost any angle without the need to have the specimen at hand. Furthermore, the images can be used to generate a calibrated photogrammetric 3D-model, allowing morphological measurements and read-out of 3D-landmarks. The whole image acquisition and analysis workflow is highly automatized and needs little manual input. Scan duration lies between 2 and 8 hours and is fully automated. Calculation of a point cloud from the image data, meshing the points to generate a closed model, and finally texturizing the model in natural colors takes about 4 hours of computing time on an up-to-date consumer system. Data analysis is a semi-automated process which needs only some visual quality inspection inbetween steps. The whole process (acquisition and analysis) requires in total about 45 minutes of human interaction. Hence, by parallelization of processes, a high throughput could be achieved. The scanner can be copied with a manageable amount of money (less than 10,000€) and technical skills. A list of all commercially available parts as well as 3D-models for printing custom-made parts, Matlab scripts for data acquisition and Python-scripts for data analysis will become available in an open-source framework for further development and optimization of the system.

MOR-O-02

**Fast X-ray imaging of fossil insects from Paleogene fissure fillings**Thomas van de Kamp<sup>1</sup>; Achim. H. Schwermann<sup>2</sup>; Tomy dos Santos Rolo<sup>1</sup>; Thomas Engler<sup>3</sup>; Philipp Lösel<sup>4</sup>; Janes Odar<sup>1</sup>; Tilo Baumbach<sup>1</sup>; Lars Krogmann<sup>5</sup>

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Synchrotron-based X-ray imaging became an established method for the examination of small animals and X-ray microtomography in particular is an important tool for non-destructive 3D imaging of insects. The imaging station of KIT's Institute for Photon Science and Synchrotron Radiation (IPS) is optimized for fast X-ray imaging and includes a high speed detector system and a sample change robot. The setup facilitates high throughput experiments and digitization of large sample numbers in a single experiment.

Despite faster acquisition times, image analysis is often still time-consuming. Especially manual segmentation of tomographic volumes is extensive and its results often show unwanted artifacts. By employing semi-automated tools, however, which were developed in the scope of the projects ASTOR and NOVA, image analysis can be accelerated and improved.

In a recent experiment, we scanned hundreds of fossil insects from the fissure fillings of the Quercy region in France, which were semi-automatically analyzed. The talk highlights the first result of this study.

MOR-O-03

**Three-dimensional reconstruction and functional morphology of leg musculature in Onychophora (velvet worms)**

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Onychophora, Tardigrada (water bears) and Arthropoda (spiders, millipedes, centipedes, crustaceans and insects) constitute the highly diverse Panarthropoda, characterized by serially arranged locomotory appendages. While arthropods exhibit articulated legs, due to their rigid sclerotized exoskeleton, onychophorans and tardigrades have unjointed limbs similar to those found in fossil Cambrian lobopodians – a paraphyletic assemblage of marine animals from which all extant panarthropod lineages derived. Onychophorans, despite being terrestrial, bear locomotory appendages that particularly resemble those of lobopodians and are thus pivotal for understanding both the terrestrialization within Panarthropoda and how unjointed legs evolved into specialized jointed appendages in arthropods. Nevertheless, the myoanatomy and functional morphology of onychophoran legs is poorly known. We therefore used new high-resolution nanoCT imaging to generate, for the first time, a 3D-reconstruction of the onychophoran leg musculature and associated structures. Furthermore, we used high speed camera recordings of walking onychophorans to analyze the operating principles behind their locomotion. This approach allowed us to trace back the versatile movement abilities to a complex interplay of 15 muscles associated with the leg and the foot. These include promotors, remotors, levators, retractors, protractors, depressors, rotators, flexors and constrictors, as well as horizontal and vertical muscle septa that divide the leg cavity into four compartments along its longitudinal axis. Our findings shed light on the evolution of walking legs and their musculature within panarthropods.

MOR-O-04

**Fish functional morphology based on 3D reconstructions and numerical modelling**

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Fish differ not only remarkably in general appearance but also in sensory adaptations, e.g. of the mechanosensory lateral line system. Although the differences in size, shape and structural complexity are commonly discussed in the context of habitat and lifestyle, the distinct origin of this diversity still remains unclear. To draw functional interpretations from morphological structures, we adapted and optimized a workflow pipeline for 3D reconstructions of the fish body including the lateral line system. We performed fluid modelling based on realistic geometries and hydrodynamic conditions used in former experiments, i.e. a small sphere vibrating close to the fish while additional bulk water flow was present in the tank. The results of our simulation demonstrate the lateral line canal obtained more reliable information on the sphere motion than superficial neuromast. This finding is in agreement with former behavioral and physiological investigations. Furthermore, our study revealed that small pits found in the anterior head portion of *Leuciscus idus* alter local flow velocity and may prevent superficial neuromast from excessive hydrodynamic stimulation by water currents. In another in-silico experiment, the bulk flow direction relative to the fish's head was varied along the medio-lateral and dorso-ventral axis. Machine-learning algorithms revealed that fish can estimate flow direction from lateral line information, i.e. by superficial neuromast and/or canal neuromast inputs. In conclusion, our contribution demonstrates that laser scanning, photogrammetry, micro-computed tomography and computational fluid dynamics provide a great methodological toolset in functional morphology. Continuing studies are intended to investigate on radiation of body shapes and associated swimming capabilities in the model system of Sulawesi sailfin silversides (*Atheriniformes*).

MOR-O-05

### Did extant tree sloths evolve divergent musculoskeletal organization of the neck to cope with mechanical head support in inverted locomotion?

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The suspensory lifestyle of sloths evolved independently in the two extant genera (*Bradypus* and *Choloepus*), while facing a similar functional constraint: the support of the head in an inverted posture and locomotion. Instead of having seven cervical vertebrae like all other mammals, species of *Bradypus* increased the number of cervical vertebrae up to nine, whereas species of *Choloepus* decreased it down to five. This occurred alongside a change in the extension of the cervical musculature. Here, we compare the musculoskeletal anatomy of sloths' necks using network analysis. First, we model the neck as a network, where nodes represent bones and muscles, and links represent physical connections among nodes. This allows us to identify the anatomical modules that make up the neck in sloths using quantitative tools from network theory, and to compare them with those found in other mammals.

Our results show that sloths share a similar axial regionalization of the neck as other mammals, despite their variation in the number of cervical vertebrae. However, differences between both genera are driven by the arrangement and modularity of their pectoral muscles associated with the head-neck functional unit. Neck modularity of *Bradypus* resembles that of long-necked mammals due to its nearly complete lack of cervical and cranial attachments of the neck/shoulder muscles. The muscles of *Choloepus*, however, are so placed to offer the greatest possible dorsal and ventral support to the head and to the scapula. Thus, its neck anatomy and modularity is closer to the general pattern of other small mammals (i.e., pronounced head support, functional connection of head and forelimb). We conclude that the modular organization of the arrangement of bones and muscles in the neck of extant tree sloths represents two possible evolutionary solutions to mechanically support the head while inverted.

MOR-O-06

### 3D imaging of the tensile deformation of a mouse [*Mus musculus*] Achilles tendon enthesis

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Several tissues contribute to the functioning of the Achilles tendon insertion into the Calcaneus. At the transition to bone, tendon fibers pass through unmineralized and mineralized fibrocartilage. But the tendon tangentially approaches the Tuber calcanei well before the insertion. The contact is mediated by sesamoid fibrocartilage and periosteal cartilage – separated by a bursa. A tip of a fat pad protrudes into this bursa. This configuration is commonly known as the enthesis organ. However, there is no comprehensive explanation for the spatial distribution and mechanical functioning of the tissues of enthesis organs.

In order to investigate their mechanical behavior, a custom-made tensile testing apparatus was inserted into a synchrotron beamline. With a phase-contrast setup we recorded radiographs of enthesis deformation and 3D images of native entheses in relaxed and loaded condition. Additionally, defined loads were applied to native entheses, which were then in the loaded condition fixed in formalin. After staining, they were scanned in the synchrotron beamline with attenuation contrast.

The resulting radiographic image series and 3D reconstructions are the first step to approach the spatial distribution of deformation in tendon-bone transitions. As expected, the tendon is stretched considerably when a load is applied. But adjacent to the Tuber calcanei, it is flattened at the same time. Furthermore, slight deformations of the mineralized fibrocartilage were detected. When the strain is maintained, the tendon shows relaxation behavior in form of a slow decrease in thickness. These findings support the interpretation of entheses as a transition with graded material properties and will be the basis for more accurate mechanical models.

MOR-O-07

**Super-sized crustacean larvae in oceans of today and in the past – the forgotten part of the plankton?**

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The term plankton refers to the entirety of organisms that live in the water column and are not capable of locomotion against the major currents. Hence these organisms do not swim in the strict sense, but float passively. Plankton has been recognised as an important part of the oceanic food web. Research on plankton is therefore of prime importance for understanding the vast oceanic ecosystems. There are different fractions of plankton, related to size, which have gained different level of attention by researchers. A fraction that seems often largely ignored is macroplankton. An important part of the macroplankton is made up of crustacean larvae. While the term 'larva' seems often coupled to small size, and hence many larvae are part of the mesoplankton, several representatives of malacostracan crustaceans have evolved large larval forms reaching well into the centimetre range. Some of these forms occur in large abundances. Still many aspects of the biology of these organisms remain obscured. Research on crustacean larvae has significantly benefitted from observations of laboratory breedings. Yet, larval forms in such cultures tend to metamorphose early during larval development, leading to shorter larval phases and smaller larval sizes than observed in the field. I present various examples from modern-day and fossil finds that provide unexpected observations of large malacostracan larvae. With these findings I aim at demonstrating that: 1) large crustacean larvae are morphologically diverse and represent an important part of the oceanic food web; 2) large crustacean larvae occur also in systematic groups that have so far not been known for this phenomenon; 3) these forms perform complex behavioral traits that are at best unexpected for marine crustacean larvae; 4) different types of large crustacean larvae have evolved at least 150 million years ago and hence do not only play an important role in modern day ecosystems, but have already done so back in the Jurassic.

MOR-O-08

**Living in caves: A comparative morphological analysis of the central nervous system in Pinelema spiders**Philip O.M. Steinhoff<sup>1</sup>; Andy Sombke<sup>2</sup>; Shuqiang Li<sup>3</sup>; Prof.'in Gabriele Uhl<sup>1</sup>

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Sensory deprivation can cause changes in receiving and processing structures deprived from sensory input. Prime examples for natural selection leading to the reduction or loss of sensory structures are blind cave-living organisms. The spider genus *Pinelema* comprises five species (eyeless or eye possessing) that all live in completely dark caves in southern China. As a starting point for a comparative analysis, we explored the anatomy of the brains of the six-eyed *Pinelema bailongensis* Wang & Li 2012, and the eyeless *Pinelema huobaensis* Wang & Li 2016, by means of paraffin-histology, microCT analysis and whole-mount immunolabelling. We compare the brain structures of the *Pinelema* species to that of salticid and ctenid spiders.

As typical for spiders, the synganglion of *P. bailongensis* and *P. huobaensis* is a highly fused, clearly demarcated mass within the prosoma. The ventral nerve cord (VNC), the pedipalpal neuromere (tritocerebrum) and the cheliceral neuromere (deutocerebrum) are structured similar to what is known from salticid and ctenid spiders. The protocerebrum is located dorsally of the deutocerebrum and comprises the arcuate body and the rather non-structured protocerebral neuropil. Visual neuropils and a mushroom body were not detected, but are clearly present in the syncerebrum of the salticid *Marpissa muscosa* and the wandering spider *Cupiennius salei*. Our data strongly suggest that ecological diversity has led to structural disparity in spider brains.

MOR-O-09

**The development of the nervous system in the bay barnacle (*Amphibalanus improvisus*) – the increasing importance of the peripheral nervous system**

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The most common representatives of the Cirripedia are the barnacles, which live predominantly on hard substrates. All adult cirripeds are sessile and their morphology, which bears scant resemblance to the bauplan of arthropods, is highly derived. Cirriped development involves two different kinds of larvae, the nauplius and the cypris. We suggest that two phases of metamorphosis occur, the first from the nauplius larva to the cypris larva and the second to the sessile adult.

To understand the process of differentiation from the nauplius larva to the sessile adult, we studied the cirripedian neurogenesis using immunohistochemical methods, confocal laser scanning microscopy and 3D reconstruction. Six nauplius larval stages show cerebral structures associated with nauplius eyes and frontal filaments, a developing ladder-like ventral nerve cord, and a peripheral nervous network. The cypris larva exhibits the most complex brain during development, with cerebral structures now associated with compound eyes. Due to a split in the dorsal head shield into a bivalved carapace, the peripheral nervous system encases the cypris laterally. In sessile adults, the protocerebrum takes on a commissure-like appearance associated with three separate nauplius eye cups. The anterior portion of the ventral nerve cord develops into a highly condensed neuropil innervated by the 4th and 5th intersegmental nerves. Both nerves are part of the peripheral nervous system, whose terminal cells extend into external setae and proceed to movable shell parts.

We suggest that the loss of the protocerebrum as a sensory integration unit is the consequence of the loss of its sensory input, while the anterior portion of the ventral nerve cord increases in importance in connection with the sessile lifestyle of adult barnacles. Additionally, we assume that the complex peripheral nervous system enables adult cirripeds to maintain contact with their environment sensorially, and mediates motor skills.

MOR-O-10

**From 2D to 3D: evaluating the limits to neuronal miniaturization in insects on ultrastructural level using 3D image information**

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Until now, most morphometric studies that have examined the limits to miniaturization in insect brains at an ultrastructural level have relied on two-dimensional data from thin-section electron micrographs imaged by transmission electron microscopy (TEM). To test their numerical validity in the third dimension, we reinvestigated previously proposed limits to miniaturization by examining a high-resolution 3D image stack (serial-section: ssTEM) of the optic neuropiles of the miniature parasitic wasp *Trichogramma brassicae* (Bezdenko, 1968). We investigated 3D volumes and their ratios and compared these with 2D profile areas of neuron cell bodies, their nuclei, and mitochondria, to examine the minimal limits for cell miniaturization as well as the minimal diameters of axons and their mitochondria in order to examine the functional, energetic demands of signal transfer in the tiniest axons. We show that incorporating the third dimension is critically important to avoid misinterpreting these quantities, and limits to the analysis of miniaturization from 2D data are discussed. We find that miniaturization within the insect nervous system extends beyond that previously reported and is already present in some cases in *Trichogramma brassicae*.

MOR-O-11

**Morphological diversity of mantis shrimps: ontogeny in focus**

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Mantis shrimps (Stomatopoda) are marine crustacean predators with a powerful raptorial appendage for hunting prey. They form an ingroup of Malacostraca with about 500 known species, occupying a broad range of marine habitats, ranging from 1500 m depth to the shore and coral reefs. Their ontogeny features several free-living larval stages, occupying pelagic habitats in contrast to their benthic adults. Most of these larvae already show the prominent raptorial appendage, arising from the 7th post-ocular segment, however being slightly different in shape to that of the adult stomatopods. Two principal adult forms are generally differentiated: “Smashers” possess a proximally bulged outer margin on their most distal appendage element (dactylus), which they use for a striking movement towards their prey, whereas “speakers” possess a (usually) spine-bearing dactylus with which they pierce their prey. In contrast to this, most larvae exhibit a spineless, more dagger- or scimitar-shaped dactylus. To quantify this morphological diversity, a morphospace approach was applied. A morphospace is a multi-dimensional and unscaled graphical representation of the variability of a specific shape within a certain group. This shape may refer to an entire organism or a specific structure of that organism. This graphical representation allows a comparison of morphological diversity of structures not only between different adult forms, but also between different ontogenetic stages. In addition to the morphological diversity of the dactylus, we also investigated those of other structures of stomatopods for which significant morphological differences have been observed. Our results indicate an unexpectedly large morphological diversity of larval forms. These findings highlight the impact of larvae for their ecosystem.

MOR-O-12

**Morphological disparity and developmental shape changes in domesticated horses**

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The morphological disparity of domesticated horses provides a rich subject to investigate the developmental bases of shape variation and its limitations within a species. Additionally, it offers a worthwhile comparison with evolutionary patterns at the macroevolutionary scale. A variable that can greatly affect shape variation in selective breeding is size, but because morphological changes coupled with size in horse domestication remain unclear, we aimed to investigate the influence of domestication on disparity. We here present the morphological disparity of domesticated horses. We examined over 180 skulls across 35 domesticated horse breeds using three-dimensional geometric morphometrics. Including horse breeds reaching from the smallest (Falabella) to the largest breed (Shire) enabled us to determine the whole breadth of shape variation. Skull shape morphotypes, as defined by coldblood, warmblood, fullblood, and pony, vary in compliance with recent phylogenetic studies, from broad and angular shape with a convex nasal bone in coldblood horses to narrow and round shape with a concave nasal bone in fullblood horses. Furthermore, we document for the first time the skull shape of the smallest horse breed, the Falabella, and quantify how some modules of the skull appear neomorphic, although size alone does not result in a significant deviation from the morphospace otherwise occupied by adult horses. Results further show that skull shape changes during development differ among breeds with a trend to more convergent skull shape towards adult stages.

MOR-O-13

**Body dynamics and gait choice in poly-pedal animals.**

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Examinations of gaits and gait-changes have been the focus of movement physiology since the very beginning of the field. While most studies focussed on bipedal and quadrupedal designs, many small species have more than four pairs of legs. Nevertheless, examinations of gait-changes in poly-pedal organisms, such as arthropods, are rare. Except for the well-known change from slow feedback controlled walking to a fast, feedforward controlled running gait, no other changes are known or are deemed to be of low significance. However, recent studies in fast moving spiders, mites and cockroaches have also revealed changed leg coordination patterns and centre of mass dynamics for the transition from intermediate to high running speeds. These changes are similar to gait transitions as found in quadrupedal vertebrates. Accordingly, the present new numerical model aims to extend available theory to poly-pedal designs and examines how the number of active walking legs affects body dynamics when combined with changing duty factors and phase relations. The study shows that higher numbers of leg pairs can prevent effective use of energy saving mechanisms and entailed advantages as significantly higher degrees of leg synchronisation are required. The model also shows that with higher numbers of leg pairs gait changes are less apparent and tend to be overlooked since small changes in the leg coordination pattern have a much higher impact onto the COM dynamics than in locomotor systems with fewer legs. In this way, the model reveals coordinative constraints for specific gaits facilitating locomotion assessment of animals with two to many pairs of walking legs.

MOR-O-14

**Adaptive convergence in the femoral shape of sciuriform rodents depends on locomotor behavior**

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Sciuriform rodents are a monophyletic group of approximately 300 extant species whose most recent common ancestor was likely arboreal. During the evolutionary diversification of this clade, fossoriality evolved three times independently and arboreality evolved once anew. We asked whether convergence in these locomotor behaviors is reflected in convergence of postcranial skeletal morphology. We used geometric morphometrics to investigate the 3D femoral shape of 142 species covering taxa with convergence in arboreal and fossorial locomotor behavior. We conducted an adaptive model comparison to estimate the most likely number of convergent shape optima for both locomotor behaviors. We generated 3D-surface-models of the non-convergent shape optima to compare differences in functionally relevant substructures. The most likely adaptive model accounts for only one shape optimum for the two arboreal taxa, but three shape optima for the three fossorial taxa. The fossorial shape optima differed in bone robustness and the relative position of the third trochanter. The latter is a muscle attachment site for the superficial gluteus muscle, which is assumed to be involved in hind limb retraction. We hypothesize that the primary role of the hind limb during arboreal locomotion (generation of powerful propulsion when climbing against gravity and jumping from tree to tree) imposes strong functional constraints on the femoral shape, limiting the diversity of morphological solutions. On the other hand, the hind limb might be less constrained in its functional role during digging behavior. This might have allowed taxa that independently acquired fossoriality to evolve different tasks for the hind limb during digging behavior, which in turn might be reflected in different femoral shape optima. Comparative studies on the digging behavior and their potentially differing biomechanical constraints on the femoral shape are needed to test this hypothesis.

MOR-O-15

**Serial and special: comparison of podomeres and muscles in tactile vs walking legs of whip scorpions (Arachnida, Uropygi)**

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Thelyphonidae are one of a small number of taxa within the Arachnida that do not walk on four pairs of post-pedipalpal legs. The second, third and fourth pair are used for locomotion, while the first pair has evolved into a pair of elongated and antenniform sensory appendages extensively covered with sensilla. These tactile legs display about six additional tarsomeres, and the terminal claw-like apotele is reduced. A typical (“knee-like”) patella as found in the posterior three pairs of legs, and in all four pairs of legs of the closely related Amblypygi and Araneae, is apparently absent. This has caused some authors to assume that the patella has fused with the tibia to form a so-called “patellotibia”. However, this hypothesis is controversial, and various authors have used a labelling of the podomeres of the antenniform pair of legs including a “patella”. To shed more light on the matter, we analyse here the morphology of the four pairs of post-pedipalpal legs in *Mastigoproctus giganteus*. Our study uses micro-computed tomography ( $\mu$ CT)-based 3D reconstructions of the intrinsic muscles and cuticle components of the podomeres to describe and compare these morphological structures. The evolutionary changes undergone by the podomeres and the muscular system in the antenniform legs of Thelyphonidae are discussed and the homologous identity between podomeres is discussed on the basis of the hypothesis of serial homology. Our findings imply a refutation of the patellotibia hypothesis.

MOR-O-16

**Morphology, microstructure and evolution of tarsal attachment pads in Phasmatodea (Hexapoda)**Thies Büscher<sup>1</sup>; Constanze Grohmann<sup>1</sup>; Sven Bradler<sup>2</sup>; Thomas Buckley<sup>3</sup>; Stanislav Gorb<sup>1</sup>

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Stick and leaf insects (Phasmatodea) use two types of attachment pads on their tarsi, in order to adhere to different substrates, the euplantulae and the arolium. Both structures generate the required attachment through adaptation to the surface profile. The euplantulae are known to possess different adhesive microstructures (AMS). The aim of our study was to describe the AMS of a variety of phasmid species and to discuss correlations of these structures and the phylogeny as well as the ecology of the species. We examined the diversity of these AMS in 116 species using scanning electron microscopy (SEM). The species were chosen from all described subfamilies and represent all oviposition modes and the whole biogeographical distribution of phasmids. Twelve different types of AMS were found and the correlation of these features and the phylogeny as well as the ecology of the species is discussed. In order to reconstruct evolution of the euplantular structures we inferred the phylogeny of stick and leaf insects based on two nuclear (28S rDNA and histone 3) and two mitochondrial (CO I and CO II) genes of 55 species that represent all major lineages within Phasmatodea and mapped the morphological data onto the phylogenetic tree. The distribution of the types of AMS within monophyletic lineages of Phasmatodea suggests multiple independent origins of the same types, or frequent reversals. The realisation of a certain type of AMS appears to be strongly associated with the ecomorph of the species. Species with smooth euplantular surfaces are primarily dwelling on trees, whilst structured surfaces with conical outgrowths are more frequently found in species dwelling on the ground, regardless of the phylogenetic position of the species. Diverse monophyletic groups include similar combinations of AMS in dependence of the ecological niche preferred by the species. Ecology and AMS are discussed under consideration of the presumed functional properties of the surface structure.

MOR-O-17

**Functional morphology of the skeletomuscular ovipositor system in parasitoid hymenopterans**Benjamin Eggs<sup>1</sup>; Annette I. Birkhold<sup>2</sup>; Oliver Röhrle<sup>2</sup>; Oliver Betz<sup>1</sup>

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In order to reach their hosts and permit greater control over egg placement, many parasitoid hymenopterans are able to actively bend their terebra in various directions, although intrinsic musculature is lacking. Modifications of the ovipositor might have facilitated the evolution of joint-free terebra movements, which in turn facilitated the acquisition of new hosts, and potentially have been a key factor in the evolution of the parasitoid life history strategy and enormous diversification of parasitoid wasps. Despite many comparative studies on the hymenopteran terebra, little is known about the mode of function of the skeletomuscular ovipositor system and the mechanisms behind the terebra kinematics. Therefore, we have described the hymenopteran ovipositor of *Venturia canescens* (Ichneumonidae) and *Lariophagus distinguendus* (Pteromalidae), including all inherent sclerites and muscles, and determined its mode of function. The ovipositor consists of the female T9, two pairs of valvifers and three pairs of valvulae derived from the 8th and 9th abdominal segments. The basally situated valvifers accommodate the operating muscles (a set of six muscles in *V. canescens*). The terebra consists of the paired 1st and the 2nd valvulae that are interlocked via aulax and rhachis (olistheter system), allowing the three valvulae to independently slide relative to one another in longitudinal direction. The anterior and posterior 2nd valvifer-2nd valvulae muscles flex the terebra from the resting to the active position. The modified dorsal and ventral T9-2nd valvifer muscles antagonistically act indirectly on the 1st valvifer, which acts as a lever arm and transfers the movements to the 1st valvulae. The 1st valvifer-genital membrane muscle and the posterior T9-2nd valvifer muscle potentially act as tensor muscles. The terebra movements are based on modifications of the 2nd valvula (i.e. a partial longitudinal cleft) and the olistheter elements, and on the distribution of resilin.

MOR-O-18

**Terminal legs of Chilopoda (Myriapoda) - A prime example of morphological disparity and functional diversity**

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The arthropodium can be regarded as one, if not the eponymous key innovation of arthropods. In taking on a sheer plethora of functions, arthropodia are one of the most versatile, most specialized and hence, one of the most widely modified features known in arthropods. This specialization is particularly evident considering the appendages of the head, commonly and in many cases independently transformed into a series of mouthparts. Comparable modifications comprise the convergent transformation of the anterior-most thoracic arthropodia which brought forth additional mouthparts. Besides the head with its cephalic sensory organs, it is the posterior end of the centipedes' body that shows a considerable disparity and diversity of appendages, namely the terminal legs. In all centipedes this last pair of legs is particularly unique as it is of unrivalled heterogeneity. Moreover, it provides an excellent opportunity to explore diverse pathways of leg transformations. Some examples are elongation and annulation in combination with an augmentation with sensory structures indicating a functional shift towards a sensory appendage. Additionally, thickening, widening and reinforcement with a multitude of cuticular protuberances and glandular systems suggest a role in both attack as well as defence. Sexual dimorphic characteristics suggest that terminal legs play a pivotal role in intraspecific communication, mate finding and courtship behaviour. We show that these transformations are by no means restricted to its outer morphology, but that this particular centipede character was subjected to a whole cascade of adaptations in terms of neuroanatomy and behavioral adaptations. This study is funded by DFG SO 1289/1.

MOR-O-19

**Head Biomechanics of a Springtail**Peter T. Ruehr<sup>1</sup>; Michael J. Fagan<sup>2</sup>; Bernhard Misof<sup>1</sup>; Alexander Blanke<sup>3</sup>1 Zoologisches Forschungsmuseum Alexander Koenig; 2 University of Hull; 3  
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Hexapoda evolved a plethora of mouthpart shapes and feeding patterns. A highly complex mouthpart system is found in springtails (Collembola) where the entognathous mandibles move with multiple degrees of freedom which results in a combination of rotation, protraction/retraction and adduction/abduction during food intake. Collembolan mouthpart movement patterns might have evolved together with a suite of head ridges and endoskeletal elements that mechanically stabilize the head capsule during biting. In order to identify such structures and explore their functional role in the collembolan head under load, we used the finite element method, an in silico technique to model the strain distribution of objects under defined loads. With sensitivity studies using different mechanical setups regarding material properties and configuration of the endoskeleton we show that endoskeletal elements play an important role for the strain distribution over the springtail head capsule during biting. Through the mechanical support by the endoskeleton, lateral, comparatively thin areas of the head capsule are relieved of high strain burdens. The endoskeleton furthermore directs strains into a thickened clypeal sclerite that spans between the genal areas of the head. The results show that this sclerite and the endoskeletal elements of springtails fulfil the same functions like the epistomal ridge and the tentorium in winged insects. Thus, a suite of non-homologous head ridges evolved to fulfil the same functions in springtails and winged insects probably in response to the similar functional requirements.

MOR-P-01

**Cell division in adult water bears (Tardigrada)**

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We are presenting results from comparing structural properties of protein-coding genes using a new tool (COGNATE) across genomes to illustrate differences and commonalities between automated and manually curated gene annotations. This is a first step in identifying the potential and the limits of the two methods in the generation and interpretation of gene structure data. We show that the choice of prediction algorithm can have a more pronounced influence on the results than manual curation. Additionally, we underline that the consideration of taxonomic lineage and assembly information can help interpreting results.

MOR-P-02

### The circulatory system of the velvet worm *Euperipatoides rowelli* (Onychophora, Peripatopsidae)

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The organization of the blood circulatory system in Onychophora – one of the closest arthropod relatives – has hardly been studied. Hence, the composition of the circulatory system in the last common ancestor of Onychophora and Arthropoda is unknown. We therefore performed 3D reconstructions based on serial semi-thin sectioning and synchrotron radiation-based X-ray micro-computer tomography (SR- $\mu$ CT), in conjunction with scanning electron microscopy, to study the circulatory system in the onychophoran *Euperipatoides rowelli*. Our study revealed two segmentally repeated channel types that direct the hemolymph into the pericardial sinus surrounding the ostiated heart. The segmental ostia of the heart are located dorso-laterally and orientated diagonally. The heart opens into the anterior supracerebral sinus, the organization of which proved to be more complex than previously thought, as it shows additional medial and antero-ventral extensions. Our findings suggest that the last common ancestor of Onychophora and Arthropoda possessed an elaborate, segmentally organized blood circulatory system, which was modified in different arthropod lineages. Nevertheless, comparative studies of additional species are still required in order to identify homologous elements between representatives of the major panarthropod groups.

MOR-P-03

### Post-embryonic development in tarantulan spiders – less direct than assumed?

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Spiders (Araneae) display a direct mode of development, as generally assumed for chelicerates. This means that in the post-embryonic development so-called prelarval and larval stages are gradually followed by a varying number of so-called nymphal stages and eventually the adult. The nymphal stages are usually thought to fully resemble the adult, except for their size. Therefore, previous research focused exclusively on the larval and the adult stages, largely neglecting the nymphal stages. However, recent investigations on mesothelan spiders (sister group to all remaining araneans = Opisthothelae) pointed to previously unexpected morphological changes during the nymphal phase. Therefore, similar investigations on the development of different characters during this phase in other araneans may hold new insights about the evolution of spider morphology. We focused our research on mygalomorph spiders with their best known representatives, the tarantulas (Theraphosidae), as sister group to all remaining opisthotelatan spiders (= Araneomorphae). We analyzed the development of chelicerae, walking legs, and prosomal sternal plate with respect to size proportions and changes in shape. Measurements were taken on shed skins (exuviae) and carcasses preserved in alcohol of three different species of tarantulas, *Heteroscodra maculata* Pocock, 1899, *Poecilotheria metallica* Pocock, 1899 and *Acanthoscurria geniculata* (Koch, 1841). We present here first results of this study, revealing a possible event of heterochrony and thus presumably supporting the possibility that the ground pattern of spider morphology might need modification.

MOR-P-04

**These legs were NOT made for walking**

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Several taxa within Arachnida are characterized by slender, elongated post-pedipalpal appendages. These antenniform legs are not used for locomotion, as the following three pairs of walking legs are, but serve instead for tactile orientation, chemosensory perception and even intraspecific communication (e.g. courtship display).

According to both morphological and molecular phylogenetic hypotheses, antenniform legs have evolved at least three times independently among Arachnida. Antenniform legs share specific features which set them apart from walking legs: they are distinctly elongated, they are smaller in diameter, the distal podomeres are annulated and they are highly mobile. Assuming that the last common ancestor of Arachnida possessed four pairs of walking legs, it is hypothesized that antenniform legs evolved from walking leg-like appendages, and that the evolution process involved a series of cuticular and muscular transformations. This is the starting point of our project. In a morphological survey, antenniform legs are compared to 1) walking legs within the same taxon and 2) to the antenniform legs in other taxa. The convergent evolution of antenniform legs may provide insights into constructional constraints in the evolution of tactile appendages in Arthropoda.

We present a morphological comparison between the walking legs and the antenniform leg in Amblypygi. On the basis of detailed micro-computed tomography scans, 3D-reconstructions are created. General aspects of the muscular anatomy of amblypygid antenniform legs are visualized here for the first time.

MOR-P-05

**Bending the sting: joint-free movement principles in the parasitoid wasp *Leptopilina heterotoma***

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Despite the lack of joints or intrinsic musculature in the terebra (ovipositor shaft), many parasitoid wasps such as *Leptopilina heterotoma* (THOMSON, 1862) (Hymenoptera: Figitidae) are able to actively bend their highly flexible terebra in various directions in order to find or reach their potential hosts. The terebra consists of two pairs of valvulae, while the second pair is fused to a singular unit, the first valvulae are interacting over the rail-like olistheter system with the second ones. Several potential movement principles can be involved in the joint-free kinematics of elongated rod-shaped structures. (1) Interlocking mechanisms of elongated elements, which can move against each other, permit some bending induced by differences between the applied longitudinal forces on these elements. (2) Offset steering due to an asymmetrical construction of the tip causes a passive bending movement induced by the mechanical resistance of the medium. To observe the movements of the terebra, high speed video recordings of female *L. heterotoma* were obtained during their host searching behaviour. To examine the material composition of the terebra, pictures of the ovipositor were taken with a fluorescence microscope, taking advantage of different autofluorescent properties of softer and sclerotized parts of the insect cuticle. Ovipositors were investigated with scanning electron microscopy to reveal potential interlocking structures. Additionally, a 3D model of the overall structure will be reconstructed from semithin sectioning. As the bending of the terebra could be observed outside the substrate, the dependence on interactions with the medium for the bending process can be excluded. In the terebra, a heavily sclerotized longitudinal line correlates with the olistheter system, whereas the rest of the body consists of softer cuticula, which may show elastic properties. Distinct interlocking structures between the valvulae were not found.

MOR-P-06

### Tuning of grasshopper songs to road noise: is the morphology of the stridulatory apparatus involved?

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Anthropogenic noise is increasingly affecting natural populations and has the potential to interfere with sexual communication in species that rely on acoustic ornaments. We showed in previous studies that males of the acridid grasshopper *Chorthippus biguttulus* from roadside habitats produce courtship signals with elevated frequency components and higher syllable-to-pause ratios compared to conspecifics from non-roadside habitats. In addition, we also showed that part of these effects can be attributed to developmental phenotypic plasticity triggered by exposure of late larval stages to experimental noise. These results are compatible with the idea that grasshoppers can escape signal masking through road noise by modifying specific song traits. However, the traits underlying the documented differences in song performance are unknown.

Here we test the hypothesis that, on a proximate level of explanation, the differential song performance is caused by differences in morphology. Acridid grasshoppers produce courtship songs by rubbing their hindlegs against their hindwings. We therefore analysed a number of selected hindleg and forewing traits known to be involved in song production for specimens used in previous studies, for specimens collected from roadside versus non-roadside populations. We found that local frequency maximum was negatively related to pronotum length and to five wing traits. Syllable to pause ratio was positively related to pronotum length and to one hindleg traits. However, none of the morphological traits under study differed between specimens collected from roadside versus non-roadside habitats. We conclude that other, possibly neurophysiological traits underlie the differential song performance of grasshoppers inhabiting roadside versus non-roadside habitats.

MOR-P-07

### Characters of the nervous system support sipunculid and amphinomid affinity

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Recent molecular studies propose a sister group relationship between Sipuncula and Amphinomida which together are part of the basal radiation of Annelida. This contradicts the traditional view, as Sipuncula was considered a separate taxon closely related to Annelida. Though their annelid affinities are well supported, sipunculid morphology makes it hard to place them within annelids. From a morphological point of view the current molecular results seem contra-intuitive since sipunculids are superficially unsegmented, sessile and do not possess chaetae and body appendages. In contrast amphinomids are clearly segmented, vagile, possess body appendages and chaetae. The segmentation is also expressed in the anatomy of the central nervous system (cns). Traditionally the cns of Annelida is supposed to be composed of a dorsal brain, circumesophageal connectives and segmentally arranged ganglia in the ventral nervous system as found in Amphinomida. The anterior part of the cns of Sipuncula resembles that anatomy, but in contrast to Amphinomida only one ventral medullary cord without any ganglia is present. However, a recent survey on the anatomy of the ventral nervous system of Annelida contradicts the traditional view and shows that a single ventral medullary cord is most likely plesiomorphic for annelids. To evaluate whether there are any characters in the nervous system of Amphinomida and Sipuncula which support their close relationship, we studied the cns of *Phascolosoma granulatum* and *Eurythoe complanata* and performed serial histological (5µm) and semi thin sections (1µm). Additionally we use immunohistology to describe the fine structure of the cns. Our results imply that the sister group relationship between Sipuncula and Amphinomida predicted by molecular analyses is supported by characters of the cns such as the anatomy of the brain, the innervation patterns of the nuchal organs, as well as the location of the cns in body integument.

MOR-P-08

### The diversity of body organisation in mites: first steps towards a quantitative approach

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Mites (Acari) are a very species-rich ingroup of Arachnida (Euchelicerata), including other well known groups such as spiders or scorpions. Some estimations reach up to one million, mostly unidentified, extant species. These species occupy very different habitats, from soil to water, also including diverse parasitic life styles. Presumably coupled to these life styles, different morphological adaptations evolved. Despite the large morphological diversity, the body of all mites shows a basic common organisation (best visible ventrally), dividing it into different functional units (tagmata) along the anterior-posterior axis. Besides this, several additional furrows and systems of sclerotic plates are present, which further partition the body. The aim of this study was to comprehend this large morphological variation and to attempt to quantify it. Previous approaches to apprehend the morphological diversity of Acari were concentrating on landmarks of distinct structures such as the attachment points of setae or details on the chelicerae, but not on the major body organization. Quantitative approaches have so far been restricted to rather closely related species. In order to achieve a broader insight, we investigated different species of Acari from a soil sample from Munich as well as certain exemplary species with an apparently rather extreme body organisation and different habitats as reference points. The documentation was performed with autofluorescence microscopy under different wavelengths. The major body features were measured and plotted to identify a possible correlation between the body organization and the lifestyle and/or the phylogenetic relationship of the investigated mites. We here present results of this study which may help to improve our understanding of the large diversity of mites.

MOR-P-09

### The terminal legs in Geophilomorpha (Myriapoda, Chilopoda) – morphological evaluation of transformed walking legs

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The last pair of legs in Chilopoda, the terminal legs, are particularly unique as no other leg in centipedes is of a comparable functional, morphological and behavioral heterogeneity. In most adult centipede species they are the largest legs, easily noticeable by their shape and by the way they are held as well as moved in relation to regular walking legs. They are never or only rarely used for locomotion but hold a variety of different functions. One particular aspect of terminal leg transformations are sexually dimorphic characteristics found in various representatives of centipedes, in particular in Geophilomorpha. For instance, only males of several genera possess prominently thickened and hirsute terminal legs featuring an intensive coverage with trichomes and sensilla at the ventral side of several podomeres. Although available experimental evidence is as yet circumstantial, terminal legs of Geophilomorpha play a role in at least certain aspects of courtship behavior, indicating the presence of mating associated sensory organs. In a broad methodological approach, histology, immunohistochemistry, scanning electron microscopy as well as microCT analysis were applied in order to explore characteristics of sexual dimorphic terminal legs in terms of leg morphology, diversity of sensory organs, and organization of associated processing centers in the nervous system in comparison with walking legs. To that end, we aim at unraveling sex-specific differences accompanying the evolutionary transformation of trunk appendages within Geophilomorpha in particular and centipedes in general.

MOR-P-10

**Comparative morphology of the stylets and the head of hematophagous Triatominae (Hemiptera: Reduviidae)**

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The kissing bugs belonging to the subfamily of the Triatominae (Hemiptera: Reduviidae) are probably best known for their role as bloodsucking vectors of the Chagas disease. Therefore, most studies concerning the Triatominae also revolve about this general subject. However, the focus of research has extended in the last few years. The remarkable manner in which the animals are able to move their heavily derived, rod-like maxillae using joint-free bending movements for the efficient localization of blood vessels has attracted the attention of biomimetic researchers. The maxillae of the animals are tightly interlocked and show a tongue-and-groove system on their inside. Their apices are strongly asymmetrical and the most distal part of the left maxilla can be seen to splay outwards just prior to the blood meal. The apices of both the maxillae are accompanied by a prominent abutment, whereby the left one shows a conspicuous 'joint'-like section that might facilitate the splaying. Since the maxillae are capable of alternating longitudinal movements and the abutments are most likely mechanical obstacles for each other during these sliding movements, we hypothesize that the collision of these two abutments and the resulting powers of resistance play the key role in the realization of the joint-free movements as well as in the splaying of the spine.

MOR-P-11

**Ultrastructure and possible role of the epidermal gland system of *Tetranychroderma suecicum* Boaden, 1960 (Gastrotricha: Macrotrichida)**

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Marine Gastrotricha are microscopic, interstitial protostomes that exhibit several adaptations to their habitat, i.e. the interstice between sand grains. Among those are differentiations of the epidermis like cushioning cells, a strengthened and often sculptured cuticle, or adhesive glands that facilitate a sticking to the substrate. The epidermis of most species of the Macrotrichida furthermore contains conspicuous glandular structures, the epidermal glands. As yet, there is no coherent hypothesis on the functional role of this organ system and there is only a single transmission electron microscopic (TEM) investigation of epidermal glands of *Turbanella cornuta* plus scattered data of few further species. In the present study, we investigated the epidermal glands of the species *Tetranychroderma suecicum* by means of serial sectioning and TEM as well as scanning electron microscopy (SEM). Aligned images were three-dimensionally analysed and reconstructed. *T. suecicum* has up to 50 pairwise arranged epidermal glands. Each gland consists of one huge glandulocyte with a basal nucleus and an apical 'chimney' carrying the cell pore. The cell is loaded with granular vesicles that are embedded within an electron-dense cytoplasm. This density probably results from fatty acids that are transferred to the glandulocyte by adjacent epidermal cells via exo- and endocytosis. Inside the vesicles, fatty acids are possibly transformed to the secretion that is released through the cell pore. Each gland is associated with a ciliary sensory cell. Different roles of the epidermal glands are discussed. Since no traces of mucus-like substances were observed on the specimens investigated by SEM, we suppose a water-soluble nature of the secretion. Hence, it could either represent a pheromone for interspecific communication or an allomone that is, for instance, used as a repellent against predators such as flatworms. These hypotheses shall be tested subsequently with experimental setups.

MOR-P-12

**Functional morphology and tagmatisation in a spirostreptid giant millipede**

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The organisation of a body into distinct functional units (tagmata) is often assumed to be one of the major factors of evolutionary success in different animal groups, resulting in large radiation events. In arthropods, different groups possess a rather distinct body organisation (tagmatisation), as exemplified by malacostracan crustaceans or insects. Other arthropod groups appear to have a less tagmatised body, with a distinct head but a not further differentiated trunk region. One of this groups is Diplopoda (millipedes). Here we present new observations on the tagmatisation of derived diplopods, more precisely spirostreptid giant millipedes (Juliformia). Details include different aspects of tergite and sternite morphology as well as the functional morphology and insertion of the appendages. Structures of the specimens were documented in situ using macrophotography under cross-polarised light. Further details were revealed by stepwise dissection and repetitive documentation. In addition to sclerotised structures also aspects of the soft-part anatomy were documented, for example, position of major muscles. Our results partly support results of previous studies on the morphology of these animals. Some of our observations draw earlier interpretations into question. The morphology of the anterior trunk segments is significantly different from the further posterior ones concerning their sternite and tergite morphology or the insertion of the appendages. These aspects indicate a certain degree of tagmatisation in the trunk in diplopod myriapods, though myriapods are often used as a prime example for an untagmatised trunk. Understanding the evolutionary success of different arthropods, which is often attributed to a specific tagmatisation, a clear view of how the body is indeed organised is of prime importance. Detailed morphological studies in further representatives of Diplopoda are planned for these aspects.

MOR-P-13

**Corrugation alters aerodynamic performance in flapping insect wings**Henja-Niniane Wehmann<sup>1</sup>; Thomas Engels<sup>2</sup>; Kai Schneider<sup>3</sup>; Prof.'in Marie Far-  
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Insect wings are flexible, corrugated, distinct three-dimensional structures. Wing veins stabilize the wing surface and often serve as shields for the axons of wing strain receptors. Thin membranes interconnect wing veins and largely function as aerodynamic surfaces. The complex compound structure of insect wings may result from different constraints during wing development, but also from constraints on propulsion such as the requirements for wing flexing during inertial and aerodynamic loading. It has been shown, for example, that elasticity helps to avoid structural damage to insect wings and may also increase lift in robotic wing models. While the 3-dimensional wing structure increases wing stiffness, its potential benefit for aerodynamic performance in flapping flight is still under debate. We approached this question, estimating the 3-dimensional wing structure of fly wings in *Calliphora* using x-ray tomography with high spatial resolution ( $\sim 10.6 \mu\text{m}$ ), and simulating the aerodynamic consequences of wing corrugation using advanced computational fluid dynamics. The simulation is based upon previously measured wing kinematics (horizontal stroke plane, 150 Hz flapping frequency,  $20^\circ$  angle of attack during mid-upstroke and  $40^\circ$  during mid-downstroke) and assuming 1.0 m/s forward flight. By comparing instantaneous flight forces and power requirements between rigid models of flat surfaces and corrugated wings, we demonstrate the aerodynamic and energetic consequences of complex wing geometries during flight of the blow fly at various flight conditions. This work is supported by the ANR-DFG research grant „Aerodynamics of Insect Flight In Turbulent Flow“. More information can be found under <https://www.tierphysiologie.uni-rostock.de>.

MOR-P-14

**Morphological adaptations on owl wings: a reality check**Hermann Wagner<sup>1</sup>; Paolo Piedrahita<sup>2</sup>

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Owls are well known for their silent flight. The silent flight is based on several specializations on the flight feathers and wings of these birds. Amongst them are a serrated leading edge of the wing, a soft, velvet-like dorsal wing surface and a fringed trailing edge. These specializations have been well documented especially in the barn owl.

The documentations available so far were typically based on material from birds living in captivity. It was unclear so far, how hunting in the wild would affect these specializations.

We set out to examine the morphology of flight feathers and wings in wild barn owls on the island Santa Cruz (Galapagos, Ecuador). On this island barn owls live in different vegetation zones. We studied behavior specifically in one of these zones, the so-called agricultural zone. We caught birds, did a short clinical examination and photographed the wing flight feathers and wings. The birds were in good condition and seemed to have eaten recently as judged by the pellets they had cast and the bloody beaks. We observed major morphological damage on wings and feathers. Specifically, the delicate serrations at the leading edge were often damaged. Moreover, many birds were molting flight feathers, missing the 10th primary feather, the feather with the serrations, on one side. In many cases, more than one flight feather was missing.

These data suggest that owls can hunt successfully in the dark, even without intact morphological adaptations. This may be interpreted in at least two different ways: either the adaptations are not necessary for successful hunting, which poses the questions why they then evolved at all: or the adaptations are so good that damage does not impair their function, which would shed light on fail-safe construction in biology. The latter point would in our view make the silent flight an either more attractive model in a biomimetic sense than held so far.

MOR-P-15

**A new method for morphology-based species identification in ciliates**

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Ciliates are cosmopolitans found in marine and freshwater systems world-wide. With about 3,500 species described and an estimated number of 30,000 actually existing species, it is obvious that they are important members of aquatic ecosystems. As the name suggests, characteristic for this group of protozoans is the presence of cilia on the body surface. Furthermore, the argyrom (i.e. the silverline-system) pattern is species specific. Additional traits are: the shapes of the nuclei, cortical kinetosomes and associated microtubules, body size and body form. Unfortunately, most of these traits are transparent and are therefore not visible under the light microscope or phase contrast, but have to be stained, in the classical method using silver-impregnation techniques. These are often laborious and time consuming. We here present a simplified method visualizing all species classification patterns. We apply immunocytochemistry staining the argyrom, kinetosomes, cilia, as well as the micro- and the macronucleus. The established protocol is a short and cost-effective method. Ciliate species can be analyzed with the help of epifluorescent microscopy and 3D reconstructions can be performed with confocal imaging. Using this protocol, we here describe three species. We verified our identification by using genetic markers. Due to their world-wide distribution and their central role in many aquatic ecosystems, a fast and cost-effective species identification system will be advantageous in many ciliate investigations.

MOR-P-16

**A comparative analysis of adult neurogenesis in malacostracan crustaceans**

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In recent years, it has become evident that adult neurogenesis is a more widely distributed phenomenon in vertebrates and invertebrates than previously recognized. The generation and integration of new neurons during adulthood persists in the olfactory system. In crustaceans, there are the so-called deutocerebral chemosensory lobes as first order processing area within the central olfactory pathway and the hemiellipsoid bodies as second order processing area. Another secondary processing area associated with the olfactory system is present in reptant decapods, the accessory lobes. In the last two decades, adult neurogenesis was only demonstrated in different representatives of reptant decapods such as crayfish, lobsters and crabs. While numerous studies are available that focus on the cellular mechanisms and regulation of the neurogenesis rate, investigations about the distribution and evolutionary aspects of adult neurogenesis within crustaceans are missing.

Using the thymidine analogon Bromodeoxyuridine (BrdU) that incorporates into the DNA of dividing cells combined with immunohistochemical detection and confocal laser-scanning microscopy we detected proliferating neuronal precursors in adult crustacean brains. To give an overview over the taxonomic distribution of adult neurogenesis, we investigated diverse representatives of malacostracan crustacean taxa such as Leptostraca (basal-branching malacostracans) and Peracarida but also basal-branching decapods as head-to-head records to reptant decapods. Our results suggest that adult neurogenesis is a common feature of the Malacostraca. However, some taxa seem to have lost the ability to proliferate new neurons during adulthood such as the Peracarida. In contrast, decapods have evolved a high disparity of adult neurogenesis. We suggest that the proliferative system in reptant decapods has undergone significant modification due to the emerging accessory lobe.

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MOR-P-17

**Sensory projections of pectines in the scorpion nervous system**

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While most arthropods utilize their antennae to perceive chemosensory input, Chelicerata evolved different organs for chemo-sensing. Pectines are specialized comb-like structures located on the ninth body segment, which are used to probe the substrate for chemo- and mechanosensory information. They are subdivided into smaller units, the so-called pegs. Afferents of these sensory appendages project into a distinct neuropil of the CNS, located behind the fourth walking leg neuropils. However, detailed neuroanatomical data concerning sensory projections are still missing. In this study, afferents of single pegs of *Mesobuthus eupeus* were analyzed by backfilling techniques, combined with immunohistological labeling of neuropilar regions. Staining of neuropil areas revealed the lobular organization of the primary posterior pectine neuropil and a second homogenously structured anterior neuropil. The latter extended anteriorly near the midline up to the level of the second walking leg neuromeres. Posterior and anterior neuropils were shown to be bilateral structures, receiving input from the respective ipsilateral pectine. The antibody staining also revealed a symmetry within one single primary pectine neuropil along the neuropil (not ganglion) midline, in horizontal sections. Sensory projections of each peg entered the posterior pectine neuropil on the ventral side and innervated distinct parts of the primary neuropil: Afferents of distal pegs projected into medial areas, whereas afferents of proximal pegs projected into lateral areas. After leaving the posterior pectine neuropil through a medially located tract, the axon bundles terminated in an anterior neuropil, with no distinct somatotopic distribution. The somatotopic organization of chemosensory afferents in the primary pectine neuropil suggests that the peg arrangement serves for differential perception of chemical gradients on the substrate, which might support orientation based on substrate-born signals.

MOR-P-18

### A crustacean invader's brain - the anatomy of the central nervous system in the Japanese skeleton shrimp *Caprella mutica* (Malacostraca, Amphipoda)

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The Japanese skeleton shrimp *Caprella mutica* Schurin 1935 is a representative of the Caprellidae (Malacostraca, Amphipoda) that has a high dispersal potential. From its discovery, it expanded its natural range from the shallow areas of the Sea of Japan to a tremendous amount of coastlines on both the northern and southern hemispheres within only a few decades and now has become an invasive species to European seas. Due to their high abundance and their global distribution in marine and freshwater bodies, amphipods constitute an important ecological part of aquatic habitats. Nevertheless, neuroanatomical studies are scarce in this taxon. We were the first to investigate the brain of *C. mutica* to give an overview of the general brain anatomy by the use of histological sections, immunohistochemistry and X-ray microtomography in combination with three-dimensional reconstruction.

The overall characteristics of the *Caprella mutica* brain correspond to that of other malacostracans. Differences to other amphipod brains could be found in the visual neuropils, the presence of a hemiellipsoid body and the deutocerebral chemosensory neuropils. Whilst the latter two structures were reported to be lacking in the brains of the amphipods *Niphargus puteanus* and *Orchestia cavimana* and the visual neuropils were reduced in these species, the brain of *Caprella mutica* shows a well-differentiated chemosensory lobe with distinct olfactory glomeruli. In addition, all three visual neuropils lamina, medulla and lobula could be identified as well as the hemiellipsoid body, although they are less pronounced as reported for many other amphipod species (e.g. *Parhyale hawaiiensis*).

MOR-P-19

### The nervous systems of onychophorans, tardigrades and arthropods shed light on panarthropod evolution

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The evolution of animal groups, such as arthropods, the most abundant and diverse animal group in the world, attracts the interest of many researchers. Nevertheless, understanding the origin and evolution of arthropods requires examining not only arthropods themselves but also their closest outgroups, the tardigrades (water bears) and onychophorans (velvet worms). Despite a recent rise of molecular techniques, the phylogenetic positions within panarthropods (onychophorans + tardigrades + arthropods) still remain unresolved, thus rendering this method alone as insufficient for clarifying the panarthropod topology. Therefore, examining morphological characters such as one of the most intriguing features of panarthropods — their nervous system — becomes inevitable for shedding light on the evolution of these animals. Therefore, we investigated the nervous system of both tardigrades and onychophorans by applying a range of different neuroanatomical and morphological techniques. Herein we present our recent findings on the nervous system in both animal groups in order to compare them not only with each other but also to put our results in context with what is recently known about arthropods. In particular, our comparative studies especially focus on the evolution of segmental ganglia, the segmental identity of brain regions and developmental perspectives. Furthermore, we summarise the current knowledge of the evolution of the nervous systems in panarthropods and finally we attempt to reconstruct the most likely scenario for these systems in the last common ancestors of arthropods and panarthropods.

MOR-P-20

**Comparative morphology and evolution of venom glands in Chilopoda**Carsten H.G. Müller<sup>1</sup>; Andy Sombke<sup>1</sup>; Hanne Thoen<sup>3</sup>; Eivind A.B. Undheim<sup>3</sup>

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Forcipules with venom glands are shared by all centipedes and are therefore considered the most important apomorphy defining them. Venom glands consist of two major components, (1) the more or less extended glandular sac, which releases secretion into (2) a strongly cuticularized duct at its distal tip projecting towards the tarsungulum where it opens through a subterminal pore. The glandular sac is surrounded by musculature and shows a modular composition. Each module represents an enormously stretched glandular unit and consists of at least one canal cell, one intermediary cell and two secretory cells of unequal size. One secretory cell is very small and contains typical secretory granules, hence called the granulated type-1 cell. In contrast, the other is very elongated and, along with adjoined ones, may even reach back to the trochanteroprefemur in some taxa. This non-granulated type-2 secretory cell surrounds a tubular reservoir filled with main portion of venom maturing while being mixed up with sc-1 secretion and moving up the partly cuticularized conducting canal established by the intermediary and canal cells. The cellular anatomy of venom gland modules and common duct system is similar across all five centipede subgroups. However, slight differences are also discernible on ultrastructural level which can be used for reconstructing the evolution of venom glands in Chilopoda. Being the morphology-focused branch of a comprehensive, multidisciplinary study on chilopod venom gland evolution, this contribution integrates data obtained by classic, invasive analytical methods, such as (immuno-)histochemistry and electron microscopy, and by non-invasive approaches like  $\mu$ -CT.

MOR-P-21

**Integrative morphological survey of *Xenotrichula intermedia* Remane, 1934 (Gastrotricha: Paucitubulatina): Implications for a pan-European species and a cosmopolitan 'X. intermedia species complex'**

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Previous morphological and molecular studies already indicated the presence of different entities that are all referred to as *Xenotrichula intermedia* Remane, 1934, a cosmopolitan, sand-dwelling intertidal gastrotrich. While investigations of the musculature using confocal microscopy (CLSM) have been used to morphologically distinguish geographically distant populations (=putative species), a detailed reconstruction of the myoanatomy based on CLSM data has never been performed. The only existing reconstruction (based on epifluorescence microscopy) displays differences to latest published CLSM data. Furthermore, ventral features have not been investigated in most of the recent studies, resulting in ambiguous species boundaries. In this study, we present a comprehensive investigation of morphological, meristic and morphometric features of a North Sea population of *X. intermedia*. In order to investigate the variability and boundaries of this species, we performed an integrative approach using CLSM, electron and light microscopy as well as computer-aided 3D reconstruction tools. While reconstructions of the musculature and ventral scale patterns show anatomical accordance to recently studied populations from the Mediterranean Sea, differences to other populations are observable, too. We conclude that European populations form a morphologically homogenous metapopulation and a distinct morphospecies. This European *X. intermedia* most likely belongs to a 'Xenotrichula intermedia species complex'. Further members of this complex are 'X. aff. intermedia' from the NW Atlantic, 'X. aff. intermedia' from the Persian Gulf, 'X. aff. intermedia' from the Indian Ocean, as well as the similar morphospecies *X. carolinensis* Ruppert, 1979. These species are rather uniform but distinguishable via morphometric, muscular or ventral features. Additionally, our results highlight the necessity to reconsider the terminology and homology of longitudinal muscles among the Paucitubulatina.

MOR-P-22

**Differences in morphometric and life history traits between two related scaly cricket species, with first data for the little-known *Paramogoplistes novaki* (Orthoptera: Mogoplistidae)**

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In a study performed in 2014 along the Krčić River in SE Croatia, altogether 142 scaly cricket specimens were collected, thereof 37 *Paramogoplistes novaki* and 105 *Mogoplistes brunneus*. Both species were found only in the karst habitat, *M. brunneus* along the entire flow and *P. novaki* exclusively in the lower reach. For the latter, this was the first record in Croatia since its description in 1888. In order to assess the reliability of diagnostic morphometric traits, a thorough comparison between *P. novaki* and *M. brunneus* was performed. Namely, the extent of variability of those traits was heretofore insufficiently known for both species. Total body length proved to be unreliable for identification, while commonly used pronotum length to width ratio was found to be reliable only in adult males. However, the shape and several morphometric traits of the subgenital plate, formerly overlooked as diagnostic traits, clearly separated the two species. Lesser variability of the morphometric traits between the sexes, along with several morphological cues, could point out to neotenic origin of *P. novaki*. Autumn-oriented activity period of *P. novaki* was much longer than the activity period of *M. brunneus*, and surface activity maxima of the two species exhibited clear temporal separation, possibly resulting from competition due to niche overlapping. Sex ratios were female-biased in both species, more strongly so in *M. brunneus*, which could be explained by the higher activity of females in the study area. By providing first substantial insight into morphometric variability and life history of these two little-known species, this study should encourage further research on European scaly crickets.

MOR-P-23

**Biomedisa: The Biomedical Image Segmentation App**

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X-ray microtomography (mCT) has established itself as a tool for the investigation of morphological questions. However, with the analysis of the data and the ever-increasing amount of data, we are constantly facing new boundaries. In particular, the segmentation of tomographic images remains one of the most challenging tasks in computer vision. It is important for phylogenetics, functional analysis and simulation. In many cases manual segmentation is still considered the “gold standard”. The web application Biomedisa (<https://biomedisa.de>) was developed as a semi-automatic tool for improving and accelerating the tedious manual segmentation of CT scans. Biomedisa can be used in addition to any segmentation tool like Amira, Fiji or ImageJ. Its segmentation process is based on a highly scalable diffusion method, which is free of hyper-parameters and thus eliminates the need for an elaborate and tedious configuration. The segmentation is performed by using patch-based weighted random walks, which begin in manually pre-segmented slices and extrapolate the information contained in these slices to the remaining volume. Users can upload their tomograms and labeled slices to Biomedisa, run the segmentation process, and visualize both the image data and the results using 3D rendering software and a 2D slice viewer. A high scalability is achieved by the independence of the random walks. This enables the use of massively parallel computer architectures such as graphics processing units (GPUs) and thus allows for an evaluation of large image data in a reasonable time. In the presentation, we compare the results of *trigonopterus* weevil (1497 x 734 x 1117 voxels, 61 labels, 54 pre-segmented slices) with a completely manually segmented weevil. Using 4 Nvidia Titan X (Pascal) the segmentation was performed in 36 min. Biomedisa is carried out with the support of the Federal Ministry of Education and Research (BMBF), Germany, within the projects ASTOR and NOVA.

MOR-P-24

### How do spiders taste and smell? Insights from ultrastructure of tip-pore leg sensilla in wasp spiders (*Argiope* spp.)

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Except vision, sensory biology of arthropods relies on cuticular sensilla. Most types of sensilla described project a rigid or flexible hair of various shape and size. These sensilla are capable of receiving mechanical or chemical (olfactory or gustatory) cues. Others may detect changes in temperature or the presence of water, CO<sub>2</sub>, or electric fields. Depending on functional diversity of receptor cells included, sensilla may serve a single or multiple function(s). Besides electrophysiological recordings, receptor modalities can be assessed by the aid of electron microscopy revealing the presence of specific functional ultrastructures, such as tubular bodies (mechanoreception), a tip pore (gustation), or numerous wall pores (olfaction).

As opposed to insects, only little is known of the structural and functional diversity of sensilla in spiders. One gap of knowledge in particular concerns those sensilla spiders may smell with. This appears astonishing as behavioral observations revealed that spiders indeed receive chemicals to detect prey, predators and mating partners. In addition, a sex pheromone has been identified recently in the wasp spider *Argiope bruennichi*. Wall-pored sensilla, usual receivers of volatile odors in insects, have not yet been reported in spiders. Instead, tip-pore sensilla, equipped with sockets, two tubular bodies, and occurring on median and distal parts of all walking legs in high numbers, are assumed to be contact-chemoreceptors and could also be candidates to receive airborne chemicals. Our SEM and TEM study on two species of *Argiope* provides further support to this view. Their tip-pore sensilla also carry a subpopulation of dendrites not projecting to the tip pore but interacting with a heterogenous shaft cuticle. Thus, olfaction may be added to gustation and mechanoreception as putative receptor functions. Future research needs to explore how volatile odors access the receptors without traversing wall pores.

MOR-P-25

### The morphology of the bulbus organ of *Parasteatoda tepidariorum*

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Sexual reproduction is one of the main drivers for evolution. With the transition to land, effective sperm transfer is crucial for reproductive success. For this purpose male spiders have evolved a unique structure: the bulbus, a pipette like organ to take up, store and transfer sperm under terrestrial conditions. The bulbus organ is situated on the tarsal tip of the pedipalp, the second appendage pair of the spider body plan. Its morphology is ranging from a simple pear-shaped protrusion with extremely complex, sclerite equipped structures and there is no known reversal to plesiomorphic sperm transfer modes. Many aspects of its postembryonic development during the last instar before the adult moult and its general morphology are still unclear.

In our lab we investigate the development, genetics and morphology of the common house spider *Parasteatoda tepidariorum*. To elucidate the structure of the bulbus in adult stages and its formation during postembryonic stages, we use a multi method approach with three dimensional imaging through micro CT with high brilliance bench and synchrotron radiation sources, bleaching and clearing techniques for CLSM and ultra-structure analysis with TEM. We focus on the development of the primordium of the bulbus, its transformation during moulting and its adult morphology. This work provides an in-depth view of the structure and development of a bulbus of the complex, sclerite equipped type.

MOR-P-26

**More than meets the eye - unravelling the morphology of Daphnia's inducible defences in 3D**

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M Waterfleas of the genus *Daphnia* are abundant primary consumers and key species in freshwater ecosystems. Many studies have shown their high degree of phenotypic plasticity against a range of predators. *Daphnia* forms so called 'inducible defences' that are temporally coherent to the occurrence of carnivores, e.g. larvae of the phantom midge *Chaoborus*. The most conspicuous inducible defences are morphological alterations found in many species of this genus e.g. spines, thorns, neckteeth or crests. These render *Daphnia* less susceptible to predators. As only full knowledge of shape alterations allows to identify the mechanisms of the defense, we performed a three-dimensional shape analysis with a new developed workflow, comparing defended and undefended morphotypes in a high resolution. Therefore, casts of the typical and induced morph are analysed statistically and averaged to 3D models for comparison. This revealed novel defensive features in a range of *Daphnia* species. We compared the morphology of the typical and predator induced morph of five *Daphnia* species against fish, Triops, Notonecta and *Chaoborus* predation. From the broad range of defensive strategies, we chose the morphological alterations of *Daphnia lumholtzi*, *D. magna*, *D. longicephala*, *D. barbata* and *D. pulex*. Animals raised in the presence of these predators showed the commonly known shifts in morphology, but additional remarkable changes that have not been described so far. Furthermore, we found dispositions in the overall surface shape. These data are indispensable in future analyses, studying the function of morphological alterations with respect to anti-predatory mechanisms.

NEU-S-01

**Amygdala circuits and the control of fear memory**

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My lab uses Pavlovian cued fear conditioning and its extinction to investigate the substrates and mechanisms underlying the expression of learned fear and its extinction in mice as model organism. A key region for the formation and storage of fear and extinction memories is the amygdala. The amygdala directly receives sensory inputs from thalamic and cortical regions and is part of a larger interconnected network with the hippocampus and medial prefrontal cortex. The latter tripartite network has been implicated in state- and context-dependent control of fear. Increasing evidence suggests that parallel processes in these circuits and inhibitory elements play a critical role in the control of fear and extinction memory.

We employ a combination of behavioral, and ex vivo electrophysiological, anatomical and optogenetic approaches in mice to delineate properties of and plasticity in fear and extinction circuits. My talk will highlight several aspects of our recent work. On the network side, I will discuss data on the functional architecture of prefrontal- and hippocampal-basolateral amygdala circuits, and the role of a specific set of local inhibitory synapses in the basolateral amygdala that participate in extinction. From a systems perspective, I will show that sleep supports the consolidation of fear extinction memory and discuss preliminary data on the associated global activity patterns during sleep. Lastly, I will describe novel connectivity of amygdala intercalated cells, a specific set of GABAergic neurons surrounding the BLA which were thought to play a key role in extinction. Our data suggest that these cells may also participate in fear learning and its expression, as they provide learning-modulated sensory feed-forward and feedback inhibition to basolateral amygdala. This puts them in a unique position to gate fear expression or its suppression.

NEU-S-02

**Serotonergic SK channel modulation promotes adaptive optimized coding of natural stimuli**

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Growing evidence suggests that neural systems are adapted to their environment in order to optimally encode natural sensory stimuli with a given set of statistics. The mechanisms underlying this adaptation are, however, poorly understood in general. Previous studies in an array of sensory systems have shown that neural responses are optimally tuned utilizing various strategies in order to efficiently process sensory information to enable matched behavioural perception to the stimulus statistics. However, what happens when those statistics change over time? Here we show, using the weakly-electric fish *Apteronotus leptorhynchus* that the electrosensory system can adapt to a given environment with differential stimulus statistics. Using a combination of electrophysiology, behavioural paradigms, and pharmacology, we demonstrate that adaptation takes place at the single-neuron level, leading to an adaptation at the behavioural level matching the stimulus statistics. Furthermore, we demonstrate that this adaptation requires feedback processes from the telencephalon, mediated by the release of serotonin (5-HT) onto 5-HT<sub>2</sub> receptors located on the pyramidal cells of the electrosensory lateral line lobe (ELL). Therefore, our study reveals the circuitry leading to adaptation to natural sensory stimuli, as well as a novel function of 5-HT<sub>2</sub> receptors in regulating adaptive optimized coding. Due to the ubiquity and similarities in homology of 5-HT<sub>2</sub> receptors in weakly-electric fish and mammals, it is likely that our results are generally applicable across sensory systems and species.

NEU-O-01

**Discovering neurons for stereoscopic 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 vision, the ability to combine images from the two eyes to compute depth. This enables it to judge the distance of a target in space and to decide whether it is in reach or not.

We study the mechanisms underlying stereoscopic vision in praying mantids with behavioural, neuroanatomical and electrophysiological approaches. We present visual stimuli on a computer screen during behavioural experiments and during electrophysiological recordings. Images intended for the left and right eye are shown in different colours, and 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 during intracellular recordings 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.

When presented a moving disc seemingly floating in front a computer screen and within catching distance, mantises strike during behavioural testing. The animals usually do not strike when the disc is simulated to be out of reach. This clearly shows that the animals use stereoscopic vision, to judge the distance of those moving targets. Our anatomical findings show that the lobula complex, a component of the insect optic lobe, is highly structured and comprises at least one nested neuropile that is not present in other insects. Within the lobula complex we find neurons tuned to specific combinations of bars shown to the left and right eye corresponding to specific distances in space. Some of those neurons are good candidates for being involved in the striking behaviour of the praying mantis.

NEU-O-02

**How bumblebees deal with conflicting visual cues when flying back home?**

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Social insects rely on the learning of visual cues to remember their nest location. Different visual cue categories can be used by them, local ones (e.g. in digger wasps) and more distant ones in the background like the panorama of the scene (e.g. in ants).

In naturalistic environments, bumblebees have access to a variety of nearby and more distant cues. Therefore, making use of a single cue may be dangerous for goal localization. For example, if only one cue is remembered and then vanishes (displaced by the wind, anthropogenic changes of the landscape, etc), the bumblebee will be lost and have to randomly search for its nest.

We investigate which visual cues are used by the bumblebees and how they are combined by placing global and background cues of different complexity into conflict, during a homing task.

The inconspicuous entrance of the bumblebee nest is surrounded by a constellation of three landmarks (i.e the local cues), giving access from the ground to a cylindrical flight arena (1.50 meter diameter). The arena walls are themselves covered by a printed image of a panorama, which will be our background cue.

The experimental procedure is the following: The Bumblebee learns a prior condition with a certain spatial arrangement between the two cues. When the bee has left the flight arena for a foraging trip through a hole leading to a feeding chamber, the two cues are rotated in the cylinder and placed into conflict to each other. Finally, when entering again the arena again, the bee's return flight is recorded and the trajectory analyzed.

The analysis quantifies the relative importance of local and the background cues based on the angular position of both cues in the arena and the return direction of the bee. We quantify also the search behavior of the bee. Our experiments reveal that both nearby and the background cues are used during homing, but are differently weighted according to the complexity of the background cue we used.

NEU-O-03

**Compass-like representation of solar position in the locust central complex**Uta Pegel<sup>1</sup>; Keram Pfeiffer<sup>2</sup>; Christine Scholtyssek<sup>2</sup>; Uwe Homberg<sup>1</sup>

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Like many other insects the desert locust *Schistocerca gregaria* likely uses a sun compass for orientation. Besides direct sunlight, several other features of the sky like the sky polarization pattern and the chromatic gradient can be exploited for navigation. Celestial E-vector orientation can give reference to solar position, but due to its symmetry the polarization pattern is ambiguous. Hence other visual cues like the position of the sun likely contribute to sun compass based navigation. In the locust brain, the central complex (CX) appears to be involved in navigational tasks. A CX neuropil, the protocerebral bridge (PB) holds a topographic representation of E-vector orientations (Heinze and Homberg 2007, *Science* 315:995). In order to study the contribution of solar azimuth information deriving from direct sunlight, we tested CX neurons to polarized light presented from zenithal direction and to an unpolarized green light spot that rotated around the head of the animal. We found that various CX neurons integrated both cues by preferring a certain E-vector orientation and a certain azimuth of the green spot. In two types of columnar neurons the preferred E-vector orientation and the preferred azimuth of green light correlated with the slice of innervation in the PB. Two types of tangential neurons of the lower division of the central body (CBL), termed TL2 and TL3, differed substantially in their response characteristics. Responses to polarized light were of higher amplitude in TL3 neurons than in TL2 neurons, whereas responses to green light were of higher amplitude in TL2 neurons than in TL3 neurons. In TL2 neurons the preferred azimuth of green light was related to the layer of innervation in the CBL. Besides the azimuth of the green spot, some CX neurons also encoded its elevation. Our results indicate a topographic representation of solar azimuth at the neuronal level and a possible elevation dependent signaling of solar azimuth information.

NEU-O-04

**Different structure same function: avian hippocampus and spatial memory.**

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Birds' hippocampus, contrary to its mammalian homolog, lacks a layered structure and its anatomical subdivisions are still highly debated. The question of how such different structures can support similar functions requires to investigate the avian hippocampus in ways that can be directly compared to mammalian studies. Here I will present the results of a series of experiments with two species of birds (zebra finches and domestic chicks) which questioned how far theories developed for mammalian hippocampus can also be applied to the avian hippocampal formation by using experimental setups equivalent to those used for rodents. In zebra finches (*Taeniopygia guttata*) using a "dry version" of the Morris water maze task we demonstrated the role of the avian hippocampus in learning and recall of this spatial task based on allocentric cues, in contrast to orientation on local cues, which like in rodents do not involve hippocampus. We also found that the visual Wulst (from which avian hippocampus receives direct visual information) is crucial for spatial orientation. With a standard reference memory task we studied the involvement of the hippocampal formation of domestic chicks (*Gallus gallus*) that used the geometrical shape of the environment to orient and locate a reward. We found enhanced neuronal activation (based on immediate early genes expression) after chicks learned to locate rewarded corners using the shape of a rectangular arena compared to chicks trained to discriminate local features in a square-shaped arena. Another study with chicks revealed a change in the neural representation of two different environmental shapes in the hippocampus, pointing to a remapping-like effect, in line with rodents' studies. This work has implications for understanding hippocampal representations in birds and the evolutionary history of complex cognition, considering apparent differences in brain structure across species.

NEU-O-05

**Stimulus dependent neural correlations in electric sensing: origins and function.**

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We use electrophysiological and mathematical approaches to investigate the effects of correlated neural activity onto information transmission in the brain. It is generally agreed that behavioral responses are determined by combining the activities of large neural populations. Understanding such population codes is however complicated by the fact that neural activities are correlated. Such correlations were observed ubiquitously in the brain and are focus of much debate because they strongly impact coding and at the same time are plastic and change depending on behavioral state, attention or in a stimulus dependent fashion. This has further led to the hypothesis that neural correlations can carry information independently from single neuron firing statistics and as such form an additional channel of information transmission in the brain. There is however no experimental evidence to support this hypothesis to date.

We use the weakly electric fish *Apteronotus leptorhynchus* to investigate how correlated neural activity arises and encodes behaviorally relevant stimuli in the medullary electrosensory lateral line lobe (ELL). These fish use stimulus amplitude to gauge inter-conspecific distance during social interactions. We found that neural correlations decreased as a function of stimulus amplitude. Interestingly, this variation was mainly due to changes in noise correlation magnitude (i.e., correlated variability) as signal correlations (i.e., correlations between the mean responses) and single neuron firing rate remained constant. We used computational means to understand how noise correlations can encode stimulus amplitude and found that stimulus-amplitude dependent correlations were due to the differential activation properties of the receptive field center and surround portions. As such, we provide evidence that noise correlations between ELL pyramidal neurons carry independent information and thus form a separate channel of information transmission.

NEU-O-06

**Learning to behave: shaping sensory flow to enable and enhance active electrolocation.**

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As nocturnal animals, weakly electric fish have developed a sophisticated sense: active electroreception. These fish rely on a self-generated electric field to navigate and capture prey in the dark. Conceptually, electrolocation can be subdivided into separate tasks: detection, characterization, and localization.

Detection involves determining whether or not a target is in the vicinity, while the characterization stage requires an assessment of various target properties that can vary along a continuum, such as size, shape, and electrical impedance. The generation of purposeful and goal-oriented behavior depends on an animal's ability to extract these properties. Action and perception form an interactive process during which the corollaries of the ongoing behavior alter the sensory signals which in turn can be used to modify the motor response. Learning hence may be defined as the adaptive optimization of behavior with respect to motor efficiency and/or sensory information gain necessary to solve a specific task. Investigating this hypothesis in *Gnathonemus petersii* we show that the adjustments of motor behavior emerge as a scaffold to actively shape the sensory flow. Reconstructing this flow shows that the changed behavior leads to an increase of the amplitude of the sensory input, which results in the animal being able to solve a detection task from further away after learning.

A crucial step towards a spatial representation of the environment is localization. We show that the geometry of the electric field can provide the physical basis for a novel non-visual parallax cue. In fact, electric fish show a behavior that is reminiscent of visual-peering, suggesting that this cue may be actively generated. We show that this cue indeed is used in electrosensory distance perception across phylogenetically distant taxa of weakly electric fish. Our results demonstrate for the first time that behaviorally relevant electrosensory information is extracted using sensory flow.

NEU-O-07

**Passive versus active sensing: stimulus induced modulation of background activity in an identified descending interneuron in the stick insect**

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Stick insects use their antennae to search and sample the environment ahead during walking. When the antennae encounter an obstacle a reaching movement of the front legs can be observed. The information required for this behaviour 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 substrate vibration. Unlike antennal afferents that arborize in the brain and also descend to the Gnathal Ganglia (GnG), afferent information from the vibration input does not descend through the circumesophageal connectives.

cONv displays highly fluctuating background activity, reaching rates comparable to what has been measured for the encoding of antennal joint angle velocity. How can cONv reliably encode single-trial joint movement in the presence of its strongly fluctuating background activity and how does it respond depending on the behavioural state of the animal and the mode of stimulation (movement or vibration)? These questions were studied by electrophysiology and antennal motion tracking in stationary animals. Substrate taps at a rate comparable to stepping during walking are reliably encoded by a single spike per tap, while reducing background activity.

The response of cONv to passive deflection of the antenna is reliable, strong and velocity-dependent. However, no movement related modulation of cONv during active exploration by the antennae can be detected, while its sensitivity to passive deflection persists. Preliminary results show that responses to interrupted active antennal movements resemble those to passive deflection, implying that cONv acts as a reliable antennal contact detector under behaviourally relevant conditions.

NEU-O-08

**Inter-leg coordination in insects: A mechanism based on local load feedback**

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Animals coordinate their legs in a flexible manner during walking and running. However, which specific mechanisms give rise to flexible inter-leg coordination during natural locomotion remains largely unknown. One hypothesis is that the neural locomotor networks of the legs can be coupled mechanically based on a transfer of body load from one leg to another. For example, a leg in stance could start its stance-to-swing transition once its load sensors detect an unloading induced by the touch-down and loading of a neighboring leg. Such reactive coordination based on local sensing of load transfer would be computationally inexpensive and inherently adaptive. To test this hypothesis, we simultaneously recorded leg kinematics, ground reaction forces and muscle activity in freely walking stick insects (*Carausius morosus*). By determining joint torques, we predict that load sensors (campaniform sensilla) on the proximal part of the insect leg reliably signal leg unloading near the end of the stance phase. The unloading is directly correlated with a switch from stance to swing muscle activity, in agreement with an intra-leg load reflex promoting the stance-to-swing transition. Furthermore, a mechanical simulation reveals that unloading of a leg can be specifically ascribed to loading of the ipsilateral posterior leg. These data support the idea that local load feedback can contribute to coordinate neighboring legs in a back-to-front sequence during locomotion, simply by exploiting the mechanical coupling between them. We propose that this mechanism is used across insect species in analogy to mechanisms proposed in mammals.

NEU-O-09

**Postmetamorphic neurogenesis in the mushroom bodies of the red flour beetle**

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With its fully annotated genome, the susceptibility for reverse genetics based upon RNA interference (RNAi) and relative longevity (up to 2-3 years), the red flour beetle *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 the beetle *T. castaneum* where neuroblasts giving birth to MB Kenyon-cells remain active after adult eclosion. To label cell proliferation in adult *T. castaneum* we successfully combined the 5-ethyl-2'-deoxyuridine (EdU) with immunohistochemistry against the glia-cell marker reversed-polarity and the use of transgenic lines expressing neuronspecific markers. We reliably labeled the progenies of the adult persisting mushroom body neuroblasts, determined their identity and counted the newborn Kenyon cells 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. To address the question whether adult proliferation of Kenyon cells depends on olfactory input, we used two approaches. First, we enriched the environment of group-reared beetles during their adult life with the food related odor *cis*-3-hexenol (leaf alcohol). Secondly, we repeated those stimulation experiments, but knocked down the common odorant co-receptor (*Orco*) by systemic RNAi, resulting in beetles anosmic to the leaf alcohol.

Our data suggest at least two proliferation phases in the early adult. A first phase, direct after adult eclosion that lasts for 3 to 4 days, seems to be independent from olfactory stimulation. In contrast, a second phase that directly follows the first phase seems to depend on olfactory stimulation.

NEU-O-10

**Characterization of the neuromuscular junction in the Cnidarian *Nematostella vectensis* and its evolutionary implications**

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The ability to control movements requires the interaction of contractible muscle cells and neurons capable of muscle innervation. Communication between the neuron and muscle cell is accomplished by a specialized synapse, the neuromuscular junction (NMJ). The majority of known animals belong to the Bilateria, which comprises the sister groups Protostomia and Deuterostomia. Within deuterostomes, the NMJ is best studied in vertebrates where acetylcholine (ACh) functions as excitatory neurotransmitter that binds to nicotinic ACh receptors on the sarcolemma of the muscle cell. Surprisingly, muscle innervation in arthropods like *Drosophila* and crayfish works completely different. Unlike in vertebrates, glutamate (Glu) rather than ACh is released from the presynaptic terminal in *Drosophila* and binds to postsynaptic ionotropic Glu receptors (AMPA/Kainate). So far, it remains unclear what kind of NMJ was present in the bilaterian ancestor. In order to unravel the evolution of the neuromuscular system in Bilateria, the condition in non-bilaterian outgroups is of paramount importance. In this respect, Cnidaria, which comprise the sister group to Bilateria, is of special interest. The anthozoan *Nematostella vectensis* is an ideal candidate, because it is supposed to have retained a number of ancestral features. Like bilaterians, *Nematostella* possesses a nervous system and elaborate muscles. However, the structure and function of the NMJ in *Nematostella* is still completely unknown.

By applying a combined methodological approach (transgenetics, genomics, gene expression, immunolabelling and correlative microscopy) we will provide a comprehensive morphological and functional analysis of the NMJ in *Nematostella*. First insights are presented here and evolutionary implications are discussed.

NEU-O-11

**Beautiful bodies, tiny brains? The protocerebral architecture and corresponding sense organs in calanoid copepods**

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Copepoda is a crustacean taxon which has traditionally been assigned to the Maxillopoda. However, molecular analyses have rendered the position of Copepoda within crustaceans unclear, and the latest sister-group relationships to have been proposed have placed Copepoda with Cirripedia in a group called Hexanauplia, or together with cirripeds and malacostracans in the taxon Multicrustacea. Little is known about the morphological details of the copepod nervous system. To fill in the gaps, we investigated the basal subgroup Calanoida using immunohistochemical labeling against alpha-tubulin and various neurohormones, combining this with confocal laser scanning analysis and 3D reconstruction. Our results make clear that the morphology of the protocerebrum in calanoid copepods is remarkably disparate. The investigated copepods only exhibit certain components of the “central complex”. The protocerebral sense organs considered here are the frontal filament organs and a photoreceptor known as the “gickelhorn organ” which was first investigated by Eloffson 50 years ago and which we compare with the arthropod compound eye. In addition, the frontal filament organs and related structures are identified and homologies drawn between different crustacean taxa.

NEU-O-12

**Aquatic Imaging: Neuronal Map Formation through the Lateral-Line System**Julie Goulet<sup>1</sup>; Vanessa Hollmann<sup>1</sup>; J. Leo van Hemmen<sup>2</sup>; Jacob Engelmann<sup>3</sup>

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The majority of vertebrates are fish and they all possess a lateral-line system that enables them to sense the velocity or acceleration of their aquatic environment. It has been a long-standing question as to whether and, if so, how a central map as a neuronal representation of the outside sensory world exists in this dispersed sensory system.

We present two-fold evidence in favour of such a map and clarify the underlying neuroanatomy of the lateral-line system of zebrafish (*Danio rerio*). Except on the head, the lateral-line system of zebrafish consists of superficial neuromasts. In the first central processing area, the MON, our anatomical data for the first time confirms a weak mapping of this input. Based on previous work we know that this crude map is refined in the torus semicircularis. We here provide theoretical evidence that explains the unique role of the rather poorly mapped representation in the MON through what one may call ‘stimulus distillation’. It seems that a poor map in MON is a requisite to decorrelates a diffuse and highly correlated velocity field by sparse coding. In the torus then the subsequent convergence and synaptic plasticity result in a stimulus distillation that enables map formation. This process can profit from, but does not necessarily need, a visual teacher stemming. In summary we present anatomical data that suggests a functional relevance of the hitherto enigmatic role of topography in the lateral line system. Using a biologically plausible minimal network model of the lateral line system we demonstrate the functional relevance of the network properties. Similar mechanisms may be at work in other distributed sensory systems and could further aid in the design of autonomous agents that employ such near-range sensory systems for navigation in the future.

NEU-P-01

### Adaptive mechanisms in the insect visual motion pathway facilitates optic flow-based spatial vision in cluttered environments

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Optic flow is the most plausible basis of spatial vision in aerial insects. It uses the fact that during translatory self-motion the retinal speed of objects in the environment depends on their distance to the animal. However, as a consequence of the ambiguous nature of optic flow measurements by elementary motion detectors (EMDs) as are known in insect visual systems, it is not trivial at all to what extent this kind of motion detectors can provide reliable spatial information for the use at later processing stages, especially when dealing with the dynamic visual input in cluttered natural environments. Therefore, we systematically modeled each stage of the visual motion pathway of insects (including its adaptive properties) based on electrophysiological data on the peripheral visual system and the lobula plate tangential cells (LPTCs) of flies. By presenting visual stimuli that mimic the time-dependent visual input during translatory flight in cluttered virtual and natural 3D environments, we could show that temporal filtering and adaptation in the peripheral visual system as well as adaptive processing at the level of EMDs facilitate the representation of spatial information at the output of motion detector arrays - irrespective of the overall brightness of the environment. This is even true under the dynamic conditions of natural flight of insects with its characteristic sequence of rapid saccadic turns and intersaccadic intervals where gaze direction is kept rather constant. Hence, our adaptive model (accounting for both brightness and motion adaptation) leads, in a computationally parsimonious way, to optic flow-based segregation of cluttered sceneries into nearby and distant objects under a wide range of brightness and dynamical conditions. This model may well be implemented also in artificial visual systems.

NEU-P-02

### Neurons in the locust central brain are sensitive to polarized light from ventral directions

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Neurons in the central complex in the brain of the desert locust and other insects are sensitive to the plane of dorsally presented polarized light, and likely use this property to exploit the polarization pattern of the sky for spatial orientation. In addition to skylight, however, light that is reflected from smooth surfaces like leaves or water is also polarized. Several insect species use these cues to detect oviposition sites on vegetation or at ponds (Kelber 1999, Nature 402:251; Wildermuth 1998, Naturwissenschaften 85:297). During long range migrations desert locusts frequently pass the ocean, but have also been observed to avoid water (Shashar et al. 2005, Biol Lett 1:472). Whether polarized light reflected from the water surface plays a role in this behavior remains to be shown.

In the present study, we therefore analyzed the responses of neurons in the locust (*Schistocerca gregaria*) brain to polarized light presented from ventral direction. The dorsal rim area of the eye, mediating sensitivity to dorsally presented polarized light, was painted black. Neurons were recorded intracellularly and stimulated with blue light from ventral direction passing through a rotating polarizer. Several types of CX neurons involved in the processing of zenithal E-vectors were completely insensitive to ventral stimulation. In contrast, some cells were strongly inhibited or excited during polarizer rotation irrespective of E-vector orientation, suggesting sensitivity to ventral light levels. We found four CX cell types and a neuron of the lobula that were E-vector sensitive, indicating a possible role of the CX for water body detection and course changes in response to the presence of water.

NEU-P-03

### A multi-compartment model based on expression patterns of structural and ion channel proteins in a multimodal cell type of the avian optic tectum

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The vertebrate midbrain is an important subcortical area involved in distinct functions such as multimodal integration, movement initiation and bottom-up attention. Our group is particularly interested in the computation of multisensory information in single neurons. Here, we studied multimodal integration in the optic tectum (TeO, counterpart to mammalian superior colliculus). In chicken, the TeO is organized in 15 layers where visual input targets the superficial layers while auditory input terminates in deeper layers.

A candidate cell for multimodal integration is the Shepherd's crook neuron (SCN), which has dendrites in both input regions. The characteristic feature of these neurons is the axon origin at the apical dendrite. To understand signal flow and cellular computation in this neuron, we analyzed expression patterns of structural proteins (NF200, Ankyrin G, and Myelin) and ion channels (Pan-Nav, Nav1.6 and Kv3.1b). NF200 is strongly expressed in the axon. Ankyrin G is mainly expressed at the axon initial segment. Myelination and Pan-Nav expression starts after the AIS. Nav1.6 has a high density in this region. Kv3.1b is restricted to the soma, the primary neurite and the axon branch. Based on these anatomical data, we built a multi-compartment model in NEURON. We assumed the same number of active synapses on the apical and basal dendrite mimicking visual and auditory input, respectively. The number of activated synapses on apical, basal or both dendrites remained always the same. A simultaneous stimulation of both sensory input regions leads to a significantly enhanced number of action potentials on the axon compared to the stimulation of one input region. Introducing a delayed onset of one sensory input, the delayed auditory signal increases the spiking rate more than the delayed visual signal. These findings point to the ability of SCNs to compute visual and auditory input in the AIS to further process the integrated information to higher brain regions.

NEU-P-04

### Responses to visual and hydrodynamic stimuli in the goldfish optic tectum

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The optic tectum in fishes receives input from the retina but also from other sensory modalities. Surprisingly, little is known about the responses of tectal neurons to hydrodynamic stimuli, although this has been studied in amphibians where visual and lateral line inputs have been shown to combine. Therefore, we are investigating whether unimodal and/or multimodal units can be found in the optic tectum of goldfish that respond to hydrodynamic stimulation.

Multi-unit recordings were made in the optic tectum of goldfish (*Carassius auratus*) using custom-made metal-electrodes. Visual stimuli (0.5 s duration) were generated by a stationary light-emitting white diode (LED) placed 10 mm in front of the fish's left eye. Hydrodynamic stimuli (0.5 s duration) were generated by a sinusoidally (100 Hz) vibrating sphere (dipole, 10 mm diameter) placed at a distance of 15 mm to the fish's trunk. Neuronal responses were analyzed with respect to discharge patterns and strengths and recording sites were verified by histological reconstruction of electrolytically placed lesions.

To date, we recorded from 156 units in the optic tectum of 13 fish. Most units ( $n = 108$ , 69 %) responded exclusively to visual stimulation. Some units ( $n = 3$ , 2 %) responded exclusively to hydrodynamic stimulation. Many units ( $n = 45$ , 29 %) were found that responded to both, visual and hydrodynamic stimulation. If the hydrodynamic stimulus was blocked by a transparent acrylic plate, these units continued to respond to the visual stimulus, but no longer responded to the hydrodynamic stimulus.

Our data show that, as expected, the vast majority of tectal units is sensitive to visual stimulation. However, our data also show that there are few cells in the optic tectum of fish that respond to hydrodynamic stimulation.

NEU-P-05

### How does an animal keep track of its heading when it moves through the world?

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Many animals maintain an internal representation of their heading as they move through the world. In *Drosophila melanogaster*, such a compass representation was recently discovered in the “compass cells”, a neural population in the central complex. In other insects, this brain region was shown to encode topographically organized sensory maps of polarized light patterns and sun position, but how the internal compass of insects functions in the absence of visual cues was unknown. Here we use single-cell electrophysiology, population calcium imaging, and thermogenetics in head-fixed walking flies to identify and characterize a population of neurons that conjunctively encodes the fly’s heading and recent rotations. We show how left-right mirror-symmetric turn responses in these “turn neurons” and their recurrent loop-with-shift connectivity with the compass cells provide an elegant mechanism for updating the fly’s neural representation of heading when the animal turns in darkness. As we could formalize in a mathematical model, the turn neurons receive the information about the fly’s prior heading from the compass neurons, combine it with the information about the fly’s recent turns, and route this output back to the compass neurons, allowing the network to update the representation of the animal’s current heading. Such a network motif was long supposed to be the substrate for an animal’s ability to update its neural compass by integration of its own movements — a hypothesis for which we are the first to provide conclusive experimental evidence.

NEU-P-06

### Estimating higher-order locomotion parameters from distributed proprioception

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Adaptability of legged locomotion relies on distributed proprioceptive feedback from the legs. Apart from low-level control of leg movements and inter-leg coordination, proprioceptive cues may also be integrated to estimate overall locomotion parameters relevant to high-level control of behaviour. For example, this could be relevant for odometry estimates of distance and direction during navigation. To date, it is unknown how overall parameters such as body inclination or forward velocity may be represented in the nervous system. If proprioceptive encoding was optimal, the afferent activity pattern of distributed proprioceptive cues from across the body should be a suitable representation in itself. Given noisy encoding in multiple afferent spike trains, the major questions become (i) how reliable the parameter estimates can be, and (ii) which parts of the distributed code are most crucial.

Here we use a database on unrestrained whole-body kinematics of walking and climbing stick insects in conjunction with a simple spiking proprioceptor model to transform sets of joint angle time courses into corresponding sets of spike trains. First results were obtained for a “full model” decoding body inclination angle from 360 spike trains: 20 proprioceptors x 18 joints, i.e., three degrees of freedom (DoF) per leg. Across 10 animals ( $n=44$  trials), a two-layered artificial neural network with 10 hidden neurons yields a body inclination estimate at an rmse of  $18.6^\circ \pm 1.4^\circ$  s.d. ( $r^2=0.37$ ). In order to test the relevance of individual DoF, we compared the “full model” with simplified models that either decoded one DoF only, or used fewer proprioceptors. Decoding levation angles only yielded an rmse of  $19.8^\circ \pm 2.0^\circ$  ( $r^2=0.27$ ), which was similarly good as decoding three DoF with a similar number of inputs (rmse=  $20^\circ \pm 1.4^\circ$ ,  $r^2=0.30$ ). This suggests that estimates of overall locomotion parameters are possible, and that femoral levation is most relevant to decoding body inclination.

NEU-P-07

**Potential mechanisms for feature invariance in passive electroreception**

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One of the major questions in sensory biology is how the nervous system maintains perceptual invariance in the face of multifeatured inputs. Perceptual invariance here refers to the ability to recognize objects independent of irrelevant stimulus variation; e.g. in vision such variations might be due to the visual angle, light intensities and background texture.

We address the question if such perceptual invariance is also possible in the passive electrosensory system. Here, prey-like stimuli that move towards a fish (*Gnathonemus petersii*) contain information on speed and distance, but a simple rate-coding approach would confound these parameters. Work on the active electric sense of South American knifefish suggests that speed and distance can be disambiguated through a specific form of power-law adaptation at the level of the afferents. However, different mechanisms would be necessary to disambiguate other parameters such as stimulus amplitude. Similarly we here show that the afferents of the passive system have power-law adaptation to natural stimuli, yet not of the form required for speed invariant encoding. Using modelling and physiology we then show that information may still be disambiguated based on the slope-to-amplitude heuristic proposed for distance detection in the active sense. Our model shows that additional factors like amplitude, orientation and direction of the movement of the stimulus can be disambiguated using this approach. Furthermore, we show how different forms of power-law adaptation may influence perceptual invariance in the face of background stimuli.

NEU-P-08

**Learning and the involvement of the telencephalon in *Gnathonemus petersii***

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Navigation is a ubiquitous challenge to animals and different strategies have been described, including map formation and spatial memory formation in higher vertebrates. Here cortical and subcortical structures are involved. Similar to bats, fish have to navigate in a three-dimensional environment, yet the homology regarding telencephalic structures of teleosts and mammals is as of yet unclear. A benefit of teleosts, however, is the comparatively simpler structure of the forebrain and the accessibility of hippocampus like areas. Their active sampling mode furthermore allows a direct quantification of attention alongside an in-depth characterization of the sensory flow in ongoing behavior. In the following we show that spatial learning in Mormyrids is based on both ego- and allocentric cues. Under most experimental condition the animals however preferred egocentric strategies. Therefore, we are currently also investigating the possibility of path integration.

Context dependent learning is another task in which the telencephalon is thought to be involved. Mormyrids are especially interesting in this regard, since they are capable of solving remarkably complex cognitive tasks despite relying on a seemingly poorly resolved sensory input, their electric sense. Here we introduce a two by two alternative forced choice set-up in which the fish has to choose between different object-place associations. In future studies we will link the behavioral experiment with tetrode recordings in the telencephalon and thereby getting access to the neuronal activity during learning.

NEU-P-09

**Stepping, searching, swing or stance: Common patterns of inter-joint coordination**

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During locomotion, the walking-legs of insects may transition from regular stepping to cyclic searching movements, for example after loss of foothold. There are two alternative interpretations of how searching may come about: (i) stepping and searching could be distinct and mutually exclusive rhythmic motor patterns (Berg et al. 2015, *Curr.Biol.*), or (ii) stepping could be an alternating sequence of swing and stance movements, each one governed by distinct control modes. In the latter interpretation, searching is but the terminal part of a swing movement that was not terminated by ground contact (Dürr 2001, *J.Exp.Biol.*). Here we study the difference between stepping and searching in two stick insect species for which the problem has been studied in the literature: *Carausius morosus* and *Medauroidea extradentata*. For this, we compare the inter-joint coordination of front legs in a large set of unrestrained walking/searching trials of these two species. Data were acquired with a marker-based motion capture system. After kinematic analysis of time-courses of four degrees of freedom per leg, and manual annotation of swing, stance and searching episodes, we asked two questions: (a) How does searching differ between the two species, and (b) how similar are the average inter-joint coordination patterns between (i) stepping and searching or (ii) swing and searching? With regard to (a) we show that duration and work range of the leg differ strongly: searching in *M. extradentata* lasts much longer and covers nearly twice the angular range of *C. morosus*. With regard to (b) we calculated average vector fields of instant velocity vectors across the entire joint angle space covered in unrestrained locomotion. The difference between distinct movement patterns was estimated by metric comparison of their vector fields. First results suggest a high degree of similarity of swing and searching for the largest part of the work range, except near the typical touch-down region of the foot.

NEU-P-10

**A second insect olfactory center in the red flour beetle**Yasmin Rein<sup>1</sup>; Janet Anders; Stefan Dippel<sup>1</sup>; Martin Kollmann<sup>1</sup>; Ernst A Wimmer<sup>2</sup>; Joachim Schachtner<sup>1</sup>

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The current picture of the insect olfactory pathway starts with the olfactory sensory neurons (OSN), mainly located on the antenna that send their axons into the paired antennal lobe, the first central olfactory processing center. From there, projection neurons send their axons to higher olfactory integration centers – the paired mushroom body and the paired lateral horn. The gustatory sensory neurons located on the antenna project to the primary gustatory center, located in the gnathal ganglion.

A recent study on the olfactory system of the red flour beetle *T. castaneum* revealed that besides the antennae also the mouthparts are highly involved in olfaction (Dippel et al., 2016. *BMC Biology* 14:90). The OSN from the mouthparts are not projecting into the antennal lobe, but to a so far not described unpaired glomerular organized olfactory neuropil in the gnathal ganglion, termed gnathal olfactory center (GOC) and to the paired lobus glomerulatus, a structure so far only being characterized in hemimetabolous insects. In summary, the olfactory system of *T. castaneum* seems to follow a different logic than hitherto thought for insects, with olfaction and taste dispersed to a high degree on antenna and mouthparts and a selective central processing of olfactory information depending on the location of the OSN.

In the current study, we aim to better characterize the neuroarchitecture of the gnathal olfactory center. To identify the neuronal components of the network, including local-, projection- and centrifugal neurons, to better describe the glomerular organization, and to reveal pathways to higher processing centers, we use various neuroanatomical techniques. The techniques include e.g. immunohistochemistry against various neuromediators, transgenic lines, antennal-, mouthpart-, and GOC fills, confocal laser scanning microscopy, and 3D-reconstruction.

NEU-P-11

**Eyes, ears, noses and the lateral line system: Experimental cross-modal and uni-modal reorganizations facilitate understanding of developmental and evolutionary principles**

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Discrete sensory information processing as well as cross-modal integration facilitate selective and integrated responses to environmental stimuli. Such integration requires organization of afferents in ocular and 'vestibular' dominance columns to achieve both aspects of information processing. Experimental work has revealed substantial cross-modal reorganizations in thalamo-cortical connections allowing visual cortex to process auditory information or alter the frequency map in age related high frequency hearing loss. Limited cross-modal changes have been reported in the brainstem with some somatosensory fibers expanding to auditory and vestibular nuclei upon deafness or loss of an ear. In contrast, rapid vestibular connection changes occur in microgravity resulting in alterations of eye movement patterns. We previously introduced ear transplantations to test brainstem plasticity as a result of an added ear and its orientation and thus stimulus acquisition relative to the native ear. We have expanded this work and use ear manipulations to demonstrate molecularly regulated specificity of distinct afferent projections leading to segregation of primary afferents in the hindbrain, including cochleotopic projections. We demonstrate that targeted projections do not depend on the presence of target neurons whereas target second order neurons critically depend on sensory input for viability and dendritic development. Transplantations of 'extra' ears in chicken and xenoplastic transplantation of mouse ears onto chicken as well as zebrafish ears on *Xenopus* show that inner ear afferents are uniquely molecularly targeted to innervate exclusively their hindbrain territory that has only limited capacity to accept nearby afferents. Inner ear afferents can navigate along lateral line afferents to reach the hindbrain but lateral line afferents do not expand into the inner ear projection area when the ear is removed. Finally, we demonstrate the transplanted noses and eyes can innervate the hindbrain but show no obvious pattern reminiscent of the longitudinal columns of native sensory projections.

NEU-P-12

**Molecular function of mechanosensory neurons in the antenna of *Drosophila melanogaster***

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*Drosophila melanogaster* employs its antenna to detect a variety of different sensory modalities. The Johnston's organ (JO) is housed in the second antennal segment and comprises approximately 500 mechanosensitive neurons. Previous work showed that the subpopulation of AB Neurons (sound receptors) are essential for hearing, particularly for active mechanical amplification of faint sounds, whereas the CE neurons preferentially detect gravity and wind. Members of the transient receptor potential (TRP) family, NOMPC (TRPN1), Nanchung (Nan) and Inactive (Iav), are essential for the mechano-electrical transduction of antennal displacement into electrical signals in the JO. In *nompC* null mutants only loud sounds evoke residual nerve responses similar to responses measured in animals missing the AB neuronal population. Additionally, the non-linear mechanical amplification of faint sounds, is lost in *nompC* null mutants. Calcium imaging experiments showed that the residual nerve responses in *nompC* null mutants stem most likely from responses of the CE neuronal population. Normal function of CE neurons was not changed in *nompC* null mutants showing their independence from *NompC*. Loss of *Nan/Iav* results in a complete loss of nerve responses, but increases the non-linear mechanical amplification. How *NompC* and *Nan/Iav* exactly interact in the AB neuronal subpopulation remains unknown, although it has been proposed that *Nan/Iav* serve as amplifiers of an electrical response elicited by mechanical gating of *NompC*. However, the channel responsible for converting the mechanical stimulus of wind and gravity into an electrical signal, which is probably also amplified by *Nan/Iav*, remains unknown. To identify novel channel candidates involved in sensory perception in the JO, we will investigate the transcriptomes of the different JO neuron subpopulations utilizing ablation experiments, followed by RNA sequencing and differential gene expression calling.

NEU-P-13

### A noise robust two-dimensional spiking neuronal network model of the electrosensory lateral line lobe of *Gnathonemus petersii*

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For any sensing organism, extracting reliable sensory information from unreliable, noisy input stimuli is a key ability. The arising need of sensory neuronal structures to compensate for refferent input and noise embedded in the perceived signal by morphology and function is a well investigated topic in sensory biology. In case of active electrolocation in the Mormyridae family of weakly electric fish, the animal perceives its surroundings by generating electric fields and detecting distortions in the self-caused carrier signal arising from the local environment with specialized electroreceptors, the so called mormyromasts.

We here present the implementation of a two-dimensional spiking neuronal network model of the electrosensory lateral line lobe (ELL) of the weakly electric fish *Gnathonemus petersii*. The network was programmed in the python-based Brian Simulator, consisting of leaky integrate-and-fire neurons and network parameters generally based on anatomical insights. Inputs to the network are achieved by a simultaneous application of artificial electric images to a set of linear integrators, which produce a latency code similar to the response that has been observed in primary afferent fibers of mormyromasts.

Our results show a sparse encoding of the stimulus by the network and demonstrate a separation of refferent input and stimulus induced response. We furthermore observe an intrinsic ability to filter out noise, while the underlying signal becomes amplified in the temporal domain.

NEU-P-14

### Quantifying sensory collisions in groups of echolocators

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Echolocating bats sense their surroundings by emitting loud ultrasonic calls and analysing the time delay and spectral properties of the returning echoes. Since these returning echoes are often very low in amplitude, their auditory analysis may be easily hampered by other louder sounds, e.g., in the presence of conspecific echolocators. However, echolocating bats of many species roost and forage in groups. On exposure to such jamming conditions, bats regularly alter call parameters such as amplitude, duration, or spectral properties, and this varies across species. These alterations might be 'anti-jamming' strategies to optimise echolocation. However, an alternative hypothesis is that these alterations are part of the bats standard reaction to close-by objects. A common conceptual understanding of why different echolocating species react differently to such potential jamming still remains lacking.

We present a simulation framework to estimate the maximum amount of potential jamming that bats may experience in the presence of conspecifics. We quantify 'sensory collisions', the fraction of own echoes that are overlapped by conspecific calls. We calculate auditory scenes from the perspective of the flying bat by including empirical physical and biological data on atmospheric attenuation, call emission and reception, and flight. Importantly, our simulations are based directly on these empirical data without further assumptions, thus allowing to test diverse scenarios and species. First, we simulated *Myotis daubentonii* bats, which call more often in pairs than when flying alone (Fawcett & Ratcliffe 2014), resulting in increased sensory collisions. We test if bats attempt to maintain a baseline rate of echoes perceived in the face of sensory collisions. Further tests will incorporate empirical data on sensory collisions in free-flying bats currently being collected in the field to reveal the sensory heuristics individuals use when echolocating in groups.

NEU-P-15

**Coordinating thorax, legs and antennae: How stick insects climb horizontal obstacles**

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As a nocturnal obligatory walker, the stick insect *Carausius morosus* relies on tactile cues when negotiating obstacles. Stick insects search and sample their near-range environment with their antennae, their main sense organs of touch. Antennal contacts are known to provide positional cues used during climbing and may induce short-latency adaptation of ongoing front leg movements. Together, this allows aimed reach-to-grasp movements towards the location touched.

Here, we study the kinematics of reach-to-grasp movements for horizontal obstacles at different height. Our objectives are (i) to test for height-dependent effects on front leg kinematics and body inclination, and (ii) to identify the determinants of grasp location relative to the preceding antennal contacts. Blindfolded animals were motion-captured as they climbed a horizontal rod placed at one of two heights (low, high), using a multi-camera setup (Vicon MX10). Contact events and movement types were annotated manually; kinematic analyses were done in Matlab.

During reaching, the front leg femur is levated depending on obstacle height. Similarly, the rate of 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. The initial antennal contacts appear to have little effect on the subsequent grasp location, as their locations spread widely on both sides of the grasp location. However, the locations of the last antennal contacts preceding the grasp have much lower spread and typically lie medially of the grasp location. This indicates a lateral-to-medial sampling sequence of the antenna, and adjustment of grasp location according to touch. Before grasping, front legs tend to touch the obstacle first with the distal tibia and then flex/retract, with the tibia sliding along the obstacle until the tarsus grasps. Thus, our results reveal the coordinated action of antennae, front legs and thorax.

NEU-P-16

**Metamorphic development of the olfactory system in *Tribolium castaneum***Björn Trebels<sup>1</sup>; Vanessa Weber<sup>1</sup>; Brigitte Götz<sup>1</sup>; Stefan Dippel<sup>1</sup>; Carolin Knoll<sup>1</sup>; Ernst A Wimmer<sup>2</sup>; Joachim Schachtner<sup>1</sup>

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The current picture of the insect olfactory pathway begins with the olfactory sensory neurons (OSN), mainly located on the antenna, that send their axons into the paired antennal lobe, the first central olfactory processing center. From there, projection neurons send their axons to higher olfactory integration centers. A recent study on the olfactory system of *T. castaneum* revealed that besides the antennae also the mouthparts are highly involved in olfaction (Dippel et al., 2016. BMC Biology 14:90). The OSN from the mouthparts are not projecting into the antennal lobe, but to an unpaired glomerular organized olfactory neuropil in the gnathal ganglion, termed gnathal olfactory center (GOC), and to the paired lobus glomerulatus (LG), so far only described in hemimetabolous insects.

In the current study, we investigate the metamorphic development of the olfactory system in *T. castaneum*. In a first step, we analyzed the development of the antennal lobes and correlated the results with the expression pattern of a partial *Orco Gal4/UAS-dsRed* line at different metamorphic stages. We found, that the glomeruli of the antennal lobes form between stages P40 and P50. Our data show expression of *Orco* in all developmental stages except in the prepupal and early pupal stages (P0 to P10). A strong fluorescent signal in distinct zones of the antennae and maxillary palps reappears in pupal stage P20, whereas the last antennal segment shows a weaker signal, which gets stronger in the subsequent stages. These data suggest similar to results found in *Drosophila* that the larval OSN expressing *Orco* undergo apoptosis and are replaced with new OSN. However, unlike in *Drosophila* expression of *Orco* reappears prior to the formation of the antennal lobe glomeruli. In a second step, we started to investigate the metamorphic development of the newly discovered GOC and the LG, to see when these structures develop and how their development relates to the formation of the adult antennal lobes.

NEU-P-17

**Immunohistochemical Characterization of the Daphnia Nervous System**Ioanna Ioannidou; Jacqueline Reinhard; Andreas Faissner; Ralph Tollrian;  
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Freshwater crustaceans of the genus *Daphnia* are small planktonic organisms ranging in length from <1 mm to 5 mm, globally found in standing water bodies. They are of high ecological importance as they are grazers controlling algae population growth but serve as primary prey for higher trophic levels. Over the last century, water fleas of the genus *Daphnia* have become a model for studying phenotypic plasticity. They are able to perceive an array of environmental factors initiating the development of adaptive phenotypes increasing organism fitness. Fundamental for the development of context-dependent phenotypes, is the capacity to detect and identify environmental cues. While the nervous system of *Daphnia* morphologically appears rather simple, it still shows an impressive capacity to respond to a vast diversity of environmental cues. The underlying signalling pathways systemic mechanisms as well as the cellular changes are not thoroughly investigated as the nervous system has only vaguely been described. We here present a method in which we mounted whole brains on poly-lysine coated object slides. This allowed us to identify explicit cell types and their modalities in the *Daphnia* brain using immunohistochemistry and confocal imaging. Our results contribute to our understanding of how *Daphnia* is able to distinguish a vast array of environmental cues.

NEU-P-18

**Aquatic Imaging: Anatomical Base of Map Formation in the Lateral-Line System**Vanessa Hollmann<sup>1</sup>; Julie Goulet<sup>1</sup>; J. Leo van Hemmen<sup>2</sup>; Jacob Engelmann<sup>1</sup>

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The majority of vertebrates are fish and they all possess a lateral-line system that enables them to sense the velocity or acceleration of their aquatic environment. In conjunction with a second presentation we here present two-fold evidence in favour of such a map using the lateral-line system of zebrafish (*Danio rerio*). Topographically organized neuronal maps are frequently found in the animal kingdom. A puzzling exception to this ubiquitous representation is the medial octavolateralis nucleus (MON) of the lateral line system. The termination pattern of the afferents in the MON crudely preserves the peripheral distribution of the neuromasts. Afferents terminate in two columns extending over the rostro-caudal length of the MON, such that neuromast input from the head region terminates medio-ventrally, whereas information from the trunk terminates dorso-laterally. If this topography is maintained at the output level of the MON is unclear, but neurophysiological data suggests that the midbrain torus semicircularis (TS), the major target of the MON, contains a topographic representation of the body that is more finely resolved than the crude head to tail separation of the afferents. We here re-investigate the apparent lack of topography at the level of the MON output neurons, revealing a weak mapping of the MON efferent system for the first time. We further provide theoretical evidence that explains the unique role of the rather poorly mapped representation in the MON through what one may call 'stimulus distillation'. It seems that a poor map in MON is a requisite to de-correlates a diffuse and highly correlated velocity field by sparse coding, leading to refined mapping through subsequent convergence and synaptic plasticity in the TS. This process can profit from, but does not necessarily need, a visual teacher stemming. In summary we present anatomical data that suggests a functional relevance of the hitherto enigmatic role of topography in the lateral line system.

NEU-P-19

**Biomechanics and proprioception of antennal bending**

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Antennae are the main tactile sensory organs of insects. In the stick insect *Carausius morosus*, antennae are very compliant, with a length:diameter ratio of 100:1. During climbing, the antennae of *C. morosus* repetitively touch objects ahead of them. As the flagellum is pulled past an object, it often bends strongly. Assuming that such bending may be a relevant cue for sensory encoding of touch events, we investigated the proprioceptive infrastructure of the stick insect flagellum that may encode bending. To this end, we mapped all campaniform sensilla (CS) from serial scanning electron micrographs of one dorsal and one ventral antennal surface: The dorsal surface carried 144 CS, whereas the ventral surface carried only 58. To test whether this asymmetric distribution of CS was consistent across animals, we compared proximal, middle and distal parts of 8 antennae (4 animals; 6 annuli per part). The density of CS per mm was significantly lower on the ventral than on the dorsal surface. Median ventral density dropped from 2.3 CS/mm at the base to zero at the tip. Median dorsal density ranged from 4.5 to 6.2 CS/mm in all parts. This suggests that a downward bend of the flagellum, as it occurs during an upward sweep against an object, may be encoded with higher fidelity than a similar upward bend. To test whether this dorsoventral asymmetry is matched biomechanically, we measured the passive static bending behaviour of the flagellum. For this, antennae were fixed at the scape-pedicel joint and deflected by a linear robot manipulator positioned at 16 different locations across the work range of the flagellum. Preliminary results show that the maximum curvature increases with deflection amplitude, and the site of peak curvature moves distally with the site of deflection. Whereas bending properties were similar for lateral and medial bends, maximum curvature tended to be larger for downward than upward bending, suggesting that bending biomechanics matches CS distribution.

NEU-P-20

**Receptive fields of polarization-sensitive neurons of the central complex in the desert locust**Frederick Zittrell<sup>1</sup>; Keram Pfeiffer<sup>2</sup>; Uwe Homberg<sup>1</sup>

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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 a range of 360° of E-vector orientations across the slices of the bridge. 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 polarized by a rotating polarizer from different positions on the hemisphere above the locust. Neurobiotin tracer injection allowed for identification of neuron types and reconstruction of anatomical relationships. We found that different types of columnar neuron show E-vector tunings arranged in concentric circles, matching the sky-polarization pattern of a distinct solar position and that this position differs between individual neurons. This matched-filter property theoretically allows a single cell to unambiguously determine the solar azimuth from the sky-polarization pattern alone. Funded by DFG grant HO 950/24-1.

NEU-P-21

**Directional sensitivity in the infrared system of a rattlesnake (*Crotalus atrox*)**Maximilian S. Bothe<sup>1</sup>; Harald Luksch<sup>1</sup>; Hans Straka<sup>2</sup>; Tobias Kohl<sup>1</sup>

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The infrared (IR) system of pitvipers is uniquely specialized to detect low-energy IR-radiation. The sensory periphery, located on the upper jaw, consists of pit-organs that are innervated by trigeminal nerve branches that ramify into smaller, topographically arranged bundles after entering the sensory epithelium. The somata of these afferents are located within the trigeminal ganglia and project centrally to the nucleus of the lateral descending trigeminal tract (LTTD) in the hindbrain, where the spatial termination pattern maintains the pit-organ topography. Here, we used an ex-vivo whole mount preparation of rattlesnake brains, with attached intact pit-organs, to perform electrophysiological recordings from central neurons in the LTTD. Neurons were activated by separate electrical stimulation of multiple nerve bundles that innervate adjacent sensory areas or by an IR-emitter that was moved across the receptive field of the pit-organ in naso-temporal and temporo-nasal directions. The recorded LTTD neurons usually displayed both strong excitatory and inhibitory responses upon stimulation. Based on response latencies, EPSPs were monosynaptic, while IPSPs had a disynaptic onset. Compatible with electrically activated responses, the moving IR emitter also caused comparable sequences of excitation and inhibition in these neurons. Based on respective magnitudes of excitatory and inhibitory components, a directional motion preference was obtained for each neuron by calculating a directional sensitivity index (DSI). Those neurons with a DSI that differed by at least 10% for opposing movement directions were classified as directional sensitive. Accordingly, the majority of neurons (52%) showed stronger activation during naso-temporal moving IR stimuli, while the remainder showed either no directional preference (24%) or stronger activation towards temporo-nasal moving stimuli (24%), indicative of an implemented IR motion detection system at the first central nucleus.

NEU-P-22

**Spike-timing precision across olfactory receptor neurons allows instantaneous odor coding**

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Recent reports of rapid olfactory processing challenge the prevailing hypothesis that odors are encoded in form of spike rate differences across olfactory receptor neurons. However, in order to read out a spike rate code, downstream neurons have to integrate over a considerable time span, at least on the order of the inter-spike interval of the least excited yet still relevant receptor neuron. Compared to a rate code, a spike timing code would allow much faster odor processing. Here we tested whether spike generation in olfactory receptor neurons is precise enough for a spike timing code. Using paired recordings from *Drosophila* olfactory receptor neurons, we found hitherto unknown fast and precise receptor neuron responses to odorant stimuli, with first-spike latencies below 3 milliseconds and a neuron-to-neuron jitter below 0.3 milliseconds. The pattern of first-spike latencies across different receptor neuron types conveyed odorant information over a wider concentration range than did the across-neuron pattern of spike rates. These data provide new upper bounds for the speed of odor processing and suggest that the insect olfactory system uses spike timing for encoding rapidly fluctuating odorants as they occur in nature.

NEU-P-23

**Visuo-motor response to rotational and translational optic flow in the fruit fly *Drosophila melanogaster***

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When flying, *Drosophila melanogaster* relies strongly on visual cues for both stabilization and guidance. Voluntary self-motion and involuntary perturbations, together with visible objects, contribute to the dynamic pattern of luminance on the retina. This 'optic flow' is a panoramic visual signal that may be processed by the brain and, ultimately, to behavior. Theoretically, the global pattern of optic flow can be decomposed into rotational and translational components. But for small fields of view, each motion type can also present similar, and thus ambiguous, motion patterns. For example, leftward motion in the left retina could arise from either forward translation or rightward yaw.

Given that motion perception in flies arises from local computations in the relatively well-characterized, retinotopic motion-processing circuitry, these motion types would not be expected to be discriminated at this level.

Using two approaches, we asked if rotation and translation are distinguished in the brain of *Drosophila melanogaster*. First, do rotation and translation lead to similar or different behavioral outputs? Second, are these two types of optic flow analyzed by the same circuitry or do dedicated pathways exist?

We use virtual reality arenas in which the flies, freely flying, are in closed-loop with the stimulus: the position of the flies, tracked by cameras, is used to display and adjust a precisely defined stimulus consisting in a cloud of random dots ("star field"). Applying a rotational or translational optic flow to this star field enables us to observe and analyze in a comparative manner the visuo-motor response of the flies. We see that *Drosophila* make fewer saccades (abrupt turns) during rotation than during translation or a control condition, which suggests that a rotation-sensitive pathway exists independently from a translation pathway and can suppress saccade generation.

With genetic tools, we performed a behavioral screen by blocking candidate visual neurons. We find neurons contributing to the response to one, the other, or in different ways to both types optic flow components. Blocking other neurons – T4/T5 cells for example – decreased responses to both rotation and translation. Our results therefore both shared and specific cell types involved in processing of rotational or translational optic flow.

PHY-S-01

**A journey of light from the eye to the physiology**

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Light plays a role in the regulation of numerous aspects of physiology and behaviour, including the entrainment of circadian rhythms. In mammals these rhythms are generated by the major pacemaker the suprachiasmatic nuclei (SCN) and peripheral clocks. The SCN synchronised to light/dark change coordinates peripheral clocks resulting in an optimal adaptation of organism's physiology and behaviour to the environment. These responses are mediated via rods and cones and photosensitive retinal ganglion cells expressing melanopsin. All three photoreceptors differ in wavelength sensitivity. My recent findings regarding impact of different wavelengths on behaviour and physiology indicate that blue (470nm) and green (530nm) light have opposing effects. 470nm light results in reduced sleep, increased corticosterone, and increased feeding behaviour whereas 530nm results in sleep promotion. These responses are attenuated in melanopsin deficient mice. Further analysis of the metabolism of melanopsin knockout animals under both normal white light/dark, 12:12hr LD cycles and long day 18:06hr LD cycles demonstrates a number of changes including in the volume of CO<sub>2</sub> produced, energy expenditure, and food intake. These findings demonstrate the first time a possible link between the photopigment function and regulation of metabolic rate under lighting condition. Light in the night has been shown in humans to be disruptive to the circadian clock and sleep. Moreover, these disruptions are associated with obesity. Here I aim to investigate whether different wavelengths may affect metabolism, and whether these effects are mediated via circadian clock the SCN or via ventrolateral preoptic nucleus (VLPO) that regulates sleep. The investigation of melanopsin's role in regulation of metabolism will provide new view on the light effect on energy intake. In addition, it provides new research avenue that addresses the fundamental question of how artificial light affects our health and wellbeing.

PHY-S-02

**A live view on endothelial cell migration in zebrafish**

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Development of the vascular system requires a tight spatiotemporal regulation of endothelial cell (EC) migration through specific guidance cues. Misregulation of these cues can result in improper EC guidance, developmental defects and has implications for disease etiologies in the adult organism.

To understand the fundamental principles of endothelial cell migration, we are using live time-lapse imaging of the developing vasculature in zebrafish embryos.

We have previously described the formation of the zebrafish common cardinal veins (CCVs), which grow by collective cell migration (Helker et. al, 2013, Development 140(13):2776-86).

To identify novel molecular regulators and mechanisms by which endothelial cell migration is regulated, we performed a comparative expression screen of FACS isolated venous endothelial cells of the CCVs. The regulatory contribution of differentially expressed genes was analyzed using gain or loss of function studies, e.g. using Crispr/Cas9 mediated genome editing.

We could show that the cell-cell contact molecule Ve-cadherin is required for controlling the directionality of the migration within the collective.

Additionally, we dissected two separate functions of Semaphorin3d: we showed, that within the same endothelial cells Semaphorin3d acts via two different mechanisms. On the one hand it guides outgrowth of the CCVs via a repulsion mechanism, on the other hand we identified a novel function of Semaphorin3d as an autocrine enhancer of migration by regulating Actin network assembly and cell morphology.

Mechanistic details of the underlying signaling cascades regulating this endothelial cell behavior will be presented. Our findings are highly relevant for the understanding of collective cell migration during development as well as in pathological situations.

PHY-O-01

**A sponge fluorescent secondary metabolite absorbs light in the UV/blue colour range and increases O<sub>2</sub> concentrations in cultures of microalgae**

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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.

Marine sponges harbor many microorganisms of different origin. 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 alkaloid Ageladine A is implemented in the thylakoid space due to the specific local pH gradient, leading to accumulation at low pH and best fluorescence at pH 4. Data implemented in a mathematical model may allow calculation and prediction of O<sub>2</sub> production. Two benefits are suggested for Ageladine A: protection from UV light and conversion to blue light (photosynthesis).

PHY-O-02

**Adipokinetic hormones: receptor-ligand studies in the desert locust, *Schistocerca gregaria***Heather Marco; Heleen Verlinden; Elisabeth Marchal; Emilie Monjon; Jozef Vandenbroeck; Gerd Gäde<sup>1</sup>University of Cape Town  
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Adipokinetic hormones (AKHs) are neuropeptides of 8-10 amino acids with blocked termini (pGlu N-terminally and an amidated C-terminus), in position 2 can be the aliphatic amino acids leucine, isoleucine or valine, or the aromatic phenylalanine or tyrosine; threonine or asparagine are always at position 3, the aromatic amino acids phenylalanine or tyrosine at position 4, the branched amino acids serine or threonine at position 5 and always the aromatic tryptophan and the simple glycine at positions 8 and 9 respectively; while at positions 6, 7 and 10 a large variety of amino acids can be found. As such, the AKHs show significant structural similarity with the red pigment concentrating hormones (RPCHs) of crustaceans, and thus these neuropeptides are grouped in the AKH/RPCH family. Moreover, AKH and RPCH are arthropod homologues of the vertebrate gonadotropin-releasing hormone (GnRH) family, effecting physiological actions via a G protein-coupled receptor, specifically rhodopsin-like G protein-coupled receptors that are related to vertebrate GnRH receptors.

In insects AKH is synthesised and secreted by neurons of the corpora cardiaca into the haemolymph, where it regulates energy metabolism, especially during intense skeletal muscle activity for energy demanding processes (eg. flight). AKH acts on the fat body: glycogen is converted to trehalose, lipids are converted to diglycerides and proline can be used as energy source. AKHs occur in all insects, to date; it is believed that the AKH ligand/receptor system is a good target for putative peptide mimetics for species-specific pest control.

We investigated 2 AKH precursor genes and the AKH receptor gene during different physiological conditions, eg. starvation, active flight, in the desert locust. We study ligand-receptor interactions and do RNAi experiments to learn about AKH signalling in a pest insect.

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PHY-O-03

**The influence of ORMDL overexpression on the gut homeostasis in *Drosophila melanogaster***

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Ormdl3 is an ER transmembrane protein that has previously been associated with sphingolipid metabolism, the unfolded protein response (UPR), Ca<sup>2+</sup> homeostasis, T cell activation and antiviral responses. In recent gene-wide and candidate-gene associated studies the ORMDL3 gene was identified as a susceptibility gene for the development of Asthma. Furthermore, it was shown that it also influences the development of inflammatory bowel diseases like Colitis ulcerosa. We used *Drosophila* as a model to study the effect of ectopically over expressed *Drosophila* ORMDL and human ORMDL3 on the gut homeostasis and epithelial integrity. We showed that ORMDL overexpression enhances the sensitivity of the gut to DSS (Dextran Sodium Sulfate) resulting in extensively shortened life span and that it triggers the epithelial regeneration by influencing stem cell proliferation. In addition, ORMDL modulates repair signaling pathways and the UPR. These results lead to the question if ORMDL also affects the microbiome of the flies' intestine.

P

PHY-O-04

**Rescue of a *Drosophila* EGFR lung cancer-like phenotype by treatment with specific inhibitors**

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Lung cancer became the leading cause of cancer death in the last decades. Late state detection and late treatment options led to a poor 5-year survival rate in non-small cell lung cancer. Since the tracheal system of *Drosophila* shares comprehensive structural and functional similarities with the human lung, it is providing the possibility to study the molecular framework underlying lung cancer development. The ectopic overexpression of several oncogenes induces cancer-like phenotypes in the larval airway system, including meta- and hyperplasia of the airway epithelial cells. We selected one of the key oncogenes for a detailed characterization of lung cancer-like phenotypes and the development of a high-throughput screening system. Ectopic activation of the EGFR pathway in the trachea by expression of a constitutively active EGFR isoform leads to thickening of the epithelium and increased number of cells indicative for epithelial meta- and hyperplasia. Finally, these larvae die due to oxygen undersupply. We used this phenotype to develop a high-throughput drug screening system based on rescuing this lethality. By screening different compounds from a FDA-approved drug library, we found that the EGFR inhibitors afatinib and gefitinib could rescue lethality. The treated EGFR larvae were able to survive the larval stages and successfully developed into pupae and adults. Epithelial meta- and hyperplasia rescue was visible by reversed epithelial thickness and decreased nuclei number.

P

PHY-O-05

**Food quality and low cadmium doses alter life history and gene expression in the nematode *Caenorhabditis elegans***

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*Caenorhabditis elegans* (*C. elegans*) as soil-dwelling and bacterial feeding animal is likely exposed to heavy metals (e.g., cadmium, Cd) in its natural habitat. High doses of cadmium (> 1 mM Cd) act as a severe stressor causing macromolecular damage. However, low doses of such a stressor may lead to positive effects in terms of elevated stress resistance (Leroy et al. 2012, *BMC Evol Biol* 12:187). In the present study, effects of incubation at 0.1  $\mu$ M Cd as well as of feeding different bacteria (*Escherichia coli* OP50 or HT115) were investigated in relation to stress resistance (high Cd doses, bad food quality), life history traits and gene expression. These studies showed, for instance, positive effects of 0.1  $\mu$ M Cd incubation and/or *E. coli* HT115 feeding on the life span and stress resistance of wild type (WT) worms. Transcriptome analyses revealed differential effects of different food bacteria on immune response genes (e.g., genes for C-type lectins). This study also showed clear relationships between the cellular responses to abiotic and biotic stressors.

PHY-O-06

**It takes two to tango: Two respiratory proteins with different functions in an animal-microbe symbiosis**

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The marine gutless worm *Olavius algarvensis* (Annelida, Tubificidae) lives in a nutritional symbiosis with chemosynthetic bacteria. These shallow-water oligochaetes harbour their bacterial symbionts in a thick layer between their epidermis and cuticle, and are intimately associated with both aerobic sulfur-oxidizing and anaerobic sulfate-reducing bacteria. The worms provide their symbionts with both oxygen and reduced sulfur substrates by vertical migration between the upper, oxic and deeper, sulfidic sediment layers.

*O. algarvensis* has two respiratory proteins, a monomeric intracellular hemerythrin and an extracellular giant hemoglobin. Hemerythrin abundances are remarkably high and account for up to 15% of the worm's proteome. In comparison, expression levels of their hemoglobins are about 30-fold lower (Wippler et al. 2016, *BMC Genomics* 17:942). To gain insights into the physiological roles of hemerythrin and hemoglobin in the *O. algarvensis* symbiosis, we analysed protein distribution and gene expression patterns by immunohistochemistry and in situ hybridisation. As in other annelids, hemoglobin was localised in the blood vascular system and expressed exclusively in the chloragog, a specialised internal tissue formed by the coelomic epithelium lining the large longitudinal vessels. Hemerythrin was highly localised and only found in the host epidermal cells underlying the symbiotic bacteria. In other annelids, homologous monomeric hemerythrins are found in muscles and coelomocytes. Hemerythrin expression in *O. algarvensis* consistently co-localised with the sulfur-oxidising symbiont that uses oxygen as a terminal electron acceptor.

We propose that *O. algarvensis* produces such high amounts of hemerythrin to supply both their oxygen-consuming symbionts and their epidermal cells with sufficient oxygen for aerobic respiration. To our knowledge, this is the first time that hemerythrin has been shown to play a central role in an animal-microbe symbiosis.

PHY-O-07

**Survival and salinity tolerance limits in the snail *Theodoxus fluviatilis*: fresh-water vs. brackish water lineages**

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It is commonly accepted that there are morphological and physiological differences between species of the genus *Theodoxus* (Gastropoda: Neritidae) but when it comes to differences within the widely distributed species *T. fluviatilis* there are still open questions. This species has formed regional subgroups (lineages) in northern Germany that appear separate in either fresh- or brackish water, yet, according to literature, are indistinguishable by morphology, anatomy and mtRNA markers. Tolerance towards challenging salinities in animals from these lineages, however, is distinct. The question, whether the observed difference in salinity tolerance is a result of local adaptation after post-glacial re-colonisation of northern Germany and the Baltic Sea or a result of the euryhalinity of this species and its phenotypic plasticity, remains. In this study physiological limits to salinity stress and range shift abilities were compared between individuals from fresh- and brackish water lineages in a 20 day common garden experiment and acclimation regime. Results confirmed that the lineages differ in their tolerance towards challenging high and low salinity levels. Brackish water animals struggled in freshwater but performed much better than freshwater individuals when directly transferred into high salinities (20‰). After slowly acclimatising the animals to their challenging salinities, individuals of both lineages achieved a shift in reaction norms and were able to survive salinity levels otherwise lethal to them. Even with this shift freshwater animals were not able to tolerate salinities as high as brackish water animals could. The explanation may lie in the better developed ability of brackish water animals to accumulate free amino acids in their foot muscle as a mean of cell volume regulation. In conclusion, the results indicate that phenotypic plasticity as well as genetic adaptation may determine osmotolerance in these two *T. fluviatilis* lineages.

PHY-O-08

**Heat flux in manatees: A new approach to estimate metabolic rates in Florida Manatees (*Trichechus manatus latirostris*)**

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Like other members of the Order Sirenia (three recent manatee species and the dugong), the Florida manatee (*Trichechus manatus latirostris*) possesses an unusual suite of adaptations to accommodate both a fully aquatic lifestyle and an herbivorous diet. Among other attributes, Florida manatees have an unexpectedly low metabolic rate and a very limited thermoneutral zone. Their relatively high lower critical temperature around 20°C limits their distribution to tropical and subtropical waters. Although they deal with their sensitivity to cold in part by migrating to warm-water refugia when temperatures decrease, the so-called “cold stress syndrome” affects and kills manatees every year during intense or prolonged cold weather, even in peninsular Florida. Beside boat strikes, cold stress is one of the major threats to Florida manatees. However, knowledge regarding some fundamental aspects of manatee thermal biology is sparse, but essential for effective conservation and management of this endangered subspecies.

We measured heat flux in two captive Florida manatees at different times of the year, in 41 sites distributed across the entire body surface of each manatee. Heat flux differed significantly between individuals, as well as among measuring sites and times of the year. The axillae and lateral tip of each pectoral flipper were identified as “thermal windows”, meaning areas with highest heat exchange. Despite exposure to constant water temperature throughout the year, the manatees in this study had significantly lower heat flux in winter than in summer. We also used heat flux values to estimate metabolic rates in individual manatees. The metabolic rates estimated in this way correspond well with those from previous studies, confirming the reliability of our approach. Our method provides simple and useful options for enhancing manatee welfare by monitoring the animals’ thermal state during potentially stressful activities such as during captures and health assessments.

PHY-O-09

**Irisin is a spermatogonial stem cell regulator in the primate testis**

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The molecular mechanisms that regulate spermatogonial stem cell (SSC) proliferation and differentiation are not fully understood. Recent studies have demonstrated the role of irisin — a cleaved and secreted fragment of the fibronectin type III repeat containing 5 (FNDC5) transmembrane protein and encoded by FNDC5 gene — in cell proliferation and differentiation in various tissues. However, analyses of irisin expression and potential action in testis have not been done. Here, we demonstrate specific expression of irisin in testicular undifferentiated spermatogonia of various primates and the tree shrew (*Tupaia belangeri*), which is a bridging species between primates and non-primates. Irisin was undetectable in spermatogonia of several non-primate mammalian species. Double immunohistochemical staining showed that almost all irisin+ spermatogonia were also SALL4 positive. Expression of both FNDC5 mRNA and irisin is altered during breeding (active spermatogenesis) and nonbreeding seasons (halted spermatogenesis) in adult rhesus monkey testis. Irisin application to testis organ fragment cultures significantly increased expression of KLF4, ID4, cKIT, and SALL4 transcript levels while it suppressed testicular mRNA abundance of Kiss1, which encodes kisspeptin, and, importantly, also FNDC5. Our results suggest that irisin is a novel molecular factor involved in the regulation of undifferentiated spermatogonial cell activities specifically in testes of primates. Moreover, in light of these findings, irisin is the first auto-regulatory factor in primates regulating spermatogonial behavior via autocrine or paracrine mechanisms.

PHY-O-10

**Seasonal telomere dynamics in a free-ranging primate**Michaël Beaulieu<sup>1</sup>; Laure Benoit<sup>2</sup>; Steven Abaga<sup>3</sup>; Peter M Kappeler<sup>4</sup>; Marie JE Charpentier<sup>5</sup>

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Telomeres have recently been used as a marker of ageing in animals in their natural habitat. However, recent studies have suggested that the relationship between ageing and telomere length may be obscured by seasonal variation in telomere length. Here, we examined whether telomere length fluctuates seasonally in free-ranging mandrills (*Mandrillus sphinx*), and investigated the mechanisms potentially underlying such seasonal variation. After controlling for significant age and sex effects on telomere length, we found that mandrills exhibited 25% shorter telomeres during the long dry season than during the long rainy season in their natural habitat in Gabon. During the long dry season, we also found that mandrills exhibited lower lymphocyte proportion in their blood (presumably because of high nematode infection and stress at that time of the year), thereby suggesting that seasonal variation in leukocyte profiles could underlie seasonal variation in telomere length. Accordingly, based on longitudinal data, we found that seasonal changes in lymphocyte proportion were reflected by corresponding seasonal variation in telomere length. Such a relationship is likely to be the result of longer telomeres in lymphocytes than in other leukocytes, as already documented in humans. As leukocytes represent the only nucleated blood cells where telomeres can be measured in mammals, our results highlight the need for future studies examining telomere dynamics to consider temporal variation in leukocyte composition in animals exposed to fluctuating infection and stress pressures.

PHY-P-01

### Transfection of human airway epithelial cells using chitosan as a non-viral delivery system

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In recent years clinical approaches for gene therapy mostly failed due to increased immune responses towards the vectors. Therefore, it is important to improve delivery of genes to target cells at the expense of minimal cytotoxicity. The natural polysaccharide chitosan (CS) is a suitable non-viral vector for gene delivery purposes because of its biodegradability and low cytotoxicity. We were able to design a CS-based delivery system for gene therapy purposes in Cystic Fibrosis (CF). CF is caused by a mutation in the cystic fibrosis transmembrane conductance regulator (CFTR) gene encoding a cAMP-dependent chloride channel expressed in epithelial cells. Defective CFTR is associated with an upregulation of the epithelial sodium channel (ENaC). Dysregulation of these proteins leads to an imbalance of ion and water transport causing problems in multiple organs, especially in the lung. As the disease is single-gene based, conventional gene therapy seems to be a promising approach of treatment. However, no DNA-based gene therapy has yet been established successfully. Hence, we developed CS-wtCFTR-mRNA complexes in order to transfect primary human nasal epithelial (HNE) cells. A cell viability assay (MTT) was conducted with the intention of testing the cytotoxicity of the complexes. The results demonstrate that CS-wtCFTR-mRNA complexes do not have a negative effect on the viability of primary HNE cells. Furthermore, we were able to effectively transfect primary HNE cells. The cells were incubated with CS-wtCFTR-mRNA complexes (0.6 µg/cm<sup>2</sup>) for 24h. Subsequently, transepithelial Ussing chamber measurements were performed in order to evaluate CFTR and ENaC activity. The functional measurements showed an increased cAMP-stimulated CFTR current as well as a decreased amiloride-sensitive ENaC current indicating functional chloride secretion and down-regulation of sodium absorption. The data show that CS-wtCFTR-mRNA complexes are a promising alternative for future CF gene therapy.

PHY-P-02

### Uptake of labeled Chitosan-wtCFTR-mRNA complexes in human bronchial epithelial cells

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The most frequent lethal disorder in the Caucasian population is cystic fibrosis (CF). It is caused by mutations in the cystic fibrosis transmembrane conductance regulator (CFTR) gene. Non-toxic vehicles like Chitosan (CS) are of special interest for gene therapy purposes. CS is a linear polysaccharide consisting of randomly distributed β(1-4)-linked D-glucosamine and N-acetylglucosamine units at different ratios. Due to its polycationic character it is able to form nanocomplexes with mRNA via self-assembly. We were already able to transfect human airway epithelial cells with CS-wtCFTR-mRNA complexes.

The aim of this study is to track the uptake of labeled CS-wtCFTR-mRNA complexes and observe the time beyond mRNA expression. On the one hand wtCFTR-mRNA was fused with GFP and otherwise it was tagged with fluorescent UTPs. Subsequently, the labeled mRNA was complexed with CS.

Transfection of CF cells (CFBE41o-) was carried out with these complexes. Additional CFBE41o- cells were transfected with Lipofectamine<sup>®</sup> as positive control. The cells were fixed in a time interval of 4, 6 and 24h. Furthermore, to underline a successful transfection, we performed antibody staining with ZO-1, a major component of tight junctions, which occurs in 16HBE14o- (human bronchial epithelial) cells and in lesser amount in CFBE41o- cells.

First results reveal that the complexes enter the cells after 6h of incubation, whereas the transfection with Lipofectamine<sup>®</sup> enables the uptake of mRNA already after 4h. Contrary to the dense assembly of tight junctions in 16HBE14o- cells, non-transfected CFBE41o- cells show a diffused and lighter tight junction pattern. Transfection with CS complexes has a small effect on the reassembly of tight junctions of the CFBE41o- cells compared to the transfection with Lipofectamine<sup>®</sup>.

Due to the minor effect of the CS transfection, the physicochemical properties of the complexes need to be checked in order to optimize and improve stability and transfection efficiency.

PHY-P-03

### The power of high resolution mass spectrometry for de novo sequencing of insect adipokinetic neuropeptides

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During the last years, state of the art mass spectrometers have been developed that can separate mass fragments at the fourth or even fifth decimal place. With such analytical instruments at hand, biologists who are interested for example, to sequence de novo small neuropeptide hormones, have a powerful tool in high resolution mass spectrometry (HR MS) to discriminate unequivocally between certain post-translational modifications and isobaric amino acids.

Two examples where HR MS played a crucial role will be discussed: both peptides are members of the metabolic adipokinetic hormone family synthesised in the corpus cardiacum of insects. Example one is a minor peptide from the hemipteran twig wilter where a decision had to be made whether the peptide was post-translationally modified by a sulphation or phosphorylation. In the second example, peptides from a hemipteran spittle bug had either a glutamine or a lysine residue at position 10 in the molecule. To elucidate the correct sequence is paramount for the next step of experimentation: structure-activity studies, in which binding with the cognate receptor will be tested. This, in turn, will be crucial to determine the “active core” of ligand/receptor interaction and will guide the design of stable and cheap peptide mimetics.

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PHY-P-04

### Characterization of ABC transporters from the red flour beetle, *Tribolium castaneum*, involved in renal excretion of xenobiotics

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ATP-binding cassette (ABC) transporters are integral membrane proteins that mediate ATP-dependent transport of a wide range of physiological and xenobiotic substrates across cellular membranes. While ABC transporters have been extensively analyzed in bacteria and vertebrates, little is known about their functions in insects. Our previous studies on ABC transporters of the red flour beetle, *Tribolium castaneum*, revealed that the genome of this beetle harbors 73 ABC transporter genes, which group into the eight known insect subfamilies ABCA to ABCH encoding half- and full-transporters. Subfamily ABCC contains many multidrug resistance proteins discussed to participate in insecticide tolerance. Notably, gene duplication events have significantly increased the number of ABCC genes in the genome of *T. castaneum*, which is known to readily adapt to different classes of insecticides.

The aim of this study is to identify ABC transporters in the Malpighian tubules of *Tribolium* larvae, which mediate tolerance to insecticides, particularly to diflubenzuron inhibiting chitin biosynthesis. For this purpose, we established a test system based on the renal excretion of the fluorescent transport substrate Texas Red (TR). We demonstrate that Verapamil, a competitive inhibitor of ABCB and ABCC transporters, and MK-571, a potent ABCC subfamily inhibitor, but neither the ABCG inhibitor Tectochrysin nor the ABCB inhibitor NSC23925, significantly inhibit TR excretion. These results suggest that TR excretion involves ABC transporters of the ABCC subfamily. Next, we analyzed the effects of verapamil on the toxicity of diflubenzuron, and found that the mortality of larvae is increased when verapamil and diflubenzuron are co-administered. In summary, we provide evidence that an ABCC transporter is involved in the elimination of diflubenzuron, and that ABC inhibitors can act as sensitizers to increase the efficiency of insecticides.

PHY-P-05

### The brain in the deep: A transcriptome analysis of the molecular mechanisms of hypoxia tolerance in the whale brain

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Diving mammals are repeatedly exposed to low oxygen conditions (hypoxia), which may have immediate effects on the oxidative metabolism and thus on brain function. In most terrestrial mammals, even brief periods of reduced oxygen supply cause severe brain damage. However, many whales and seals must have developed strategies of hypoxia tolerance that allow them to dive for up to 2 h without surfacing.

Physiological adaptations in diving mammals have been examined extensively, but little is known about the molecular mechanisms underlying the hypoxia tolerance of the diving brain. Recent studies have suggested a unusual shift in the oxidative energy metabolism from neurons to astrocytes in deep-diving phocid seals which would explain an enhanced hypoxia tolerance. Such shift has not been observed for Cetaceans. In the brain of the minke whale (*Balaenoptera acutorostrata*) and the harbor porpoise (*Phocoena phocoena*), enzymes of the oxidative metabolism reside mainly in neurons as in terrestrial mammals.

For a better understanding of the molecular adaptations in the cetacean brain, we compared Illumina-generated transcriptomes of the deep-diving pilot whale (*Globicephala melas*) and the killer whale (*Orcinus orca*) with a terrestrial relative, the cattle (*Bos taurus*). We analyzed the abundances of transcripts in the visual cortex and the cerebellum as well as mRNA expression levels of enzymes of the energy metabolism and typical stress-related genes. The results were compared with a similar approach, in which the brain transcriptomes of the hooded seal (*Cystophora cristata*) and the ferret (*Mustela putorius furo*) were compared. The results suggest divergent evolutionary strategies in whales and seals to sustain the demands for metabolic energy during cerebral hypoxia.

PHY-P-06

### Tissue-specificity of zebrafish globins

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Unlike most mammals, many fish species live and survive in environments with low and changing levels of oxygen. Respiratory proteins like myoglobin (Mb), neuroglobin (Ngb) and cytoglobin (Cygb) bind or store oxygen, thus possibly enhancing its availability to the respiratory chain in the mitochondria. Teleost fish usually harbour one Mb, one Ngb, one GbX, one Adgb, and two Cygb genes. Duplicated Cygbs are most likely the result of a teleost-specific whole-genome duplication. Some teleosts – for example several icefish or the stickleback – have lost the Mb gene, while duplicated or even triplicated Mb genes have also been observed in other teleost species. Our studies revealed the main sites of expression of the zebrafish globins, which provides hints to their functional context. As expected, the heart is the main site of Mb mRNA expression, although it displays a more widespread expression in various tissues. In fact, Mb is the most highly expressed tissue-globin in most tissues, except brain and gonads. Ngb is most highly expressed in the brain, confirming its role in the nervous system. Cygb1 and Cygb2 genes display distinct patterns: Cygb2 is mainly expressed in the brain and eye, suggesting a role in the nervous system, while Cygb1 displays a more widespread pattern. Surprisingly, GbX is most highly found in the gonads, while previous studies showed expression in parts of the nervous system. We also confirmed the testis-specific expression of Adgb. Together these data indicate a specific role of each globin in the zebrafish globin repertoire.

PHY-P-07

**Unprecedented globin diversity in lungfish**Julia Lüdemann<sup>1</sup>; Angela Fago<sup>2</sup>; Igor Schneider<sup>3</sup>; Thorsten Burmester<sup>1</sup>

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The lungfish are obligate air-breathers and the closest living relative of terrestrial vertebrates. There are six extant lungfish species, four of them in Africa, the other two occur in Australia and South America. Lungfish first appeared in the Devonian period and are an interesting model to study evolutionary key events leading to the transition from water to land.

We study the diversity of globins in lungfish. Globins are small respiratory heme-proteins able to bind O<sub>2</sub> and play an important role in the respiratory metabolism. Notably, some lungfish globins were found amplified in the lungfish genome and have unprecedented expression domains.

In contrast to other vertebrates, lungfish harbor multiple myoglobin (Mb) genes. The West African lungfish *Protopterus annectens* has seven distinct Mb genes that show tissue-specific expression patterns. For example, distinct Mbs occur in the heart and skeletal muscle, and highest levels of Mb were found in the brain. Recombinant Mb proteins have distinct O<sub>2</sub> binding characteristics and enzymatic activities. The data suggest that the Mbs carry out distinct functions and that the Mb genes evolved by neofunctionalization and/or subfunctionalization after gene duplications. Other lungfish species (*P. dolloi*, *Lepidosiren paradoxa*, and *Neoceratodus forsteri*) show a similar Mb diversity, suggesting that Mb gene amplification occurred in the lungfish stem lineage.

Globin E (GbE) was initially identified in the eye of sauropsids (birds and reptiles). In those species, GbE has an Mb-like role in O<sub>2</sub> supply to the metabolically active retina. In lungfish (*P. annectens* and *L. paradoxa*), GbE was found very highly expressed in the ovary, suggesting a role in the O<sub>2</sub>-supply in the developing embryo, analogous or complementary to the embryonic and fetal hemoglobins found in other vertebrates.

PHY-P-08

**Aquaporins of the medicinal leech, *Hirudo verbana***

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Aquaporins are transmembrane proteins that facilitate the passive transport of water and, depending on the subfamily, small uncharged solutes (e.g. glycerol, urea or ammonia). They have been identified in archaeal, bacterial, and eukaryotic organisms (including both plants and animals) representing the three domains of life. Aquaporins are present in almost all types of cells and play a crucial role in fundamental physiological processes like cell volume control, osmoregulation, and secretion. Based on the molecular characteristics and nomenclature of human aquaporins, four subfamilies can be defined: the Aqp1/4-family of classical aquaporins (encompassing Aqp0, 1, 2, 4, 5 and 6), the Aqp3-family of aquaglyceroporins (Aqp3, 7, 9 and 10), the Aqp8-type aquaammoniaporins (Aqp8) and the unorthodox aquaporins (Aqp11 and 12).

Upon feeding on its host, the medicinal leech, *Hirudo verbana*, transfers a broad range of bioactive substances into the host's wound to prevent premature hemostasis and blood coagulation. These substances are produced in unicellular salivary gland cells, stored in densely packed granules and injected into the wound through tiny ductule openings in the jaws. While the exact mechanism of secretion still remains elusive, it can be assumed that the formation of an aqueous saliva requires water fluxes between extracellular compartments, the gland cells and the granule bodies within.

Having access to a preliminary genomic database of *Hirudo verbana* (kindly provided by Eduardo Macagno, UCSD), we conducted a data mining project in order to identify putative aquaporin encoding genes. So far, 23 complete or partial sequences of different aquaporins of all four subfamilies could be predicted. For complete sequences, we furthermore tested the actual presence of aquaporins in salivary gland tissue and obtained positive evidence of expression for representatives of the Aqp1/4 and Aqp3-subfamilies.

PHY-P-09

### Hormons and Immunity - Biogenic amines regulate the cellular immune response in *Drosophila melanogaster*

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The cellular immune response of *D. melanogaster* is mediated by hemocytes which are capable of phagocytosis and production of antimicrobial peptides (AMPs). It is known that neuroendocrine factors like biogenic amines (BAs) have an impact on phagocytic activity in invertebrates and are suspected for modulating properties on the immune response.

Our aim is to unravel the interplay between BAs and the hemocyte mediated immunity. The fruit fly has proven to be a perfect choice to elucidate those interactions between blood cells and immunocompetent organs, due to its absence of an adaptive immunity and multifaceted *in vivo* experimentations.

At first, an expression profile of BA receptors in primary hemocytes (PHs) was made and confirmed the expression of nearly all BA receptors. Here we present the immunomodulatory relevance of octopamine (Oct $\beta$ 1, Oct $\beta$ 2) receptors. To determine a potential regulatory effect of BAs on the phagocytotic activity, PHs were incubated with octopamine and fluorescent particles and the phagocytic intensity was assessed. Concurrently, phagocytosis of adult hemocytes devoid of the octopamine receptor was monitored, and we could verify that larval and imaginal hemocytes are strongly controlled by BAs in their ability to phagocytose. Furthermore, in imagos this observation correlated with a reduced survival of *P. carotovorum* infected Oct $\beta$ 1- and Oct $\beta$ 2-knock outs and a disturbed AMP response of these individuals, which resulted in an uncontrolled bacterial replication within the fly. Although the detailed mechanism of this hormone-immune-interaction is still subject of research, our findings demonstrate that the activation of octopamine receptors (Oct $\beta$ 1, Oct $\beta$ 2) is indispensable for elimination of invading pathogens, by affecting two major defense mechanisms: 1) phagocytosis and 2) antimicrobial peptide release. This shall show that any influence of the hormone system can directly affect the immune defense, not only in insects but surely in all animals.

PHY-P-10

### Characterisation of *Plasmodium falciparum* populations selected on the human endothelial receptors P-selectin, CD9, CD36 and ICAM-1

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According to the WHO 'world malaria report 2015' approximately 214 million cases of malaria occurred worldwide. A malaria disease is caused by an infection of the protozoan parasite *Plasmodium*. There are 5 *Plasmodium* species known to infect humans, whereas *P. falciparum* is responsible for almost all cases of death. To evade the host immune system the parasite invades erythrocytes and the infected erythrocytes (IEs) adhere to various endothelial receptors of its human host. Depending on the location of the binding, cytoadhesion can have severe consequences for the host, including tissue damage and ultimately, organ failure. Currently, only one protein family is known to be involved in these receptor-ligand interactions, the *Plasmodium falciparum* erythrocyte membrane protein 1 (PfEMP1) family. Every parasite has a variety of 60 different var-genes, coding for PfEMP1, while only one gene is expressed at any certain time and the respective PfEMP1 is localized on the IE membrane. So far, 23 human receptors are described binding IEs but for the majority the respective PfEMP1 ligand is unknown.

In this study we identified for the first time the PfEMP1 molecules involved in binding to P-selectin and CD9 by analyzing transcriptomes of parasite populations enriched for binding to these receptors. Interestingly, although a binding of IEs to E-selectin and CD151 is described in the literature, no parasite ligands could be identified in the present study. This implies that the corresponding ligands for these receptors have either weak binding capacity or do not exist on the IE surface.

Furthermore, the cytoadhesion of *P. falciparum* populations selected on the receptors CD36, ICAM-1, CD9 and P-selectin was characterized using a laminar flow system. Based on these results, a new hypothesis for the dynamics of cytoadhesion of IEs to endothelial cells was proposed.

PHY-P-11

**Novel antistasin-like proteins in the medicinal leech (*Hirudo verbana*)**

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European medicinal leeches (*Hirudo spec.*) are ectoparasites feeding on body fluids of animals from all vertebrate taxa. During feeding they secrete up to 100 salivary proteins into the wound inflicted on the host skin. These supposedly bioactive compounds allow leeches proper feeding by suppressing defensive actions of the host and by long-term blood storage in leech crop. Apart from the thrombin-inhibitor hirudin and a few other proteins, most salivary proteins are structurally and functionally uncharacterized. Given that the parasites have to overcome defensive actions of the host, their saliva may contain substances with anesthetic properties, anti-complement and anti-inflammatory factors or substances interfering with the blood coagulation cascade, e.g. inhibiting diverse serine proteases (blood clotting factors, thrombin).

We set out to investigate such putative protease inhibitors and screened *Hirudo sp.* genome data provided by Eduardo Macagno for sequences that potentially encode proteins of the antistasin family. In other leech species such members have been recognized as inhibitors of factor Xa. We identified three different sequences encoding putative antistasin-like proteins including signal peptides. Two of them include conserved antistasin-motifs, the 3rd sequence-type displays remarkable alterations in the antistasin-motif. This raises the question if that 3rd protein may have a different function than the other two. We derived individual primer pairs for each sequence and separated full length-PCR products, using total RNA preparations from *H. verbana* and reverse transcription. The cDNAs were purified and cloned into pBlueScript II KS(-) vector for plasmid amplification and control sequencing. The results provide strong evidence for the expression of at least three previously unknown antistasin-like proteins in *H. verbana*. We started experiments generating the recombinant forms of all 3 variants for functional characterization.

PHY-P-12

**Marine mammals down under: adaptations of the brain to hypoxia during diving**Cornelia Gessner<sup>1</sup>; Andrej Fabrizius<sup>1</sup>; Mariana Leivas Müller Hoff<sup>1</sup>; Lars Folkow<sup>2</sup>; Thorsten Burmester<sup>1</sup>

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While the brain of most terrestrial mammals suffers from irreversible damage during only short periods of low oxygen levels (hypoxia), marine mammals are excellent breath-hold divers that have adapted to hypoxia. The neurons in the cortex of the deep-diving hooded seal (*Cystophora cristata*) have an intrinsic tolerance to withstand hypoxia. We aim to understand the molecular basis facilitating this neuronal tolerance to hypoxia.

A comparative expression analysis in the cortex of the hooded seal and the ferret, a non-diving carnivore, revealed several genes with significantly higher expression levels in the hooded seal. We determined whether the proteins of these genes are located in different cell types in the seal compared with the ferret and mouse. Further, we assessed whether genes expressed in the hooded seal cortex show signs of positive selection compared to non-diving mammals.

We found that clusterin and S100B, both known to have roles in the response of the brain to oxidative stress, show high expression rates in the hooded seal. However, both genes show no signs of positive selection in diving mammals and their protein localization does not differ from terrestrial mammals. Our results suggest that a possible neuroprotective role of both genes might be mediated by a change in expression levels but not by functional changes.

PHY-P-13

**Molting genes in the onychophoran *Euperipatoides rowelli* – first insights into the ancestral mode of ecdysis in panarthropods**

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Molting or ecdysis is a characteristic feature of the most diverse and abundant animals on Earth – the ecdysozoans, which include arthropods, nematodes, priapulids and allies. The animals shed their cuticle periodically during the molting process which is controlled by several genes, proteins and enzymes. Ecdysteroids, especially the prohormone ecdysone and 20-hydroxyecdysone, are defined as molting hormones in the clade Ecdysozoa. The molecular mechanisms of molting have been analyzed in a few arthropod species, including decapod crustaceans and insects, but only little is known from their closest relatives, the onychophorans (velvet worms) and tardigrades (water bears). In onychophorans, both ecdysone and 20-hydroxyecdysone have been identified previously, but neither the function nor the synthesis sites of related molecules are known. We are therefore analyzing the expression levels of candidate genes in the onychophoran *Euperipatoides rowelli* to clarify the ancestral set of genes involved in molting of panarthropods. Moreover, a comparison between different physiological states and tissues of *E. rowelli* might help to identify ecdysteroid-expressing tissues in Onychophora.

P

PHY-P-14

**Significance of calcium signaling in flight of transgenic *Drosophila* expressing the laser light-triggered calcium ion channel channelrhodopsin (ChR) in the asynchronous flight muscle tissue**

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Flight is an energetically costly form of locomotion mainly depending on inertial forces and friction. In flying animals, such as *Drosophila*, the asynchronous indirect flight muscle (A-IFM) provides mechanical power for wing flapping. To study calcium control in A-IFM, we employed the Gal4/UAS system and genetically modified muscle calcium control by genetic insertion of the calcium channel channelrhodopsin, expressed under the Act88F promoter. By application of laser light, the selected approach allows us to elicit artificial changes in intracellular calcium concentration in flying flies. During level flight, A-IFM power output is thought to precisely match the power requirements for wing flapping. If the animal provides calcium-dependent mechanical power in excess to what is actually needed for wing flapping, the wing hinge must destroy waste power to avoid structural damages, which leads to a reduction in flight efficiency. Alternatively, the animal might allow changes in wing kinematics that potentially lead to unwanted changes in body posture stability. To distinguish between these two strategies, we tested the consequences of laser-triggered calcium activation by flying transgene fruit flies in a virtual reality flight simulator under closed-loop feedback control. Data show that during laser activation, muscle calcium alters stroke amplitude only weakly, while stroke frequency decreases. The latter result is quite unexpected because aerodynamic theory predicts that an increase in muscle calcium concentration reinforces muscle power that should lead in turn to an increase in wing flapping frequency and not vice versa. The finding might highlight a more sophisticated control mechanism for wing kinematics as previously assumed. A possible explanation for our results is that the increase of calcium influx causes an increase in muscle stiffness, hampering thorax resonance and thus stretch activation of the asynchronous flight muscle.

P

SYS-S-01

**Evolution of body organisation in arthropods and its implications on systematics and character transformation**

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Evolutionary modifications of body organisation of metazoan animals has been attributed to the evolutionary success of various groups. Evolutionary changes in body organisation can, for example, be coupled to changes of feeding strategies or changes of locomotion. Within Euarthropoda – insects, crustaceans, myriapods, spiders and their kin – such changes in body organisation can be recognised easier than in many other groups due to their segmented body. Several segments with similar functional morphology are organised into functional units and can thus be recognised as distinct body regions or tagmata. On a coarse scale it may appear that only few principal tagmatisation patterns are realised among the different groups of Euarthropoda. Yet, on a more detailed level a range of variations within different subgroups can be recognised. Based on a phylogenetic framework, such smaller changes can be traced and used as a detailed reconstruction of character evolution.

In addition to detailed investigations on modern-day representatives of Euarthropoda, existing gaps in character evolution can be filled by including exceptionally preserved fossil representatives of various lineages. Such individuals often reveal character states not existing in modern-day fauna, with this representing “steps-in between”. I will present cases in different arthropod lineages in which a seemingly stereotypic body organisation can indeed be differentiated into several differing types of body organisation, representing such cases of stepwise character evolution. Highly detailed character evolution as proposed here improves the quality and explanatory power of phylogenetic reconstructions. Only in this way it becomes possible to reintegrate phylogenetic reconstructions into a larger biological framework via the principles of reciprocal illumination.

SYS-S-02

**A decade of cutting edge insect phylogenomics**

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SYS-O-01

**Three new onychophoran species from Tasmania shed light on the origin of New Zealand velvet worms**

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Onychophorans, or velvet worms, are a relevant group for studying animal evolution and biogeography, but their impact on each of these fields is blurred by the incomplete existing data for key taxa. For example, assessing the evolutionary history of these animals in New Zealand is currently hampered by the limited information available for onychophorans from Tasmania, which is believed to be the past bridge between New Zealand and mainland Australia. The origin of New Zealand onychophorans has been controversially discussed and divergence time estimates spanned a period that overlapped with both the rifting of New Zealand from Australia and its subsequent putative submersion during the Oligocene. Therefore, it is not yet possible to decide whether New Zealand lineages had an early vicariant or late dispersal origin. To shed light on this topic, we investigated three new and two described onychophoran species from Tasmania using morphological, karyological and molecular methods, and compared our data with those available in the literature for the mainland Australian and New Zealand taxa. Our morphological and karyological data suggest the existence of four distinct groups of onychophorans in Tasmania, including three matrotrophic viviparous groups, and one oviparous group. Molecular phylogenetic analyses, including additional taxa from the three landmasses revealed, however, that the oviparous Tasmanian species most likely represent two lineages, with oviparous species from the Australian mainland nested within one of them. These two lineages form, together, the sister group of all New Zealand oviparous onychophorans. On the other hand, the Tasmanian matrotrophic viviparous onychophorans form a monophyletic group, which is closer related to the New Zealand than to the mainland Australian taxa. These results suggest a single, early vicariant event for both New Zealand clades, including oviparous *Ooperipatellus* and the matrotrophic viviparous *Peripatoides* species.

SYS-O-02

**Knocking trees, spiders fall: fourteen new species of *Shaanxinus Tanasevitch, 2006* (Araneae, Linyphiidae, Erigoninae) from Taiwan and Vietnam**Shou-Wang Lin<sup>1</sup>; Lara Lopardo; Gabriele Uhl<sup>1</sup><sup>1</sup> Zoologisches Institut und Museum Greifswald[shouwanglintaiwan@gmail.com](mailto:shouwanglintaiwan@gmail.com)

Male dwarf spiders (Erigoninae) show a great diversity in their sexually dimorphic prosomal structures, which are accompanied by secretory glandular tissues, of which the products function as nuptial gift during copulation. Sexual selection on these traits might be one of the reasons why this group is the most diverse subfamily in Linyphiidae, representing the largest spider family in the northern hemisphere. Consequently, erigonines are an ideal group for studying the impact of sexual selection on character evolution and species diversification. However, the erigonine diversity in East Asia is still poorly assessed and phylogenetic relationships are unclear. For instance, only 12 species are currently known for Taiwan, of which most genera are represented by a single species.

Surveys of Taiwanese dwarf spiders were conducted in 2014, 2015 and 2017, during which 13 undescribed arboreal species of the genus *Shaanxinus Tanasevitch, 2006* were collected by tree-branch-knocking. In addition, one undescribed *Shaanxinus* species from Vietnam was found during the inspection of undetermined museum material. Previously, only two Chinese species of this genus have been described. We present intrageneric relationships of *Shaanxinus*, inferred from morphological characters based mainly on male secondary sexual traits. The monophyly of species, as well as male-female matching, were confirmed by the use of three genetic markers: COI, 16S and 28S. Furthermore, we present the internal dimension of male prosomal glandular tissues in three species reconstructed using micro-CT.

Considering the species richness of this group in Taiwan, we expect to find many more *Shaanxinus* species and other dwarf spiders in Taiwan and on continental East Asia if suitable collecting methods are applied. Increased knowledge of species diversity and their phylogenetic relationships will help to elucidate the evolution of male prosomal modifications and assess the role of sexual selection in diversification.

SYS-O-03

**Are there really four species of giraffe?**Sven Winter<sup>1</sup>; Julian Fennessy<sup>2</sup>; Axel Janke<sup>1</sup>

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Due to a 40% decline in numbers, there are only 100,000 giraffe left in Africa. Therefore, giraffe (*Giraffa camelopardalis*) have been recently considered “Vulnerable” on the IUCN Red List. However, the threat of extinction may be more grave, because there might be more than one species. Traditionally giraffe are assigned to a single species with nine subspecies, but this classification is solely based on pelage pattern, ossicone morphometrics, and geographic distribution. Genetic analyses based on mtDNA found reciprocal monophyly of the matrilineages among seven subspecies. This raised the question, whether giraffe clades might be genetically more distinct and form in fact species. Detailed analyses based on nuclear loci demonstrated that four clades of giraffe are genetically distinct species (Fennessy et al. 2016). The question remains whether the four giraffe species are reproductively isolated and what amount of gene flow exists. Here, we present an extended dataset of 137 giraffe individuals, and gene flow/migration analyses to investigate if an increased dataset and more detailed analyses are consistent with the hypotheses of four giraffe species. These findings have important implications for giraffe conservation, because the 8,700 individuals of the reticulated giraffe (*G. reticulata*) species and 5,200 individuals of the northern giraffe (*G. camelopardalis*) species, would be as endangered as wild black rhinoceroses.

SYS-O-04

**What are cryptic species? – A process-driven perspective**

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‘Cryptic species’ is nowadays a commonplace term in systematics, evolution, and ecology and with the advent of barcoding approaches increasing numbers of species are shown to be supposedly cryptic. However, the usage of the term is inconsistent in the literature and a unifying framework for studying cryptic diversity is generally lacking. Moreover, processes related to cryptic species are generally not taken into account. These processes comprise (I) recent divergence, (II) parallel or (III) convergent phenotypic evolution, or (IV) strong selection for phenotypic stasis. This causes confusion and imprecision in attempts resolving origins and evolutionary trajectories of cryptic species. For example, studies attempting to relate the incidence of cryptic diversity to ecological parameters do not take into account the distinctions in how cryptic species are generated, biasing results and conclusions.

Herein, a conceptual framework for cryptic species is presented based on the four processes underlying their generation of recent divergence, parallelism, convergence, and stasis. These four categories differ from each other in their temporal scales, phylogenetic context, and evolutionary processes implicated in their creation. The practical importance of such an approach is shown by a literature survey indicating the lack of a hypothesis-driven framework for understanding the evolutionary basis and meaning of cryptic species. The survey

further underscored the need for much higher genetic and morphological standards in the empirical investigation of cryptic species. Indeed, there was a general lack of consistency and experimental rigor in the designation of cryptic species. This inconsistency can hamper the designation of taxa into different categories of cryptic species, complicating analysis of underlying process. The refined concept of cryptic species has the potential to reveal hidden pattern and process increasing the understanding of evolution and biodiversity.

SYS-P-01

**The endemic New Zealand spider family Huttoniidae (Araneae, Arachnida)**Tim Martin Dederichs<sup>1</sup>; Raymond Forster; Cor J. Vink; Peter Michalik<sup>2</sup>

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The spider family Huttoniidae is known only from New Zealand and the only described species is *Huttonia palpimanoides* O. Pickard-Cambridge, 1879. The description of this species was based on a single female specimen collected in the Dunedin area of the South Island. Huttoniids are a member of the superfamily Palpimanoidea, which also includes the families Stenochilidae, Palpimanidae, Mecysmaucheniidae and Archaeidae. The present study is based on material collected over almost five decades by comprehensive collecting programs. Our examination of the material revealed a considerable species diversity, which is distributed throughout mainland New Zealand, but appears to be absent in the outlying Chatham and Subantarctic Islands. Moreover, the disproportionate number of immature to mature spiders in Berlese samples suggest that adult huttoniids live above the forest floor. This is supported by collecting programs covering a full range of habitats that clearly indicate that most adult huttoniids were found in dried fronds of tree ferns. There are 13 new huttonid species, the majority in the genus *Huttonia* and two new genera. Most of the species appear to be locally endemic.

SYS-P-02

**Repeat landscapes in the genomes of Cirripedia (Crustacea)**Sebastian Martin<sup>1</sup>; Henrik Glenner<sup>2</sup>; Lars Podsiadlowski<sup>1</sup>

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One of the most striking examples of the force of evolution on body shape is the extremely derived morphology of parasitic barnacles (Cirripedia: Rhizocephala). Their closest relatives, the acorn barnacles (Cirripedia: "Sessilia") and goose barnacles (Cirripedia: Pedunculata), are sessile Crustacea, with their body enclosed in a couple of cuticular skeleton plates and a set of appendages used for suspension feeding. All cirripeds share a unique free living larval stage, the cypris larva.

In non-parasitic species these larvae settle on solid ground and undergo metamorphosis into juvenile barnacles. Larvae of the parasitic Rhizocephala settle on an appropriate host, penetrate its body wall or gill epidermis and inject an infectious stage into the body cavity. Adults of Rhizocephala lack almost all characteristic features of arthropods – they do not possess appendages, mouth, gut, respiratory and excretory organs. Instead they grow as a fungus-like system of tubes in their hosts hemocoel. To what extent genomic changes are correlated with this fundamental change in morphology is focus of our current research.

Here we present an analysis of NGS-data of three cirriped species, *Chelonibia testudinaria* (epizootic lifestyle), *Anelasma squalicola* (ectoparasitic), and *Sacculina carcini* (endoparasitic). REPEATEXPLORER was used to trace the landscape of repetitive elements in their genomes. These elements, formerly known as "junk DNA", are putatively involved in genome evolution by increasing, rearranging and diversifying the genetic repertoire of their hosts. Tandem repeats and transposable elements show diverse patterns in cirripeds and represent an impressive portion of 60-70% of their genomes. Not many of these elements are shared between the three species.

SYS-P-03

**Trans-oceanic dispersal shaped distribution of Branchiopoda**Martin Schwentner<sup>1</sup>; Stefan Richter<sup>2</sup>; Gonzalo Giribet<sup>3</sup>

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Branchiopoda live predominately in small, temporary aquatic habitats with no means of active dispersal. Their resting eggs, however, are well adapted for passive dispersal via wind, birds or other animal vectors. Phylogeographic studies have shown that passive dispersal can be very effective at local and in some cases even continental scales. Several branchiopod genera are distributed across multiple continents. Whether this reflects Pangaeian, Gondwanan or Laurasian distributions, or later trans-oceanic dispersal is unknown. Branchiopoda have a rich fossil record, but only few fossils have been attributed to extant genera, providing relatively little information regarding the historic distribution of these taxa.

Based on the most comprehensive phylogenomic dataset for Branchiopoda, we were able to estimate the divergence times of several widely distributed genera using fossil calibrated molecular clock analyses. The obtained age estimates suggest that the break-up of continents predate the divergence of most of these widely distributed taxa. Therefore, their wide distribution across continents seems to be the result of multiple trans-oceanic dispersal events. Migrating birds could have dispersed resting eggs between continents, and indeed most trans-oceanic dispersal events seem to have occurred after the evolution of modern birds.

SYS-P-04

**The oldest antlion-like larva, the challenges of diagnostic characters, and morphometrics as a possible strategy**

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In different animal groups, early free-living developmental stages, often called larvae, may exhibit very different morphological features and lifestyles than their corresponding adults. Prominent examples of larvae occur within winged insects, for example, the caterpillars of butterflies, or the maggots of flies. An especially aberrant-appearing type of larvae are those of antlions and their close relatives (Myrmeleontiformia, Neuroptera), which exhibit a predatory lifestyle. Their most obvious morphological specializations are prominently elongated hook-like mandibles with a large groove (functionally) ventrally, which is covered by the maxillae. In this way, these mouthparts form a functional tube for suction-feeding and in some cases venom injection. The so far oldest fossil finds of such larvae are 100 million years old and preserved in amber. We report here a single specimen from Cretaceous limestones from the Brazilian Crato formation of about 108 million years age. This specimen exhibits the characteristic body shape and mouthpart specializations of antlion-like larvae. A major challenge for further interpreting this fossil is its preservation. Despite being exceptional, it still does not provide morphological details which are generally used in the taxonomy of modern forms. This is a general phenomenon encountered in fossil vs. extant comparisons. The suggested approach is trying to identify alternative additional diagnostic features. Here we explore the potential of using morphometric methods for such an enterprise. A more precise phylogenetic interpretation of the fossil is crucial: as the fossil represent the oldest report of such a larva, it represent an important calibration point for evolutionary reconstructions.

SYS-P-05

**Species Identification and Delimitation in Nemerteans - Meet me half way between morphology and molecular-based taxonomy**

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Studying ribbon worms (Nemertea) involves the exploration of species diversity and the phylogenetic relationships among species. However, working on nemertean taxonomy is challenging, since external and internal morphology yield only relatively few diagnostic characters. As observed in many other taxa, identification and delimitation of nemertean species has shifted from morphology-based to DNA-based methods. In DNA-based taxonomy, a barcode sequence for species identification or a broad set of sequences for species delimitation are used. Compared to the traditional, morphological approach, this allows for assessing the diversity of this taxon in a faster and more efficient manner, especially when dealing with cryptic species. Nemertean species descriptions and re-descriptions are considered valid if they are based on the barcode sequence, a description of external characters in combination with color photographs, and voucher specimens in ethanol. However, at this point, our knowledge about the internal morphology of nemerteans represents an amount of information that is not yet matched by molecular data. We therefore consider it as crucial to provide additional data on the internal morphology as supplement to species description whenever this information is available.

We collected data on nemerteans sampled from the European Atlantic and North Sea Coasts of Europe. We compile a species catalogue that includes voucher material, sequence data, color photographs, descriptions on external characters, and links to histological section series/ $\mu$ CT scans, which are uploaded in public data repositories (MorphDbase). We aim at clarifying the status of some type species and species that are overall difficult to delimit from congeners. In the future, this will provide a backbone for the revision of ambiguous sequence data in Genbank and will enable the successful application of DNA-based taxonomy.

SYS-P-06

**The development of *Thalassema thalasseum* (Echiura) provides novel insights into the evolution of trochophore larvae**

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The lophotrochozoan clade Echiura (spoon-worms) comprises non-segmented, mainly deposit-feeding, marine worms. While originally having been considered a separate phylum, echiurans are nowadays recognized as derived members of the annelid radiation, based on several molecular phylogenetic analyses. More recent analyses of the development of the nervous system have lent morphological support to this hypothesis. As in Annelida, the ventral nerve cord develops in an anterior to posterior progression as a metamericly arranged, initially paired primordium that fuses later in development. The ancestral type of development in Echiura, however, is presently unclear. The last common annelid ancestor is assumed to have had a trochophore larva with an apical organ comprising few serotonergic and FMRFamidergic flask-shaped cells and trochal neurite bundles, underlying the trochal band of elongated cilia and also showing serotonergic and FMRFamidergic immuno-reactivity. However, considerable variation due to differing life history strategies is seen in extant annelid species. While echiuran species show both lecithotrophic and planktotrophic development a representative of their assumed closest relative, *Capitella teleta* develops via a lecithotrophic larva. Investigation of the development of a basal representative of Echiura, *Thalassema thalasseum* reveals considerable differences to other echiuran species. While there are correspondences to *C. teleta* that support the assumed close affiliation of Echiura to Capitellidae the data also suggest that, unlike in *C. teleta*, the ancestral mode of development in Echiura was via a planktotrophic trochophore larva.

Abaga, S..... 254  
 Aboelsoud, R ..... 119  
 Aisenberg, A ..... 136  
 Albrecht, T ..... 101, 102  
 Albrechtová, J ..... 101  
 Althaus, V ..... 220  
 Amen, R ..... 153  
 Ammersdörfer, S..... 36  
 Amson, E..... 172  
 Anders, J ..... 228  
 Anichini, M ..... 54  
 Arnold, P..... 163, 172  
 Atika, B ..... 73  
 Baasner, J-S..... 145  
 Baer, B ..... 133  
 Bährle, R ..... 178  
 Bangel-Ruland, N... 255, 256  
 Bauch, C..... 121  
 Bauer, E..... 62  
 Baues, M..... 222  
 Baumbach, T..... 160  
 Beaulieu, M ..... 42, 254  
 Becker, K ..... 192  
 Becker, S ..... 64  
 Beckers, P ..... 184  
 Behr, R ..... 253  
 Beleyur, T..... 232  
 Beltz, B..... 72  
 Benda, J ..... 8  
 Beninde, J ..... 144  
 Benoit, L ..... 254  
 Bertrand, O..... 38, 57  
 Bester, M ..... 61, 62  
 Betz, O ..... 175, 182, 187  
 Bianco, G ..... 64  
 Bickmeyer, U..... 245  
 Biedermann, M..... 185  
 Bilde, T..... 31  
 Birkhold, A..... 175  
 Blanke, A..... 177  
 Blüthgen, N..... 97  
 Bogenberger, K ..... 90  
 Bohrmann, J ..... 75  
 Bollatti, F..... 136  
 Bölting, S ..... 46  
 Boonekamp, J ..... 121  
 Bornemann, H ..... 84  
 Borner, J..... 126  
 Bossen, J ..... 248  
 Bothe, M..... 239  
 Böttinger, L ..... 105  
 Botton-Divet, L..... 172  
 Bradler, S ..... 174  
 Braig, F..... 169  
 Brandl, H..... 92  
 Breedveld, M ..... 27  
 Brenneis, G ..... 72  
 Brigic, A ..... 199  
 Bruchhaus, I..... 264  
 Brückner, A ..... 63, 85, 97  
 Bruyn, N..... 61, 62  
 Bucher, G ..... 71  
 Buckley, T..... 174  
 Burmester, T126, 259, 260, 261, 266  
 Büscher, T ..... 174  
 Cadahia, L ..... 149  
 Campione, E ..... 241  
 Caspers, B ..... 19, 106, 124  
 Caspers, B..... 40, 92  
 Castillo, R..... 107  
 Catania, F..... 151  
 Chacron, M..... 206, 211  
 Chakarov, N..... 145  
 Charpentier, M ..... 254

Chen, L..... 69  
 Chicca, E ..... 231  
 Christaller, F..... 62  
 Clark, M ..... 110  
 Clauss, M ..... 170  
 Cleary, A..... 61, 62  
 Cory, A-L ..... 30  
 Csilléry, K ..... 109  
 Dalla, S..... 146  
 Dallmann, C ..... 214  
 D'Alvise, P ..... 80  
 Danchin, E..... 152  
 de Bivort, B..... 7  
 de Jong, B ..... 66  
 Deckert, J ..... 104  
 Dederichs, T..... 275  
 Demandt, N ..... 34  
 Dickhaus, T ..... 137  
 Dieker, P..... 138  
 Differt, D ..... 57  
 Dippel, S ..... 215, 228, 234  
 Dittrich, C..... 26  
 Dobler, S ..... 130, 146  
 Dölling, R ..... 249  
 Donath, A ..... 127  
 Dörpinghaus, M..... 264  
 dos Santos Rolo ..... 160  
 dos Santos Rolo, T ..... 160  
 Doussot, C ..... 208  
 Drozd, D..... 194  
 Druckmann, S ..... 223  
 Drummer, C ..... 253  
 Dubilier, N..... 250  
 Duda, M..... 149  
 Dümmer, B..... 95  
 Dürr, V213, 214, 224, 227, 233, 237  
 Eberhard, M..... 42, 43, 253

Eberhart-Phillips, L ..... 32  
 Eccard, J..... 27  
 Edme, A ..... 102  
 Effertz, T ..... 230  
 Egelhaaf, M.. 38, 56, 57, 208  
 Eggs, B ..... 175, 182, 187  
 Ehrlich, I..... 205  
 Ekvall, M ..... 64  
 Emde von der, G44, 45, 49, 50  
 Engel, K..... 92, 106  
 Engelmann, J55, 60, 114, 212,  
 218, 225, 226, 231, 236  
 Engels, T ..... 190  
 Engler, T..... 160  
 Erdsack, N..... 252  
 Esteve-Altava, B..... 163  
 Eweleit, L ..... 123  
 Exnerova, A..... 104  
 Exter, A ..... 237  
 Fabre, A-C..... 172  
 Fabrizious ..... 266  
 Fabrizious, A ..... 259, 260  
 Fagan, M..... 177  
 Fago, A..... 261  
 Faissner, A..... 235  
 Farge, M..... 190  
 Fawcett, K ..... 110  
 Feldhaar, H..... 26  
 Fennessy, J..... 273  
 Fernandez, A A ..... 21  
 Fernández, E F ..... 255  
 Ferreira, R S ..... 53  
 Feulner, P..... 99  
 Fink, C..... 247, 248  
 Fischer, K..... 81  
 Fischer, M ..... 163, 164  
 Fischer, S..... 168

Fokkema, R ..... 111  
 Folkow, L ..... 259, 266  
 Foraita, M ..... 131  
 Forcada, J ..... 61, 62, 112  
 Forster, R ..... 275  
 Forstmeier, W ..... 101  
 Fragueira, R ..... 42  
 Franconville, R ..... 223  
 Franke, A ..... 101  
 Franke, S ..... 130  
 Frase, T ..... 167, 217  
 Fricke, C ..... 135  
 Fritz, S ..... 12  
 Fritzs, B ..... 229  
 Fröhlich, M ..... 25  
 Frohn, J ..... 202  
 Frommolt, K-H ..... 54  
 Fuchs, B ..... 62, 253  
 Fulford, S ..... 250  
 Fürstenwerth, F ..... 264  
 Füser, H ..... 88  
 Gaddi, R ..... 225, 226  
 Gäde, G ..... 246, 257  
 Galipaud, M ..... 132  
 Ganske, A-S ..... 201  
 Geisen, S ..... 77  
 Gerth, M ..... 117  
 Gessler, B ..... 140  
 Gessner, C ..... 266  
 Giannakara, A ..... 139  
 Gienapp, P ..... 109  
 Giribet, G ..... 277  
 Glenner, H ..... 276  
 Goerlitz, H 24, 37, 47, 51, 52  
 Goldsworthy, S ..... 61, 62  
 Gollin, A ..... 224  
 Golüke, S ..... 19  
 Goodheart, J ..... 127  
 Göpfert, M ..... 230  
 Gorb, S ..... 174  
 Götz, B ..... 234  
 Goulet, J ..... 218, 236  
 Goycoolea, F ..... 255, 256  
 Grams, M ..... 173  
 Griebeler, E-M ..... 94  
 Griffith, S ..... 92  
 Grohmann, C ..... 174  
 Groothuis, T ..... 66  
 Gross, V ..... 178, 196  
 Großmann, M ..... 37  
 Gruhl, A ..... 250  
 Guenther, A ..... 22  
 Guillaume, F ..... 109  
 Guinet, C ..... 61, 62  
 Günter, F ..... 81  
 Günzel, Y ..... 227  
 Haase, M ..... 115  
 Hachmeister, H ..... 88  
 Hack, L ..... 216  
 Hahn, I ..... 65  
 Halitschke, R ..... 104  
 Hammel, J ..... 164, 179  
 Haneke-Reinders, M ..... 138  
 Hansson, L-A ..... 64  
 Haring, E ..... 149, 150  
 Harl, J ..... 149  
 Hartke, T ..... 133  
 Harzsch, S ..... 193  
 Hasselmann, M 80, 118, 140  
 Haug, C116, 169, 180, 185, 189,  
 269, 278  
 Haug, J116, 165, 169, 189, 278  
 Haugg, E ..... 59  
 Haupt, S S ..... 213, 237

Hausen, H ..... 70  
 Heck, L ..... 170  
 Heckel, D ..... 91  
 Heethoff, M63, 85, 97, 159, 200  
 Heimerl, D ..... 180  
 Heine, H ..... 247, 248  
 Held, C ..... 84  
 Helder, J ..... 89  
 Helfenrath, K ..... 260  
 Hellinger, J ..... 41  
 Helm, C ..... 70  
 Hering, L ..... 125, 267  
 Herlitze, S ..... 41  
 Hernik, M ..... 67  
 Herzog, H ..... 162  
 Herzog, W ..... 244  
 Heubel, K ..... 78  
 Heuveline, V ..... 200  
 Hildebrandt, J-P251, 262, 265  
 Hipp, A ..... 164  
 Hochkirch, A ..... 144  
 Hoffman, J61, 62, 103, 110, 112, 113  
 Hoffmann, S ..... 256  
 Hofmann, V114, 211, 212, 225  
 Hohberg, K ..... 89  
 Hoinville, T ..... 214  
 Hollmann, V ..... 218, 236  
 Holm, C ..... 31  
 Holtzheimer, J ..... 202  
 Homberg, U207, 209, 220, 238  
 Homolka, I ..... 129, 141  
 Hörnig, M ..... 116  
 Horstmann, M ..... 203  
 Howell, K ..... 133  
 Hu, Y-G ..... 71  
 Huang, C ..... 206  
 Hügel, T ..... 51, 52  
 Humble, E .. 61, 62, 112, 113  
 Hurst, G ..... 117  
 Huser, T ..... 88  
 Hussain, T ..... 268  
 Ihle, M ..... 101  
 Immler, S ..... 11  
 Ioannidou, I ..... 192, 235  
 Isabel, G ..... 152  
 Jäckel, R ..... 130  
 Jägers, P ..... 41  
 Jahn, H ..... 161, 179  
 Jakobs, R ..... 79  
 Janke, A ..... 273  
 Jarrige, A ..... 148  
 Jayaraman, V ..... 223  
 Jerome, N ..... 200  
 Joly, M ..... 36  
 Jünemann, S ..... 106  
 Jung, S N ..... 225, 226  
 Junghanns, A ..... 31  
 Kaack, L ..... 35  
 Kaiser, S ..... 37  
 Kalberer, S ..... 20  
 Kalinowski, J ..... 106  
 Kalke, P ..... 167  
 Kallsen, K ..... 247  
 Kalnins, L ..... 48  
 Kammerer, D ..... 278  
 Kappeler, P ..... 254  
 Karmeinski, D ..... 127  
 Kaučič, R ..... 37  
 Kaul-Strehlow, S ..... 216  
 Kempenaers, B ..... 101  
 Kenning, M ..... 176, 186  
 Kepecs, A ..... 13  
 Kersten, A ..... 49  
 Kieneke, A ..... 188, 198

Kirchhof, S.....	93	Kuchenreuther, S.....	137	Lucks, V.....	60	Mukagatare, L P.....	245
Kirchner, S.....	150	Kumar, S.....	70	Lüdemann, J.....	261	Mulder, E.....	121
Kirschbaum, F.....	114, 153	Kumerics, A.....	161	Luksch, H.....	221, 239	Müller Hoff, M L.....	266
Klockmann, M.....	143	Künzel, T.....	221	Lydersen, C.....	61	Müller, C79, 91, 96, 251, 262, 265	
Knief, U.....	101	Küpfer, C.....	122	MacIver, M.....	15	Müller, C H.....	176, 197, 201
Knoll, C.....	234	Küpfer, S.....	43	Mai, M.....	248	Müller, M.....	57
Knörnschild, M.....	21	Kupschus, D.....	50	Majdi, N.....	87, 88	Müller, T.....	96
Koch, F.....	180, 245	Kurth, A.....	44	Maraci, Ö.....	124	Münter, L.....	198
Kohl, T.....	239	Kurtz, J.....	34, 119	Marchal, E.....	246	Nachtsheim, D.....	84
Köhring, S.....	164	Kurvers, R.....	34	Marco, H.....	246, 257	Nagel, R.....	114, 153
Kokko, H.....	10	Ladurner, P.....	134	Martin, C.....	196	Nakadera, Y.....	154
Kolb, T.....	189	Lattenkamp, E.....	37	Martin, K.....	101	Nehring, V.....	86
Kollmann, M.....	228	Leese, F.....	110	Martin, S.....	276	Neiman, M.....	115
Kolonko, A K.....	255	Lehman, K.....	110	Mätz-Rensing, K.....	253	Nichols, H.....	103, 113
Komdeur, J.....	66	Lehmann, A.....	137	Mayer, G74, 125, 161, 178, 179, 196, 267, 271		Niehuis, O.....	107, 108, 155
König, K.....	129, 141	Lehmann, F-O.....	190, 268	Mayer, U.....	67, 210	Nityananda, V.....	207
Kopmann, A.....	200	Lehmann, G.....	28, 54, 137	McCully Phillips, S.....	252	Nitzlaff, S.....	256
Koppik, M.....	135	Lehmann, S.....	73	McLellan, W.....	252	Nöbel, S.....	152
Korioth, S.....	145	Lemke, S.....	262, 265	McMinn, C.....	110	Nyakatura, J.....	172
Korsten, P.....	66, 102	Lengerer, B.....	134	Meinertzhagen, I.....	168	Odar, J.....	160
Koschmieder, M.....	132	Lepreux, G.....	213	Mendelski, M.....	249	Oettler, J.....	100
Koselj, K.....	37	Lewanzik, D.....	24, 51	Menzel, F.....	97	Ohmes, M J.....	58
Kovacs, K.....	61, 62	Lewis, J.....	212	Merzendorfer, H.....	258	Oliveira I.....	271
Krämer, D.....	279	Li, J.....	219	Mesanovic, A.....	227	Oliveira, I.....	161
Kraus, S.....	23, 92	Li, S.....	166	Methou, P.....	250	Opatová, P.....	101
Krause, J.....	34	Lin, S-W.....	272	Metwally, N.....	264	Owsianowski, N.....	84
Krause, T.....	39	Lindemann, J P.....	38	Metzen, M.....	206	Pabst, A.....	252
Krebs, N.....	83	Lindholm, A.....	120	Meusemann, K.....	270	Paijmans, A.....	61
Kreifelts, V.....	195	Linn, S.....	29	Michalik, P.....	275	Panfilio, K.....	155
Krieger, J.....	116, 195	Lischka, K.....	221	Misof, B.....	5, 155, 177	Pannhausen, S.....	45, 50
Krings, M.....	76	Lopardo, L.....	272	Möbius, W.....	202	Papenmeier, S.....	263
Krist, M.....	102	López, A I.....	116	Mogdans, J.....	222	Paul, R.....	249
Krogmann, L.....	160	Lorenzi, E.....	67	Monjon, E.....	246	Pedraja, F.....	212
Kruckenhauser, L.....	149, 150	Lösel, P.....	160, 200	Monteagudo, J.....	56	Pegel, U.....	209, 220
Krüger, A.....	259	Lowther, A.....	61	Moore, H.....	110	Pei, Y.....	101
Krüger, O.....	20, 23, 113	Lu, Z.....	168	Moris, V.....	108	Peretti, A V.....	136
Kubetschek, C.....	62	Lubiana, P.....	264			Petróczyki, K.....	183

Petschenka, G.....	104	Rodríguez, A .....	26	Schenk, J.....	89	Steinmetz, R .....	84
Pfeffer, S .....	35, 59	Roeder, T .....	247, 248, 263	Scheumann, M .....	29	Stemme, T .....	194
Pfeiffer, K .....	209, 238	Rohlfing, K .....	130	Schielzeth, H.....	138	Stevenson, P .....	196
Pfeiffer, L.....	105	Rohlfs, M .....	128	Schilling, C .....	164	Stoffel, M.....	113
Picker, M.....	43	Röhrle, O.....	175	Schirmer, A .....	27	Stökl, J .....	105
Piedrahita, P .....	82, 191	Römer, C I .....	65	Schmelzle, S.....	85, 200	Straka, H .....	239
Pika, S .....	25	Römer, U.....	65	Schmidtke, D.....	36, 58	Struck, T.....	274
Pilger, C.....	88	Rommel, S .....	252	Schmitt, T.....	107, 108	Sutt, F .....	41
Pilorz, V.....	243	Rosa-Salva, O.....	67	Schmitz, J.....	214	Szyszka, P.....	240
Pjeta, R .....	134	Rösner, J.....	258	Schmitz, T .....	143	Taborsky, B.....	9
Plate, C .....	260	Rosner, R.....	207	Schmoll, T102, 145, 148, 183		Tarawneh, G .....	207
Podsiadlowski, L .....	276	Roskamp, L.....	76	Schneider, A.....	55	Tauch, A.....	106
Pokorny, T.....	90	Rosumek, F B .....	97	Schneider, J.....	30, 190, 261	Tautscher, B .....	149
Pollmann, M .....	129, 141	Roth, L .....	264	Schnier, J.....	188	Technau, U.....	216
Pötter, L .....	83	Rouault, H.....	223	Schöler, V.....	40	Telesca, L .....	110
Prosche, A.....	96	Roy, J.....	186	Scholtyssek, C .....	209	ter Hofstede, H .....	52
Prpic, M N.....	147	Ruf, I .....	157	Schomburg, C .....	147	Thiedmann, M .....	248
Prpic, N-M .....	202	Ruhmann, H.....	135	Schöning, C.....	118	Thoen, H.....	197
Ptatscheck, C .....	95	Rühr, P .....	177	Schotthöfer, S-K .....	75	Thoms, S.....	245
Quade, F .....	202	Runge, J .....	173, 181	Schou, M F.....	31	Thünken, T.....	18
Ramm, S 132, 134, 139, 154		Runge, J-N.....	120	Schrader, L.....	39	Tiedemann, R .....	114, 153
Read, J .....	207	Ruther, J.....	6, 90, 105	Schultz, M.....	237	Tilic, E .....	184
Rebrina, F .....	199	Salditt, T.....	202	Schumann, I.....	267	Tilly, A-K.....	264
Rehn, T.....	264	Sampalla, B.....	182	Schütt, W .....	17	Tinbergen, J .....	111
Reichelt, J .....	125	Sánchez-Villagra, M .....	170	Schweiger, R .....	79	Tollrian, R64, 83, 142, 192, 203, 235	
Reil, D .....	27	Santos-Carballal, B.....	255	Schwentner, M .....	72, 277	Töpperwien, M .....	202
Reim, E.....	81	Sartori, J.....	164	Schwermann, A .....	160	Traunspurger, W87, 88, 89, 95	
Rein, Y.....	228	Sartoris, F-J .....	245	Seelig, J.....	223	Trebels, B.....	215, 234
Reinhard, J.....	235	Sattmann, H.....	149	Segev, O .....	26	Treffkorn, S .....	74
Reinhold, K ....	123, 138, 183	Sattmann, S .....	150	Sesterhenn, J .....	190	Treschnak, D .....	42
Reininger, V.....	47	Sauer, J.....	92, 106, 123	Simek, P.....	257	Trienens, M.....	128
Reynolds, J.....	252	Saus, B .....	34	Small, S.....	133	Trillmich, F .....	20
Richter, C .....	84	Schaal, J .....	141	Sombke, A158, 166, 176, 186, 197		Trogant, S.....	142, 192
Richter, S.....	167, 217, 277	Schachtner, J..	215, 228, 234	Sørensen, A B .....	31	Tull, T .....	187
Ristau, K.....	89	Schärer, L .....	134	Stange, M .....	170	Turner-Evans, D .....	223
Rödel, M-O .....	26	Scharsack, J P.....	34	Steidle, J .....	129, 141	Ubels, R .....	111
Rodrigues, M .....	134	Schedwill, P .....	86	Steinhoff, P .....	166		

Uhl, G31, 143, 166, 201, 272	Weigel, S..... 221
Uliczka, K ..... 248, 263	Weihmann, T..... 171
Undheim, E..... 197	Weiss, L64, 69, 83, 142, 192, 203, 235
Vallortigara, G..... 67	Weiss, M..... 110
van de Kamp, T..... 160, 200	Wells, W ..... 103
van Hemmen, J L ... 218, 236	Werner, J..... 94
van Heteren, A..... 172	Wibberg, D ..... 106
Vandenbroeck, J ..... 246	Wiesenthal, A ..... 251
Vavakou, A ..... 233	Wilbrandt, J ..... 155
Veith, M ..... 144	Wilden, B ..... 87
Vences, M..... 26	Wimmer, E73, 215, 228, 234
Vendrami, D..... 110	Winkler, A ..... 106
Verhaegen, G ..... 115	Winter, M ..... 146
Verhulst, S..... 121	Winter, S..... 273
Vering, J ..... 267	Wippler, J..... 250
Verlinden, H..... 246	Wirkner, C..... 173, 181
Victor, R ..... 150	Witte, H ..... 164
Vink, C..... 275	Wittfoth, C..... 193
Vogel, H ..... 91	Wittig, M..... 101
von Beeren, C ..... 33	Wittig, R..... 25
von Döhren, J..... 279, 280	Wittlinger, M..... 35
von Engelhardt, N..... 46	Wolf, H..... 35, 55, 59, 194
von Hadeln, J ..... 207	Wölfer, J ..... 172
Wägele, H ..... 127	Wolf-Homeyer, S..... 55
Wagner, C ..... 263	Wolz, M ..... 143
Wagner, H..... 76, 82, 191	Worm, M ..... 45, 49
Wagner, P ..... 169	Wulff, N C..... 28
Wahab, F ..... 253	Wunderer, J ..... 134
Wallberg, A..... 118	Würz, Y ..... 23
Walther, T ..... 231	Zeymer, M..... 44
Wang, D ..... 101	Zhang, N ..... 230
Weber, M..... 134, 255, 256	Ziegler, E ..... 126
Weber, V ..... 234	Zimmermann, E... 29, 36, 58
Webster, M ..... 118	Zittrell, F ..... 238
Wegener, S..... 223	Zobac, P ..... 102
Wehmann, H-N..... 190	Zopp, L..... 149
Weigand, H..... 110	

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