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Abstracts

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- Charlotte Förster (University of Würzburg)
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Subject Groups

- *Behavioral Biology* (Mirjam Knoernschild, Anja Günther, Tobias Krause)
- *Developmental Biology* (Nico Posnien, Natascha Turetzek)
- *Ecology* (Gerlind Lehmann, Marko Rohlfs)
- *Evolutionary Biology* (Claudia Fricke, Volker Nehring, Monika Eberhard)
- *Morphology* (Andy Sombke, Conrad Helm, Ellen Schulz-Kornas)
- *Neurobiology* (Basil el Jundi, Tobias Kohl)
- *Physiology* (Sarah Lemke, Hans Merzendorfer)
- *Systematic, Biogeography and Biodiversity* (Manuela Sann, Sabrina Simon)

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Developmental Biology
Oral presentation: Invited Talk

Molecular mechanisms orchestrating growth, sexual maturation, and reproductive timing in *Platynereis*

Andreatta, Gabriele; Broyart, Caroline; Borghgraef, Charline; Vadiwala, Karim; Kozin, Vitaly; Polo, Alessandra; Bileck, Andrea; Beets, Isabel; Schoofs, Liliane; Gerner, Christopher; Raible, Florian

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Developmental and reproductive events need to be properly coordinated with environmental and physiological information to maximize reproductive success and survival. However, little is known on how animals integrate external stimuli with internal physiological status to regulate major developmental/reproductive transitions. We investigate these aspects in the marine bristleworm, *Platynereis dumerilii*, which orchestrates sexual maturation with body growth and the lunar cycle. Given its role in coordinating vertebrate sexual maturation, we focus on the functionally unexplored gonadotropin-releasing hormone (GnRH)-like system of this species. We found especially one of *Platynereis* GnRH-like preprohormones, corazonin 1 (crz1) upregulated in sexually mature animals, after feeding, and in specific lunar phases. Interestingly, our data demonstrate crz1 knockouts are characterized by reduced growth and regeneration, as well as a significant delay in maturation, caused by impaired energy homeostasis. In sum, our findings suggest *Platynereis* Crz1 coordinates metabolism to regulate growth and sexual maturation. In line with these data, we present additional insights on the molecular mechanisms which integrate environmental and internal information to orchestrate developmental and reproductive events.

Behavioral Biology
Oral presentation

Fitness consequence of polyandry in the common house spider, *Parasteatoda tepidariorum*

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Arthropods, and especially spiders have evolved several unique and complex mating strategies and behaviours. Polyandry, where females mate with multiple partners, is common and widespread across sexually reproductive animals, challenging the traditional concept of choosy and monogamous females. By mating with multiple partners females may gain indirect benefits for their progeny, by accessing higher quality or most compatible males. While the mating behavior of some spider species is well-studied, broad genetic approaches are still lacking as high-quality genomes are only available for a handful spider species. Aiming for an adaptive evolutionary and genetic explanation of female polyandry, we studied the mating behavior and its fitness consequences in the well-established genetic spider model, the common house spider *Parasteatoda tepidariorum* (Theridiidae). Females were either paired twice with the same male (monogamy) or with different males (polyandry) and mating success was scored. The latency to egg laying, number of fertilized and unfertilized eggs, as well as the hatching success were measured and used as indicators for female fitness. If females gain indirect benefits by mating with multiple partners, we predict a higher mating success and fitness in polyandrous mating compared to monogamous mating. Results will be discussed in the light of mating systems evolution and the natural history of Theridid spiders and are the foundation for future studies on the influence of different mating behaviors in spiders to genotypic evolution.

Systematics, Biogeography & Diversity
Oral presentation

Historical DNA, new fossils and an updated molecular phylogeny: insights into rates of morphological evolution among sengis (Afrotheria, Macroscelidea)

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Sengis are small African mammals with an odd character combination and a long independent evolution. They have traditionally been divided into four morphologically well-defined genera: *Macroscelides*, *Petrodromus*, and *Elephantulus* (Macroscelidinae, soft-furred sengis) as well as *Rhynchocyon* (Rhynchocyoninae, giant sengis). Molecular analyses, however, revealed that *Macroscelides* and *Petrodromus* are deeply nested within *Elephantulus*. While both former genera are characterized by multiple unique traits, *Elephantulus* is solely defined by the absence of derived characters. This suggest that rates of morphological evolution have been low in *Elephantulus* species but high in *Macroscelides* and *Petrodromus*. Due to the limited fossil record and the lack of genetic resources for some rare extant species, this hypothesis could not be tested in a phylogenetic framework yet. Using techniques adapted for highly degraded DNA, we were able to retrieve sequence data from historical museum skins collected up to 120 years ago for all living species. This data set, in combination with recently described fossils, allowed for reconstructing an updated temporal framework of sengi evolution, with older divergence within and among genera than previously reported. Rates of morphological evolution, inferred from a matrix of 107 characters, are highly variable among branches. Soft-furred sengis rapidly evolved novel characters compared to giant sengis. In contrast to our expectations, morphological rates were not considerable high in *Macroscelides* and *Petrodromus* due to the long time available for accumulating derived traits. Unambiguous morphological support for *Elephantulus* is still lacking and deep intrageneric divergence recalls for a reevaluation of the taxonomic status of the genus.

Systematics, Biogeography & Diversity
Oral presentation

Millipede microendemism: first insights into the pattern of diversity, composition, speciation and endemism among millipedes of the Indian Western Ghats

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Millipedes are slow-moving soil arthropods with low dispersal ability, living in the leaf litter in humid forests. The Diplopoda of India are a poorly studied taxon with 270+ nominal species, although India holds two biodiversity hotspots: Indo-Burma in the north-east and the Western Ghats (WG) in the southwest. The Indian millipede fauna was chiefly studied during colonial times and is almost unstudied for a century. To get a first overview of the diversity of Indian millipedes, we did a biodiversity inventory study among the millipedes of the WG, using COI barcodes, a first in Indian millipedes. We sampled eight forest sites, four highland and lowland forests, in the Southern WG of Kerala, India. A total of 470 specimens belonging to 11 millipede groups (eight orders and four families) were barcoded. 422 COI (89% success) barcodes could be analyzed using two species delimitation methods (ABGD, bPTP), revealing 144 putative millipede species. The species diversity discovered in the eight forests already accounts for 53% of the current total Indian species, and 61 % of the millipede species were previously known from southern India, exposing the hidden millipede diversity of the ISC. The delimitation threshold (uncorrected pairwise distances) varied in each Indian millipede group. An independent composition of the millipede fauna was observed in the eight forests, with only 17% of species being widespread. The high genetic distances between the sympatric millipede species of the same genus suggest allopatric speciation, while 75% of the collected species are currently considered microendemic to an area <10 x 10 km. This study still lacks a morphological examination of the specimens, however, it presents the first COI DNA barcode library on Indian millipedes.

Behavioral Biology
Oral presentation

Dialogue of the Deaf? Vocalization and navigation behavior in normal-hearing and hearing-impaired bats

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Bats are acoustic specialists. Not only do they orient and forage with their ears, but they also communicate with each other using a rich repertoire of complex calls. Unlike most mammals, where the vocal repertoire is innate, bats have been considered vocal learners. Vocal learning refers to an animal’s ability to acquire new vocalizations through imitation. Known best for this trait are of course humans and birds, and the only other known examples are marine mammals and elephants, both hard to study. So, bats are the ideal model species. An animal learning a new vocalization must be able to hear and imitate new sounds, and then improve this imitation using auditory feedback. Deafening experiments are therefore critical to verify vocal learning. In this talk we will have a look at the vocalization and flight behavior of both normal-hearing bats and bats that were acoustically deafened at birth. Pups of both groups thrived and grew into adults that are socially integrated in the colony and eager flyers. Together, these bats give us some surprising insights on what they may or may not hear and how it affects the way they move through their environment.

Systematics, Biogeography & Diversity
Oral presentation

On second sight: Revisiting the evolution of flight in stick and leaf insects (Phasmatodea)

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The re-evolution of complex characters is generally considered impossible, yet, studies of recent years have provided several examples of phenotypic reversals shown to violate Dollo's law. Along these lines, the regain of wings in stick and leaf insects (Phasmatodea) was hypothesised to have occurred several times after an ancestral loss. However, these results were highly criticised partly due to overestimation of the potential for trait reacquisition as well as to the lack of taxonomic data. We reconstructed the phylogeny of over 500 representative phasmatodean species to infer the evolutionary history of wings. For all tested alternative topologies, our results support an ancestral loss of wings and that the ancestors of most lineages were wingless. We also investigated the presence of ocelli, the photoreceptive organs usually found in winged insects: Our results show that the evolution of ocelli is dependent on the presence of (fully-developed) wings and that ocelli nevertheless are found in only less than a third of all examined winged species further substantiating the hypothesis of trait reacquisition. While we find high support for the regain of wings especially under the consideration of the disjunct presence of ocelli in only five of the major lineages, evidence from the fossil record as well as future studies focussing on the underlying genetic mechanisms are needed to assess the evolutionary process of these phenotypic reversals.

Ecology
Oral presentation

Bergmann`s rule in insects: Body-size of non-biting midges shows latitudinal and phylogenetic variations

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Size is one of the most outwardly obvious characteristics of the animals, determined by multiple phylogenetic and environmental variables. Numerous hypotheses were put forward towards explaining the relationships between the animal body size and the geographic latitude. Bergmann’s Rule well known positive relationship between the size of the endotherm animals and the geographic latitude. Werther or not insects are exhibiting similar pattern have long been a subject for debates. In this paper we are showcasing strong latitudinal size gradient in the representatives of the non-biting midges (Diptera, Chironomidae), based on the examination of the 4870 specimens of the midges from around the world. We have found that the length of the wing in Chironomidae representatives is increasing away from the equator in both southern and northern hemisphere. Geographic latitude, phylogenetic position of the species as well as mean size of the specimens in the genus to which the specimen belongs, were all significant predictors of the wing length in Chironomidae representatives. Non-biting midge’s wing and body size is growing by about 0.02 mm per one degree of geographical latitude, as one moves from the equator. We speculate that latitudinal size gradients are owing their existence to the temperature variation on the insect metabolic rate and oxygen availability for the larvae of merolimnic insects.

Physiology
Oral presentation: Invited Talk

Tissue regeneration in the African spiny mouse

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Why tissue regeneration occurs in some animals but not in others remains enigmatic, and it is not clear why even some closely related species have different responses to the same type of injury. Using naturally regenerating African spiny mice in comparative approaches with poorly regenerating mammals, we investigate the molecular mechanisms that promote scar-free regeneration in different spiny mouse tissues.

Neurobiology
Oral presentation

Manipulation of the circadian clock gene Pigment Dispersing Factor in honey bees via CRISPR-Cas9

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The honey bee is the perfect model organism for studying the significance of the circadian clock for pollination ecology, insect societies and complex behavior like time-compensated sun compass orientation or time-place learning. While we have a good idea about the genes contributing to the central feedback mechanism of the clock, the link between the circadian clock and these behaviors is largely unknown. This is partially due to the lack of efficient tools to genetically manipulate clock genes in the honey bee with its highly complex reproduction system typically for insect societies. In the honey bee colony, only the queen bee and the male bees (drones) reproduce, while thousands of sterile female worker bees take care of the brood, forage, build new combs and protect the hive. The neuropeptide Pigment Dispersing Factor (PDF) is part of the circadian clock system in the honey bee and it is expressed in a subset of clock neurons with somata situated in the lateral brain. These neurons connect clock centers and regions involved in the regulation of downstream behavioral processes such as locomotion, sleep or learning and memory. In order to assess whether PDF is a key neuromodulator responsible for relaying time of day information, we generated PDF mutant bees via CRISPR-Cas9. We applied this new method to introduce mutations into worker bee eggs and raised the manipulated bees in the laboratory. Genotyping revealed that we were able to induce different mutations in the pdf gene. In a behavioral assay monitoring locomotion, we studied effects of the mutations on circadian rhythm generation. We found that bees that carried homozygous frame shift mutations were all arrhythmic in behavior under constant conditions, while heterozygous mutations eliminated a behavioral rhythm only in a subset of individuals. With our study, we aim for developing an efficient method to generate loss-of-function clock mutants, which will enable us to shed light on the molecular mechanisms connecting the circadian clock with the honey bee's complex behavior.

Neurobiology
Oral presentation

Flight-induced generation of a compass in the brain of monarch butterflies

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North-American monarch butterflies migrate every year over 4,000 kilometers to their overwintering habitat in central Mexico. During this enormous journey, they use a compass that is housed in a brain region called the central complex. Although the anatomical outline of the central complex is highly conserved across insects, it remains unanswered whether the monarch butterfly compass is adapted to allow a robust heading coding during their migration. Until now, the monarch butterfly central complex has only been characterized in restrained animals. To understand, how the compass encodes heading during steering flight, we here developed tetrode recordings from the central complex of tethered flying butterflies. During flight, many neurons changed their angular sensitivity to a sun stimulus, an effect that could be mimicked by applying an octopamine agonist (Chlordimeform). Moreover, many neurons shifted their preferred firing direction as soon as motor efference copies and reafferent signals were integrated into the heading-direction network while actively steering during flight. This converted the heading-direction network from a frontally biased heading representation in quiescent animals to a proper compass representing 360° of angular space in flying monarch butterflies. Taken together, our data show that multimodal inputs are required during flight to establish a functional compass that allows the migrating butterfly to effectively maintain any geographical direction while rapidly navigating through space.

Physiology
Oral presentation

NO synthesis in immune-challenged locust hemocytes and potential signaling to the CNS

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Like vertebrates, insects are exposed to a broad variety of pathogens, including viruses, bacteria, fungi, and others. The innate insect immune system provides several response mechanisms, including RNA interference, phagocytosis, melanization, synthesis of antimicrobial peptides or cytotoxic compounds. The cytotoxic component nitric oxide (NO) has been reported to be involved in the response to bacterial infections in various insects. Few studies, however, have shown the actual production of NO in hemocytes. In addition, NO is also an important messenger in the nervous system. We quantified NO production in hemocytes of *Locusta migratoria* challenged with diverse immune stimuli by immunolabeling the by-product of NO synthesis, citrulline. Whereas in untreated adult locusts less than 5% of circulating hemocytes were citrulline-positive, the proportion rose to over 40% after 24 hours post injection of heat-inactivated bacteria. Hemocytes surrounded and melanized bacteria in injected first instar locust nymphs, a process referred to as capsule formation. Such sessile hemocytes, both distributed in the tissues and capsules also produced NO. Similar to the situation in other insects, many activated locust hemocytes could be found dorsally, close to the heart. In addition, we frequently observed citrulline-positive hemocytes as well as capsules near the ventral nerve cord. In response, first instar locust CNS neurons synthesized the second messenger, cGMP, as revealed by immunofluorescence after inhibition of phosphodiesterases by IBMX. Such a response could even be obtained in sterile locust embryos in response to 30 min. contact with purified hemocytes from immune stimulated adult locusts. We conclude that hemocytes can mediate a response in the CNS of an infected animal via the NO/cGMP-signaling pathway.

Physiology
Oral presentation

Comparison of two assays to measure the activity of thrombin

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Thrombin is a serine protease and an important factor in the blood coagulation cascade. Hence, it is a prominent target for many blood sucking parasites, like the medicinal leech (*Hirudo medicinalis*), to prevent blood coagulation while feeding on their hosts. Inhibitors of thrombin are the well-known hirudins and some of the only recently discovered hirudin like factors (HLF's). There are different methods to specifically investigate and measure the thrombin-inhibitory potencies of these factors: the coagulation-based thrombin time assay (TT) and a newly established fluorescence based thrombin activity assay. Here we compare these assays in terms of sensitivity, reliability, information content and further potential applications.

Physiology
Oral presentation

Transcriptomic insights into the physiology of the terminal tracheal cells in *Drosophila*

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Tracheae have to fulfill a number of different tasks with gas exchange being the most important one. The *Drosophila* tracheal system with its dorsal trunks and primary, secondary, and terminal branches shares comprehensive structural and functional similarities with the mammalian lung on one hand and blood vessels on the other. The terminal tracheal cells (TTCs) are tightly connected to all tissues and organs to ensure oxygen supply. The TTCs are so far characterized by their structural plasticity in response to nutritive cues and hypoxia similarly to endothelial tip cells. Beyond that, an inter-organ communication of these cells with intestinal cells was determined recently. Due to their branched structure and their distribution throughout the whole body, dissection and detailed investigations on a molecular level are challenging. We developed a protocol for dissection of these not easily accessible cells and performed RNA-sequencing. By this we were able to get more insight into the transcriptomic profile of these specialized cells. Based on our results, we were able to substantiate previous results and get new insights underlaying the molecular mechanisms regarding different physiological aspects. With this we successfully contribute to the characterization of these cells that are of special interest in endothelial cell research and associated pathogenesis.

Developmental Biology
Oral presentation

Temporal control on RNAi reveals that segmentation breakdown is reversible after knock down of even-skipped but not after Wnt-signaling in a beetle

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The red flour beetle *Tribolium castaneum* anterior segments are patterned during the blastoderm stage, while posterior segments are progressively added from a Segment Addition Zone (SAZ) analogous to vertebrate segmentation. SAZ setup during early blastoderm stages requires Wnt and torso signaling. Subsequently, the three primary pair rule genes, even-skipped (eve), runt (run), and odd-skipped (odd) oscillate to specify segments. RNAi-mediated knock-down of any of these genes leads to a segmentation breakdown inducing severe posterior truncations. However, it has remained unknown whether the break-down is irreversible or whether it can re-establish itself when the knocked-down components are brought back into the system. We developed a novel genetic tool where a Viral Suppressor of RNAi is expressed via heat-shock (hsVSR). We showed for the secondary pair rule gene Tc-paired, that parental RNAi can be blocked during elongation by a heat-shock lading to a rescue of posterior segments. Using this procedure, we then showed that rescue of Wnt or Torso pathway components did not rescue segments. In contrast, rescue of eve, runt or odd at posterior elongation stages led to rescue of abdominal segments and to the re-establishment of a SAZ with normal expression of pair rule genes. These results indicate that interfering with the Wnt signal leads to irreversible breakdown of the SAZ. In contrast, the primary pair-rule gene network shows a large degree of self-organizing property. The VSR technique allows for temporal but also spatial restriction of RNAi, which opens new technical opportunities.

Ecology
Oral presentation

Crossing the line: Genomic architecture of cuticular hydrocarbon variation in the parasitoid jewel wasp *Nasonia*

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Cuticular hydrocarbon (CHC) profiles play two fundamental roles in insects: protection against desiccation and chemical signaling. This pivotal dual functionality renders this complex trait essential for insect survival, diversity, reproductive success, and adaptation. Curiously though, most research on the biosynthesis and genetics of CHCs has been restricted to the Dipteran model species *Drosophila melanogaster*. However, how exactly this knowledge can be transferred to other insect taxa, for instance the economically and ecologically important Hymenoptera, remains poorly understood. Focusing on *Nasonia*, a genus of parasitoid jewel wasps suitable as a Hymenopteran model organism for genomic research, we investigated the genetics governing CHC biosynthesis and variation. Taking advantage of their haplo-diploid sex determination and cross-species fertility, we mapped quantitative trait loci (QTL) for CHC variation in recombinant F2 hybrid males from interspecific crosses between different *Nasonia* species. We complemented the QTL mapping with identifying and localizing orthologs of *Drosophila* CHC biosynthesis genes in the *Nasonia* genome. We discovered multiple genomic “hotspots” governing CHC variation between the different *Nasonia* species. Intriguingly, these hotspots coincide spatially with the genomic location of various CHC biosynthesis candidate genes. Our results particularly shed light on the so far little-known genetic underpinnings of the variation in methyl-branched alkanes, the most wide-spread and diverse CHC compound class in our investigated taxa. These findings also have considerable implications on how these fundamental complex traits can be governed, produced and maintained in Hymenoptera in general.

Neurobiology
Oral presentation

Transcriptional control of central complex connectivity in *Tribolium* and *Drosophila*

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Proper connectivity among the neurons of the brain is a prerequisite for coherent behaviour and physiology of the animal. The insect brain is made up of thousands of different neuronal subtypes each of which displays a specific axonal projection and synaptic partner choice. The ability to establish specific neuronal connections depends on the repertoire of differentiation genes expressed by individual neuronal subtypes. Therefore, the question of which gene-regulatory mechanisms govern the establishment of connectivity is at its core the question of how neuronal subtype identity is specified and of how individual neuronal features are brought about by differentiation genes. Regulatory mechanisms which specify subtype identity of central complex (CX) neurons are the subject of intense investigation. The CX is a compartment within the brain common to all insects and functions as a “command center” which directs motor actions. It is made up of several thousand neurons with more than 60 morphologically distinct identities. Accordingly, transcriptional programs must effect the specification of at least as many neuronal subtypes. We demonstrate a role for the novel homodomain transcription factor Shaking hands (Skh) in the differentiation of *Tribolium* embryonic CX neurons. The developmental dynamics of skh expression are characteristic for regulators of differentiation programs. In the embryonic brain, skh expression is restricted to a subset of neurons, many of which survive to adulthood and contribute to the mature CX. skh knock-down results in severe axon outgrowth defects thus preventing the formation of the CX primordium. The as yet unstudied *Drosophila* skh is expressed in a similar embryonic pattern as its *Tribolium* orthologue and is required for axon elongation of a subset of CX neurons suggesting that Tc- and Dm-Skh have similar functions in the establishment of the CX connectivity. We plan a detailed comparison of Skh neurons and Skh target genes in both species to address the evolution of insect brains.

Morphology
Oral presentation

Walking leaves – sticky eggs: comparative functional morphology and evolution of the adhesive system of leaf insect eggs (Phasmatodea: Phylliidae)

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Walking leaves (Phylliidae) are herbivorous insects exhibiting cryptic masquerade. They almost perfectly imitate angiosperm leaves and their eggs often resemble plant seeds structurally, but also functionally. In spite of overall morphological similarity of adult Phylliidae, their eggs reveal a signficant diversity in overall shape and exochorionic surface features. Previous studies have shown that the eggs of *Phyllium philippinicum* possess a specialised attachment mechanism with hierarchical exochorionic fan-like structures (pinnae), which are mantled by a film of an adhesive secretion (glue). The folded pinnae and glue respond to water contact, with the fibrous pinnae expanding and the glue capable of reversible liquefaction. In fact, the eggs of other phylliids appear to exhibit varying structures that were suggested to represent specific adaptations to the different environments the eggs are deposited in. We investigated the diversity of phylliid eggs and the functional morphology of their exochorionic structure. Based on the examination of all known eggs of phylliids, we were able to characterise several different morphological types. We explored the adhesiveness of these different egg morphotypes and experimentally compared the attachment performance on a broad range of substrates with different surface roughness, surface chemistry and tested whether the adhesion is replicable after detachment. Furthermore, we used molecular phylogenetic methods to reconstruct the evolutionary history of the different egg types and their adhesive systems within this lineage. Our results suggest that the egg morphology mostly corresponds with the phylogenetic relationships within Phylliidae and that the differences are likely caused by adaptation to the specific environmental requirements for the particular clades as the egg morphology has an influence on the performance regarding the surface roughness. Furthermore, we show that specific morphological features evolved convergently in different species, and that the adhesive glue has been repeatedly lost.

Physiology
Oral presentation

A proton channel, Otop2L promotes intracellular pH homeostasis critical for skeletogenesis in the sea urchin larvae

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Otopetrins belong to a novel family of proton channels that play a pivotal role in the formation of statoconia and otolith in the vertebrate inner ear. Knock-down and mutations of otopetrins lead to the agenesis of CaCO3 structures in the vertebrate inner ear with the underlying mechanisms remaining unknown. Using the sea urchin larva, we identified a proton-selective ion channel homolog, Otopetrin (Otop2L), which is exclusively expressed in the calcifying primary mesenchymal cells (PMCs) that generate the larval skeleton. Otop2L starts to express in PMC during gastrulation and mRNA abundance strongly correlates with the growth of the CaCO3 skeleton. Morpholino knock-down Otop2L impairs spicule formation associated with changes in the intracellular pH regulatory properties of PMCs. While 70% of PMCs regulate pHi in a Na+-dependent manner 30% of PMCs recover from the acidosis in the absence of Na+. H+ currents in these PMCs are sensitive to Zn2+ and Otop2L knockdown, reduced proton permeability of the cell. Skeleton regeneration experiments under a wide range of pH indicate a reduction in calcification under acidified conditions underlining of the importance of transmembrane proton gradients in the calcification mechanism. Our results provide a first mechanistic understanding how otopetrins contribute to the mineralization process. Protons generated by the calcification process are exported through the proton-selective channel, Otop2L driven by the negative membrane potential. Since this process is strongly dependent on the proton gradients across the plasma membrane these findings have strong repercussions on our interpretation of reduced calcification rates in marine species exposed to increased seawater acidity.

Behavioral Biology
Oral presentation

The Impact of Stress and Personality on Learning

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Stress is known to have an impact on cognition, with mildly stressful situations improving learning abilities, while strong or chronical stress impairs them. If a specific situation is perceived as stressful or not and the way an organism reacts to this situation could be different from one individual to another through some intraspecific variation such as personality. We therefore investigated two personality traits (stress coping in an open field test and exploration in a novel environment test) and spatial learning abilities in a low-stress and a mildly stressful maze with a group of 30 female wild mice. For each test, physiological stress has been assessed by measuring body temperature with infrared thermography. Learning abilities were not significantly repeatable between both tests despite similar complexity, which indicates that the stress level induced by the test has a great influence on learning. On top of that, there were some correlations between personality and learning measures in the mildly stressful maze. Individuals that are more explorative in the novel environment and have a higher stress level in the open field are better learners. On the other hand, no correlation has been found between personality and the low-stress maze. This could suggest that in a mildly stressful situation, learning is more influenced by personality traits as exploration and sensitivity to stress than in a low-stress situation. These findings could explain some of the contradicting findings regarding personality-cognition links plaguing the literature and argue for very careful design of cognitive test setups especially in non-model species.

Behavioral Biology
Oral presentation

Cuticular hydrocarbon diversification correlates with aggression levels in the invasive ant *Cardiocondyla obscurior*

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Cuticular hydrocarbons (CHCs) are important cues for nestmate recognition and intraspecific aggression in ants. In invasive ants, CHC profile similarity among colonies has been hypothesized to contribute to the ecological success of populations by diminishing intra-specific aggression. The ant *Cardiocondyla obscurior* has successfully colonized habitats around the world, reaching high local population densities. However, despite being invasive, antagonistic interactions between non-nestmates do occur in introduced populations of this species. Using behavioral experiments and gas-chromatography coupled with mass spectrometry (GC-MS), we show that (1) individuals with depleted CHC profiles receive virtually no aggression from conspecifics and (2) in untreated individuals, aggression levels are significantly correlated with CHC profile differences between colonies. These findings provide first empirical evidence for a role of CHCs and chemical diversity in antagonistic interactions between *C. obscurior* colonies, with important implications for population dynamics of this invasive ant.

Morphology
Oral presentation

Innervation areas of mechanosensory hair sensillae on the scorpion pectines

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The scorpions' pectines are ventral comb-like appendages that detect two different sensory modalities. The apical tips of the comb teeth, the so-called pegs, bear chemosensory sensillae which are used for probing the environment chemically, while hair sensillae collect mechanosensory information. All sensory information of the pectines is relayed to and integrated by the posterior section of the fused part of the ventral nerve cord, the synganglion, with specific pectine-associated neuropils. In previous experiments, we uncovered the innervation pattern of the entire pecten nerve afferents and identified a putative mechanosensory neuropil. In the present study, we investigate the projection patterns of single mechanosensory sensillae in more detail. We successfully traced tactile hair afferents using neurobiotin forwardfills and visualized the corresponding mechanosensory innervation areas by immunohistochemistry. The results revealed an extensive mechanosensory pathway, starting in the posterior part of the synganglion and ending in close vicinity of the walking leg neuromeres. While ventral sections of the synganglion showed inconspicuous lateral mechanosensory neuropils at the level of the pectine neuropils, these neuropils formed protrusions located dorso-laterally in the synganglion. From these protrusions, several tracts ran towards the ganglion midline, ascended anteriorly and ended close to the walking leg neuromeres. These results imply a direct connection from the first integration centre in the lateral mechanosensory neuropil to the walking leg neuromeres, which in turn, will result in fast and sensitive behavioural responses and adjustments with regard to tactile stimuli in the environment.

Behavioral Biology
Oral presentation

Bumblebees use scent marks to find their nest entrance in visually ambiguous situations

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Most social insects such as ants, honeybees, and bumblebees are excellent navigators. For example, bees can learn multiple locations in their environment, like flower patches and their nest. While navigating from one location to another, bees mainly rely on their vision. In general, the visual environment of a bee such as a meadow or a garden is reliable; yet it can be prone to rapid changes such as moving shadows or the displacement of an object in the scenery. Therefore, bees may use multimodal guidance to ensure their return to their goal location. Alternatively to vision, they might use another well-developed sense: olfaction. Olfaction is used for a wide range of functions such as communication, mate recognition or designation of depleted flowers. However, little attention has been paid so far to a role of odour in navigational tasks. In addition, potential odour cues are often not considered in common experimental designs. Therefore, we tested whether bumblebees (*Bombus terrestris*) use scent marks deposited by them around their nest during homing behaviour in visually ambiguous situations. Bees were trained to return to their inconspicuous nest hole in an indoor flight arena by using a specially designed visual scenery and scent marks around their nest entrance. Upon a forager's return, the visual scenery was altered so that it now indicated two possible nest locations. One of them was additionally marked with scent collected from the original nest hole. The time bees spent searching at either location was interpreted to indicate the weight associated to visual and olfactory guidance, respectively. We show that bumblebees actively shape their search behaviour at the potential nests and can use natural scent marks to disambiguate a visually ambiguous situation.

Morphology
Oral presentation

The influence of phylogenetic history on a highly functional trait, the orthopteran mandible

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Orthoptera (grasshoppers, crickets, and allies) are the most speciose group within Polyneoptera and show almost all diet types known for biting chewing insects. A strong link between the shape of the mandibles and diet types is assumed as a truism, however, selective feeding pressures do not necessarily produce a simple match between mandible phenotype and ecology. Here, we analysed mandible shape, biting efficiency, and their potential correlation with diet types in a phylogenetic framework for ~ 350 orthopteran species covering almost all families. Our aim was to understand how mandible shape is linked to biting efficiency and diet, and how these traits are influenced by phylogenetic history and allometric effects. Preliminary results show that despite a factor of ~100 in size, biting efficiency does not contain significant allometric signal. Moreover, diet is not an unequivocal predictor of mandible shape which contrasts earlier qualitative results. We further discuss a potential dependence of mandible shape on global climatic, and thus vegetational, zones and the interplay of phylogenetic signal in this highly functional trait.

Evolutionary Biology
Oral presentation

Molecular underpinnings of division of labour among workers in a socially complex termite

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Division of labour characterises all major evolutionary transitions, such as the evolution of eukaryotic cells or multicellular organisms. Social insects are characterised by reproductive division of labour, with one or a few reproducing individuals (queens) and many non-reproducing nestmates (workers) forming a colony. Among the workers, further division of labour can occur with different individuals performing different tasks such as foraging, brood care or building. While mechanisms underlying task division are intensively studied in social Hymenoptera, less is known for termites, which independently evolved eusociality. We investigated molecular mechanisms underlying task division in termite workers to test for commonalities with social Hymenoptera. We compared similar-aged foraging workers with builders of the fungus-growing termite *Macrotermes bellicosus* using transcriptomes, endocrine measures and estimators of physiological condition. Based on results for social Hymenoptera and theory, we tested the hypotheses that (i) foragers are in worse physiological conditions than builders, (ii) builders are more similar in their gene expression profile to queens than foragers are, and (iii) builders invest more in anti-ageing mechanism than foragers. Our results support all three hypotheses. We found storage proteins to underlie task division of these similar-aged termite workers, the genes encoding them characterise reproductive division of labour between queens and workers. This implies a co-option of nutrient-based pathways to regulate division of labour across lineages of termites and social Hymenoptera, which are separated by more than 133 million years.

Morphology
Oral presentation

Functional adaptations to locomotion in the humerus of frogs and toads

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Frogs and toads (Lissamphibia: Anura) in general show a conserved Bauplan, yet, previous studies pointed out that the humerus (proximal bone of forelimb) varies between species that utilize different locomotor modes. However, skeleto-muscular adaptations of the humerus system with regard to bone strength and effects of different muscle configurations to varying locomotor modes remained unclear. Therefore, we combined geometric morphometrics to quantify humerus shapes, with modelling of muscles across the shoulder joint to analyze muscle effectiveness, and finite element analyses to assess stresses within the bone under different loading scenarios. The shape analysis showed that the humerus of headfirst and backward burrowing species significantly differs from each other and, additionally, from all other locomotor groups (i.e., walking-hopping, jumping, swimming, climbing). Musculo-skeletal modelling revealed that certain humeral shapes in combination with specific pectoral girdle configurations increase theoretically achievable forces at the distal end of the humerus. This force increase allowed for different evolutionary adaptations to specific locomotor modes, in particular burrowing. Further, the finite element analyses showed a significant correlation of cortical thickness with von Mises stresses which was independent of the humerus shape and locomotor group. The stresses generally increase distal to the crista ventralis, a bony crest at the proximo-ventral part of the humerus. This increase might indicate a stabilizing effect of the crista ventralis and the forces produced by the attaching muscles, and thus bears the potential to increase the mechanical strength of the humerus as a response to specific locomotor demands.

Developmental Biology
Oral presentation

Of tracts, lineages, and evolution: A developmental atlas of the *Tribolium* brain

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Insect brains are complex organs that despite their small cell number cause equally complex behaviours. Each species has a brain adapted to specific environmental surroundings and for specific behaviours, hence why the insect clade has diverged strongly in its brain architecture. Of course, such differences are realized in each insect's developmental period. Therefore, studying brain anatomy and its development is essential to understand adaptative processes in insects. I want to present our current work on the brain of *Tribolium castaneum*, the red flour beetle. While previous efforts have examined four classic brain areas, our approach goes further by taking the whole brain into account. Using a simple acetylated tubulin staining, we were able to determine compartments, fascicles, and tracts of the *Tribolium* brain at three different developmental stages. Moreover, the tracts, particularly visible in the freshly hatched larva, can be assigned to developmental neural lineages. Using the large database already available in *Drosophila melanogaster* we compared tracts, fascicles, and compartments between the two species, in an – to our knowledge – unique way with respect to its completeness and simple methodology. With certain limitations of our approach in mind, we were able to find interesting differences with respect to the timing of neuroblast proliferation, and the differentiation of specific neuron populations. The differing extents of metamorphosis and external sense organ development might underlie these differences in neural development. We hope that this work is a scaffold for future studies in *Tribolium*. Moreover, we think that this approach can be used in many insect species to generate a more complete understanding of brain anatomy, development, and evolution in the future.

Ecology
Oral presentation

Food quality mediates the interaction between top-down and bottom-up control of stream biofilms

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In food webs, both bottom-up and top-down factors control the biomass on intermediate trophic levels such as benthic algal biofilms. Both mechanisms were demonstrated to be significant, but with strong variations in the strength of top-down control in different natural settings. We here investigated the hypothesis that the strength of top-down control of algal biofilms is determined by the food quality of the algae, which is in turn regulated by allocation of essential resources. We tested this hypothesis on different scales and complexity levels in both highly controlled laboratory experiments and field-related mesocosm experiments. This includes the homogenous local patch size, the multi-patch level with spatial heterogeneity and the choice for gazers as well as high-complexity level under consideration of growth and migration behaviour of grazers in mesocosm experiments. Our data show that anthropogenic eutrophication leads to a reduction of top-down control exerted by herbivores via both alterations in grazing activity and spatial structuring of the biofilms. This demonstrates how the strength of top-down pressure on biofilms is regulated and contributes to our understanding of eutrophication control in natural surface waters.

Morphology
Oral presentation: Invited Talk

Small eyes, large data: visual systems of tiniest insects in 3D ultrastructural resolution

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Up to date ultrastructural investigations of insect visual systems are mainly limited to two dimensions for the reason that they are based on selected single sections, due to the large size of the photoreceptors. In case of miniaturized insects however, complete ommatidia and stemmata are within a size range that can be investigated by serial-sectioning transmission electron microscopy (ssTEM) in order to gain 3D information on ultrastructural level. Three-dimensional data sets are of great importance for a detailed description and analysis especially of spatial constraints discussed in relation to miniaturization. Besides generating numerical and volumetric information of cells and cell organelles, the data sets also allow for the investigation and evaluation of general features such as symmetry planes, retinula cell homologies and also possible interpretation burdens that occur on basis of single 2D sections. The talk will present first case studies demonstrating the potential and value of such studies and gives an overview of the insights gained from various high-resolution 3D ultrastructural analyses of both compound eyes and stemmata of insects.

Behavioral Biology
Oral presentation

Magnetoreception during initial learning walks and re-learning walks in *Cataglyphis* ants

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When *Cataglyphis* desert ants leave their nest for the very first time, they have to calibrate their compass systems and learn the visual panorama around the nest entrance. For that, they perform well-structured initial learning walks. During rotational body movements (pirouettes), naïve ants (novices) gaze back to the nest entrance to memorize their way back to the nest. To align their looks back to the nest, they rely on the geomagnetic field as an earthbound reference system. Rotating the horizontal component of the magnetic field experimentally, leads to a predictable change in gaze direction of novices. In contrast, experienced ants (foragers) use celestial compass cues for path integration during food search. If the panorama around the nest entrance has changed, foragers perform re-learning walks prior to heading out on new foraging excursions. Importantly, initial learning walks and re-learning walks are structurally different. Novices explore different sectors around the nest entrance during several initial learning walks whereas foragers perform a spiral-shaped re-learning walk before continuing as a foraging trip. In addition, foragers do not use the magnetic field as a compass cue to align their gaze directions during re-learning walk pirouettes. Nevertheless, magnetic alterations during re-learning walks under manipulated panoramic conditions induce changes in nest-directed views indicating that foragers are still magnetosensitive in a cue conflict situation. This study has been funded by the German Research Foundation (projects: FL1060/1-1 to PNF and RO1177/7-1 to WR) and has been further supported by the Klaus Tschira Foundation gGmbH (project GSO/KT 16 to PNF).

Neurobiology
Oral presentation

The Visual Ecology of the Honeybee's Polarization Compass

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Skylight polarization forms part of the honeybee's solar compass system, which allows them to orient when the sun itself is blocked from view. Honeybees have also been demonstrated to integrate information from different sky regions to resolve the ambiguity, obtaining a robust compass reference. While the interpretation of each region appears strongly influenced by sensitivity, the combined effects of intensity and degree of polarization remain poorly defined. We present data from ongoing behavioural experiments, designed to determine how the honeybee's polarization compass trades off flexibility against generalisation. We record the waggle dances performed by returning foragers to quantify how different artificial sky stimuli affect their orientation performance. We set out to measure the functional range of the honeybee's polarization compass, with reference to measurements of real-world polarized skylight performed during experiments.

Behavioral Biology
Oral presentation

Behavioral physiology and division of foraging labor in six honeybee subspecies in a common apiary

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The mechanisms underlying division of labor are among the most intensely studied topics in social insects. In honeybees, a tight correlation between division of labor and individual sensory response thresholds was described. However, all studies have so far focused on commonly used stocks derived from only a few *Apis mellifera* subspecies. We here compared division of foraging labor and sensory responses across and within honeybees of different genetic origins by placing together colonies of *A. m. carnica*, *ligustica*, *macedonica*, *mellifera*, *ruttneri* and *iberiensis* in a common apiary. Both sucrose responsiveness of pollen foragers and non-pollen foragers was affected by subspecies affiliation. In addition, our data show that bees of different subspecies differed in their resource use and workforce composition. The present results demonstrate a clear yet different division of foraging labor in the different subspecies and suggest that sensory responses are adapted to local habitat and climate.

Neurobiology
Oral presentation

Temporal Differences of Load & Movement Signal Integration in the Sensorimotor Network of the Insect Leg

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Proprioceptive feedback is an essential component of adaptive locomotion and posture control. It arises from distinct sensory modalities, including limb loading and joint movement. In insects, cuticular forces on the leg are perceived by campaniform sensilla (CS). and movement of the femur-tibia joint is monitored by the femoral chordotonal organ (fCO). Previous studies have shown that both types of feedback are integrated by a distributed, antagonistic network of local premotor nonspiking interneurons (NSIs). Based on this spatial summation of multimodal proprioceptive signals, we analyzed whether temporal summation of load and movement signals is simultaneous in the femur-tibia control loop of the stick insect. Given the distance between the sense organs on the insect leg, we hypothesized a temporal shift between signals from the distal tibial CS (tiCS) and the more proximal fCO. Intra- and extracellular recordings demonstrated that tiCS signals were indeed delayed along the entire sensorimotor pathway in comparison to fCO signals. tiCS signal transmission time to the local network was longer, and within the network the latency-inferred network connectivity of mono- and polysynaptic connections from sense organs to NSIs or motor neurons (MNs) added to the required signal processing time. The resulting timeline of proprioceptive processing showed a marked temporal shift between tiCS and fCO signal processing which persisted into the motor output. Surprisingly, the signal timing of proximal CS groups resembled that of the tiCS, despite their spatial proximity to the fCO. The results suggest a general temporal shift between load and movement signals with implications for motor control, as it allowed delayed load signals to alter ongoing movement processing.

Evolutionary Biology
Oral presentation

The confused flour beetle, *Tribolium confusum*: A model for investigating *Wolbachia* - host interactions

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Wolbachia is a maternally inherited endosymbiotic bacteria that belongs to Alphaproteaobacteria, and found to be present in arthropods and nematodes. *Wolbachia* is known to manipulate the host reproductive biology to increase its own chances of transmission by parthenogenesis, male killing, feminization and cytoplasmic incompatibility (CI). Despite its importance as a manipulator, *Wolbachia*'s evolutionary dynamics have been poorly studied from a genomic viewpoint, and only few genomes have been sequenced from only a few hosts and strains, mostly focusing on Diptera so far (eg., *Drosophila*, *Anopheles*). The confused flour beetle, *Tribolium confusum* Jacquelin du Val, 1863 (Coleoptera: Tenebrionidae), is a cosmopolitan pest of stored products, which can naturally be infected with a single *Wolbachia* strain (wCon). Moreover, beetles of the genus *Tribolium* have been established as model systems for genetic and developmental biology as they can be easily cultured in the lab and have short generation time. Most studies on the biology of *Wolbachia* focussed on *Drosophila* vinegar flies, mosquitos or filarial nematodes, and only some few studies are available for *Tribolium confusum*, e.g., demonstrating the induction of CI, as well as suggesting to enhance male fertility at the expense of female fecundity. However, there has been no detailed characterization of the genome of this *Wolbachia* strain as well as its CI-inducing genes up to this date. In this study we show the potential of *Tribolium confusum* as a model system to investigate *Wolbachia*. We present the genome assembly and annotation of a *Wolbachia* strain isolated from *Tribolium confusum*. In addition, we tested the effect of high temperature on the *Wolbachia* density and also its impact on the CI. As for genome assembly, we used Oxford nanopore long reads and Illumina short reads to assemble the genome. The nanopore long reads enable to resolve complex repeat regions which is difficult to resolve with short-read sequencing. We discuss the content of the genome with a specific view on the presence of CI-inducing genes. Our genome assembly will serve as a resource for detailed studies of wCon and related *Wolbachia*.

Behavioral Biology
Oral presentation

Partners smell alike: Preen oil chemical composition in pied flycatchers

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Birds possess a specialized gland, the preen gland, that secretes a waxy mixture called preen oil. Preen oil serves diverse functions, including plumage maintenance, waterproofing and defence against parasites. Preen oil is also a major source of odour and may be involved in chemical intra-specific communication (e.g. sexual signalling during mate choice) and inter-specific communication (e.g. olfactory crypsis during incubation). We analysed the chemical composition of preen oil of a common passerine, the pied flycatcher (*Ficedula hypoleuca*). In females sampled twice during the breeding season, we found seasonal changes but no within-individual similarity. In breeding pairs sampled during nestling rearing, we found sex differences and within-pair similarity. These results allow us to speculate on the role of preen oil in this species, and bring new insights in the chemical ecology of birds.

Neurobiology
Oral presentation

Implications of local motion adaptation for navigation in dense environments

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Many flying insects cross dense vegetations and meander between tree-branches, flowers-stems, or grass. Navigating through dense environments come with a risk to collide with obstacles, and therefore efficient navigation involves a robust collision avoidance mechanism. Many insects avoid a collision by using the apparent motion of the object on their retina during locomotion (optic-flow). Nearer object appear to move faster on the retina than farther objects. In flying insects' brain, the optic-flow is estimated by an array of elementary motion detectors. These detectors not only respond to the distance between an observer and an object, but also to the contrast between the object and the background. Neurophysiological evidence and simulation suggested that local motion adaptation facilitates the isolation of nearby objects from the background. By combining model simulation and behavioural experiments, we assessed the implication of local adaptation for bumblebees crossing a cluttered environment. The bees crossed a tunnel containing 49 objects and meandered around the objects efficiently. We reconstructed and replayed the visual experience of the bees through the environments. The perceived optic-flow by the bees was modelled with different arrays of elementary motion detectors, notably with and without local adaptation. We analysed the response profile of the different models and investigated the implication for an agent guided by local collision avoidance and a goal-direction on efficient navigation through dense environments.

Neurobiology
Oral presentation

Acquisition of the Solar Ephemeris: Rotation of the Sky Triggers Neuronal Plasticity in *Cataglyphis* Ants

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Many animal species show impressive capabilities to navigate in challenging habitats, from highly complex to uniform environments. Desert ants are extraordinary navigators with a powerful brain. Using a set of navigational cues, they always find their way back home after far-ranging foraging trips. To spend as little time as possible in the blazing heat of the sun, foragers steer back to their nest in the shortest way possible – the beeline. *Cataglyphis* ants integrate directional information from a celestial compass and distance information from a step integrator into a vector pointing homewards. Since the position of the sun and related celestial cues change throughout the day and season, ants have to learn the sun's daily course (solar ephemeris) when they switch from interior tasks to outdoor foraging. To do so, the ants perform initial learning walks (LW) for up to three days before first foraging. Using the earth's magnetic field as a compass reference, *Cataglyphis* nodus calibrate their navigational systems and learn the landmark panorama. During this early learning phase, substantial neuroplasticity occurs along two visual pathways to higher brain centres. We show that only the performance of LWs under rotating skylight conditions triggers learning-related (Hebbian) plasticity in the mushroom bodies and the central complex, whereas sensory exposure to skylight cues in the absence of LWs leads to light-spectrum dependent homeostatic plasticity in synaptic complexes upstream the central complex. This suggests that LWs are necessary for both sky-compass calibration and panoramic memory formation in the ants' visual guidance systems. This work was supported by the DFG project: FL1060/1-1 to PNF, and project Ro1177/7–1 and DFG equipment grant INST 93/829-1, both to WR.

Morphology
Oral presentation

Morphology of the Gill Arch System in Five Ram Feeding Fish (Scombriformes, Clupeiformes)

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Filter-feeding fish are suspension feeders which separate plankton particles from the ambient water for nutrition. Their filtration system consists of gill arches with elongated gill rakers and denticles to form meshes and retain particles. Ram feeders, which engulf water by swimming forward with an open mouth, use cross-flow filtration: the water streams tangentially towards the filter medium and the particles are thus transported towards the esophagus. However, for many ram feeding species the morphology of the mouth is unknown so that the details of the filtration mechanism are unclear. We studied the mouth morphology of five ram feeders with µCT and optical microscopy in order to understand how plankton separation is achieved. We determined relevant filtration parameters in addition to video analysis of filter-feeding individuals. Species within the orders Scombriformes and Clupeiformes show differences in gill raker morphology, denticle abundance, filtration area, and mesh size, which indicates that the two groups use variations of cross-flow filtration. We suggest that *S. scombrus* and *R. kanagurta* (Scombriformes) use surface structures and mucus as adhesive material to increase particle retention, whereas *Scomber scombrus*, *Sardina pilchardus*, and *Engraulis encrasicolus* (Clupeiformes) use a purely mechanical separation mechanism. This is the most thourough study of filtration mechanisms in ram feeders to date. In combination with further experimental data and numerical fluid dynamics, our data could aid in the design of bio-inspired filtration technologies.

Evolutionary Biology
Oral presentation

Built-in disinfection: Metapleural gland secretions and uses in a clonal ant

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Ant societies are exposed to a large number of detrimental microorganisms. Ants have therefore evolved a great diversity of chemical and behavioral defenses to face such threats. The metapleural gland (MG) is known to play a key role in sanitizing ant colonies. Previous studies have mainly focused on the antimicrobial defenses of more derived ant genera like *Atta* and *Acromyrmex*. Here we report on the function of the MG in the ponerine ant *Platythyrea punctata*, a clonal species with simple social organization. Colonies of *P. punctata* are small and, contain one, seldom more, reproductive workers that reproduce by thelytokous parthenogenesis, while the majority of individuals has inactive ovaries. Reproductive division of labor is based on rank orders established by young workers through fighting. We analysed the MG content of *P. punctata* by gas chromatography / mass spectrometry and found tryptophol (indole-3-ethanol) to be the major constituent. Tryptophol proved to be active against a variety of microorganisms in vitro. Furthermore, intranidal workers carried more tryptophol than foragers. Finally, tryptophol quantity differed between reproductive and non-reproductive workers.

Morphology
Oral presentation

Comparative morphology of the venom delivery system of selected atractaspid, elapid and viperid snakes using micro-CT based 3D modulation

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Despite a century and a half of morphological and phylogenetical research, the evolution of the venom delivery system in snakes remains unresolved. While venom glands and associated teeth share the same developmental origin, their structure is fundamentally different on an interfamilial level, making it difficult to trace their evolution, especially with the remaining lack of a strongly supported phylogenetic tree. The present work dealt with the morphology of the venom delivery system in the snake families Atractaspididae, Elapidae and Viperidae. To this end, *Atractaspis irregularis*, *Elapsoidea nigra* and *Atheris chlorechis*, which were chosen as respective representatives for these families, were stained with phosphotungstic acid and scanned using micro computed tomography. The images were then processed into 3D models, which were used to describe and compare the morphology and inner structure of the venom glands. The results generally confirmed those of previous studies that relied on other methods (dissection, histology), demonstrating that MicroCT based 3D models are a reliable non-destructive method for depicting the form, structure and natural position of the venom delivery system.

Systematics, Biogeography & Diversity
Oral presentation

The Caucasus Barcode of Life (CaBOL) - Project

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The Caucasus region is one of the biodiversity hotspots of our planet. The BMBF-funded Caucasus Barcode of Life (CaBOL) project aims to catalog numerous animal and plant species of the Caucasus and store them in a reference database for public access. In order to establish a reliable reference database of DNA barcodes, animals and plants are collected and identified from various habitats in Armenia and Georgia. Based on the resulting DNA barcodes, a wide range of future applications can be built, all of which have in common that they rely on fast and accurate species identifications; the discovery of new species will equally be facilitated. A species catalogue based on DNA barcodes allows the efficient detection of differences in the biodiversity of individual regions and habitats (also over time). These data, along with the DNA barcodes themselves, will promote Caucasian biodiversity research as a whole. In addition to creating DNA barcodes, the project is concerned with identifying potential refugial areas in the Lesser Caucasus during the Last Glacial Maximum (LGM). During the LGM, the regions around Kintrishi (Georgia) and Yenoqavan (Armenia) likely served as refugia for various forest habitats and organisms.

Behavioral Biology
Oral presentation

Home sweet home: Effect of size and scent on shelter selection in two scorpion species

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Behavioural studies on Chelicerata in general, and scorpions in particular, are comparatively rare. As scorpions are mostly nocturnal animals, they have to find a save shelter for surviving daytime. In this context, the choice of an appropriate shelter is a pivotal task, but information how scorpions solve this challenge is almost uninvestigated. To test the attractiveness of shelters, we conducted a two-choice assay: Two shelters which vary in size and/or scent were placed in a rectangular plastic box. We placed a scorpion in each box and filmed its movements overnight. The final hiding place after dawn and the duration of contact with each shelter throughout the night were analysed. This experiment was done with 16 different shelter combinations of large, small, female scent, male scent, cricket scent, rosemary oil, and mineral oil. We monitored 20 females of *Euscorpius italicus* (distributed in moderate climate), as well as 14 females of *Mesobuthus eupeus* (arid climate). Comparing final hiding places, species from moderate and from arid habitat equally favoured the larger shelter in a neutral situation. Most animals were hidden under the large shelter in a large vs. small situation, no matter which of the shelters was perfumed with the scent of conspecifics. In direct comparison (2 large shelters), both species preferred female instead of male scent. Differences occurred in cricket scented tests: only *M. eupeus* preferred hiding places with cricket scent over neutral. On the other hand, *E. italicus* seem to avoid rosemary scented shelters. Our results provide a comprehensive overview on natural aspects that influence scorpion shelter choice. These observations may help to reduce accidental encounters between scorpions and humans.

Morphology
Oral presentation

Reconstructing aspects of reproduction of extinct insects based on fossils

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Insects today possess an extremely wide range of lifestyles and strategies e.g. regarding aspects of reproduction or investments in offspring. Even if it is not obvious at first glance, fossils can provide important information for investigating the evolution of these different strategies. Certainly, direct observation of behaviour of extinct organism is not possible. However, there are several approaches which can be used for reconstructions, especially based on morphological aspects of adults, youngs, but also eggs, with a comprehensive comparison to today living animals. Very rare, but very useful for reconstructing behavioural aspects are cases of the so-called ‘frozen behaviour’, were the organisms were enclosed during a specific moment, such as mating, egg laying, or hatching. Cases of ‘frozen behaviour’ of insects are especially known for amber inclusions. The insects were trapped in the still viscid resin that fast, that there are often preserved in nearly life-like conditions. Beside the behavioural aspects, these cases are especially interesting for adding further pieces in the knowledge of morphology extinct insect species, as these can allow to bring together different developmental stages, eggs with corresponding adults and/or nymphs or different sexes of the same species. Here, we present some examples of fossils preserved in Cretaceous limestone from the Crato formation in Brazil and Miocene, Eocene and Cretaceous amber contributing to reconstructions of reproduction, from mating to egg laying strategies, egg morphology and hatching in different insect groups.

Ecology
Oral presentation

Costs and benefits of inducible defences in *Daphnia cucullata*

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Phenotypic plasticity, and especially inducible defences protect prey species via for example morphological or behavioural alterations that are only expressed when necessary. They are well-known to yield strong advantages, in particular a reduced predation rate. A key evolutionary aspect of inducible defences is that there are costs associated, as otherwise they would be permanent. While some studies could reveal advantages, the costs of inducible defences are mostly unknown. Therefore, we investigated inducible defences of *Daphnia cucullata*, which forms adaptive morphologies under changing environmental conditions. For example, water temperature and turbulences, which are discussed as indicator for a predation threat, as well as presence of different predators elicit changes in morphology and behaviour. These defences enable the animals to perform better in e.g., predation experiments. Nevertheless, the mechanistic reason for this observation is still unclear. With the help of three-dimensional models of the unexposed shape, as well as the turbulence- and *Chaoborus*-exposed morph, we investigated the material investment and therefore material costs. We furthermore measured the swimming velocities of the three morphs and combined them with the respective shapes. That way, we were able to simulate drag forces to determine the energy necessary for locomotion, which may increase through the altered morphologies. This is especially interesting as one morph is elicited by turbulence and was previously supposed to be disadvantageous in colder, viscous medium. Considering all these aspects, we can form a holistic description of the alterations observable, as well as the potential mechanisms behind these defences. Even more, it allows initial approximations of the costs associated with inducible defences.

Neurobiology
Oral presentation

Stimulus distillation: How the lateral-line system of fish and the infrared system of snakes use inhibitory feedback to generate a perceptible map out of heavily blurred input

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A map is a neuronal representation of the outside sensory world. Amongst other functions, it allows for fast reactions, essential to survival. Many modalities such as hearing and seeing generate their own maps before they are integrated into a multimodal composite in the Optic Tectum (or Superior Colliculus in mammals) but does the same hold true for other modalities? Particularly, for the lateral-line system of fish and infrared vision of snakes, which both start with heavily blurred input. The many velocity detectors of lateral-line system are positioned all over the surface of the fish and, though the fish length is an approximate upper bound of its range, an aquatic object in general generates a blurred image on the skin. For a snake, its infrared image is at least as bad since it is generated by a “pinhole camera” with a huge hole – or worse. On the other hand, the lateral-line or infrared map existing in the optic tectum is at least as good as the one due to normal vision or audition. On the basis of the existing anatomy, we have shown for fish that the lateral-line map precedes multimodal integration and is nevertheless as good as the maps due to the other modalities. For snake’s infrared vision we have found that a similarly structured mathematical model shows the very same. The procedures in both classes are based on inhibitory feedback in conjunction with stimulus distillation, an anatomical construct of a huge excitatory expansion followed by severe reduction. For fish we have provided a solid anatomical and theoretical, i.e., mathematical, basis whereas for snakes the data are still scarce but the similarity seems to be far more than just accidental. The present argument suggests that sensory maps arise as such before they get integrated into multimodality.

Evolutionary Biology
Oral presentation

Evidence for female resistance traits in traumatically mating Strepsiptera (Insecta)

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Traumatic insemination is an example for sexual conflict. It is characterised by males penetrating the body wall of the female partner to inject sperm. Females unable to avoid unnecessary mating have been predicted to tolerate or resist by developing defence traits reducing damage caused by mating. Evolution of tolerance traits has so far only been demonstrated in the bed bug, where the male's penis penetrates the cuticle of the female's paragenital organ. However, tolerance was also suggested for Strepsiptera. Here we show on the example of *Stylops ovinae* (with paragenital organ) and *Xenos vesparum* (without paragenital organ) that female defence against traumatic penetration is also realised via resistance in this insect order. Using confocal laser scanning microscopy, we show that areas where traumatic insemination takes place do not differ from control sites in the material composition of the cuticle and that both contain large proportions of resilin. Micro-indentation experiments revealed that the force required to penetrate the cuticle at the wounding sites is significantly higher than at control sites. Our results demonstrate that resistance of Strepsiptera females is a direct result of an increased thickness of their cuticle at the wounding site, rather than changes in material composition. A comparison of the shape of the penises of different species of the genera *Stylops* and *Xenos* suggests that antagonistic co-evolution resulting from female resistance is restricted to *Stylops*, where allospecific males were unable to penetrate the female's paragenital organ. Our results suggest that resistance can be a driver of trait diversity.

Developmental Biology
Oral presentation

Duplication and divergence of the transcription factor Pax2/shaven in chelicerates and its role in sense organ development

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Paired box (Pax) genes are conserved across animals and encode transcription factors that play key roles in embryonic development. A chief example of this is the gene shaven (sv), the *Drosophila* ortholog of the vertebrate Pax2/5/8 genes. In *D. melanogaster*, sv is known to play a role in the development of the compound eyes, as well as the sensory hairs that are scattered across the body of the animal. This makes sv a prime candidate to study the evolution of arthropod sense organs on a genetic basis. Despite this, previous studies have failed to identify an ortholog of sv in chelicerates, the sister group to all other arthropods. Here we report the expression of an sv ortholog in the common house spider *Parasteatoda tepidariorum*, a model organism for chelicerate development. Similarly to the situation in *D. melanogaster*, we find that sv is expressed both in the developing eyes and sensory hairs of embryos of *P. tepidariorum*. Furthermore, we report the expression of a paralog of sv, which arose as a consequence of a whole genome duplication in the last common ancestor of spiders and scorpions. This paralog is not expressed in the developing eyes and shows a different expression pattern in sensory hairs, which hints at a possible case of sub- or neofunctionalization, and thus at an opportunity to study the evolution of functional gene divergence.

Neurobiology
Oral presentation

Bumblebees dashing through an artificial forest - following routes in cluttered environments

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Following habitual routes to commute between locations is an everyday task and a wide-spread navigational strategy used by many animals. Bumblebees, *Bombus terrestris*, as well as other foraging insects, are excellent navigators that can travel long distances to look for food sources. They were observed to travel along routes and optimize routes between multiple feeding locations. While foraging in cluttered environments, obstacles like trees and flower stems require the bees to deviate from their path in order to avoid collisions. However, it is not entirely clear how bees establish these routes and how experience affects the flight paths of bees in clutter. On the one hand, route following might be visually guided, and bees establish routes by matching the current view with familiar visual memories along the previous journeys. On the other hand, route following might be a by-product of bees following path integration (the continuous integration the distance travelled and turns made) and spontaneous reaction to avoid collisions. By recording flights of bees in an artificially cluttered environment, we show that bees quickly learn to efficiently cross the clutter and follow distinct routes to return to their hive. With increasing experience in the cluttered environment, bees optimize their flight time and the distance they keep to objects along the routes. Our findings shed light on the route following mechanisms that may drive bees at different stages of its foraging life.

Behavioral Biology
Oral presentation

The use of supervised learning models in studying agonistic behavior and communication in weakly electric fish

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It is long known that weakly electric fish use electric signals, also known as electric organ discharges (EODs), for both localization and communication purpose. However, studying electro-communication in weakly electric fish has been challenging, in particular in pulse-type weakly electric fish. Due to the nature of the electric field and the very brief and stereotypic waveform of the EOD it is difficult to assign EODs to individuals in a group. In addition, EOD rates in the species investigated here, *Gnathonemus petersii*, vary from a few Hz up to 120 Hz. These constraints have restricted research on electro-communication to short interaction sequences. Here we show that supervised network approaches, mainly based on open resource software, offer a promising tool to automate or semi-automate the workflow, and thereby allow the analysis of much longer episodes of behavior in a reasonable amount of time. We present a detailed workflow and verify its potential for future research using different experimental conditions, including agonistic encounters in dyadic interactions.

Physiology
Oral presentation

Aminergic modulation of honeybee thermogenesis

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For many species, including humans and honeybees (*Apis mellifera*), heat generation is essential for survival as an important part of a thermoregulation strategy. Especially in times of climate change, these abilities are of vital importance. It is known for a long time, that workerbees use their flight muscles for this purpose, but the exact molecular mechanism and the associated modulation is not yet completely understood. Some hints point to the involvement of biogenic amines as key player in this process. The purpose of this study was to provide new insights into this complex physiological process of shivering thermogenesis by combining methods of both fields, behavioral pharmacology with analytical chemistry. We were able to lower the content of biogenic amines in the respective tissues of the honeybee and confirm this via high performance liquid chromatography measurements. This reduction in biogenic amine levels caused a change in the heating behavior of the different treatment groups in thermographic analyses. From our results, we conclude that biogenic amines are essential for thermogenesis in honeybees. Furthermore, this is the basis of deeper analysis of the underlying molecular and cellular mechanisms.

Ecology
Oral presentation

A beetle’s Achilles heel: Glyphosate inhibits symbiotic bacteria in saw-toothed grain beetle

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Glyphosate is widely used as a herbicide, but recent studies begin to reveal its detrimental side effects on animals by targeting the shikimate pathway of associated gut microorganisms. However, its impact on nutritional endosymbionts in insects remains poorly understood. Here, we sequenced the tiny, shikimate pathway encoding symbiont genome of the sawtoothed grain beetle *Oryzaephilus surinamensis*. Decreased titers of the aromatic amino acid tyrosine in symbiont-depleted beetles underscore the symbionts’ ability to synthesize prephenate as the precursor for host tyrosine synthesis and its importance for cuticle sclerotization and melanization. Glyphosate exposure inhibited symbiont establishment during host development and abolished the mutualistic benefit on cuticle synthesis in adults, which could be partially rescued by dietary tyrosine supplementation. Furthermore, phylogenetic analyses indicate that the shikimate pathways of many nutritional endosymbionts likewise contain a glyphosate sensitive 5-enolpyruvylshikimate-3-phosphate synthase. These findings highlight the importance of symbiont-mediated tyrosine supplementation for cuticle biosynthesis in insects, but also paint an alarming scenario regarding the use of glyphosate in light of recent declines in insect populations.

Morphology
Oral presentation

A case of frozen behaviour: A putative parasitoid flat wasp with a beetle larvae in its grasp in 100 million years old amber

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Parasitism is one of the most common feeding strategies amongst all organisms, though especially in animals. Parasitism *sensu lato* (*s. l.*) describes a malignant form of symbiosis in the wider sense where one organism (the parasite) lives off of another organism (the host), taking nutrients and influencing that organism otherwise negatively. Parasitoidism is a form of parasitism *s. l.* wherein the parasitoid kills its host upon leaving it. Particularly within hymenopteran insects parasitoidism is supposed to be one of the more ancestral feeding strategies and is potentially responsible for the massive diversification of Apocrita, the group of wasp-waisted hymenopterans. Within parasitoid wasps, mostly the immature stages are parasitoids attached to or even inside their hosts and the adults are free-living forms, these wasps are thusly larval parasitoids. Bethylidae is a small, lower branching in-group of aculeatan wasps that are larval parasitoids. All representatives of Bethylidae or flat wasps are ectoparasitoids of mostly immature coleopteran and lepidopteran insects, meaning that the immature stages develop externally on their host organisms. Since flat wasps are aculeatan wasps, their ovipositor is modified into a stinger with which they paralyse the host organism of their progeny (mostly) permanently after a suitable host has been found. The female flat wasps then either carries the paralysed organism away and then oviposits onto it or does so directly on site. The immatures, once hatched, attach themselves to their host organism and take nutrients from their host until their development is completed and the host is killed. Here we present a new finding of a flat wasp holding onto and potentially stinging into a coleopteran immature preserved in 100 million year old amber from Myanmar.

Physiology
Oral presentation

Na+/K+-ATPase and V-ATPase in *Theodoxus fluviatilis* under changing environmental salinity

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The aquatic gastropod *Theodoxus fluviatilis* occurs in wide areas of Europe and adjacent areas of Asia. In Northern Europe the snail has formed two genetically closely related subgroups. Other than the freshwater ecotype, the brackish water ecotype survives in salinities of up to 28 ‰. Coastal aquatic ecosystems may be affected by climate change due to salinisation limiting survival of sensitive organisms. Thus, we investigated how the two *Theodoxus* ecotypes adjust to changes in environmental salinity especially focussing on the question whether Na+/K+-ATPase or V-ATPase are regulated on the transcriptional, the translational or at the activity level under changing environmental salinity. Animals were gradually adjusted to higher salinities (both ecotypes) or to lower salinities (brackish water ecotype) in aerated containers under long-day conditions and constant temperature. Whole body RNA- or protein extracts were prepared. Semi-quantitative PCR- and Western Blot-analyses did not reveal major changes in transcript or protein abundances for the two transporters under hypo- or hyperosmotic salinity stress. No significant changes in ATPase activities in whole body extracts of animals maintained under hypo- or hyperosmotic stress conditions were detected. We conclude that constitutive expression of ATPases is sufficient to support osmotic and ion regulation in this species under changing salinities given the high level of tolerance with respect to changes in body fluid volume.

Morphology
Oral presentation

The interplay of morphology and hydrodynamics in the predatory strike of two dragonfly larvae

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Dragonflies and damselflies (Insecta: Odonata) capture prey with a fast moving, highly modified mouthpart - the prehensile labial mask. Within dragonflies (Odonata: Anisoptera) two basic shapes of the prehensile labial mask have evolved with an either flat and slender or concave - 'spoon-shaped' - distal segment (prementum). While the former is a pure grasping device, the latter is also capable of scooping up smaller prey items to retain them inside the cavity by arrays of setae. Although some hypotheses exist about the hydrodynamics of the prehensile labial mask, it has not been investigated either theoretically or experimentally so far. Based on 3D µCT-data, we used computational fluid dynamic (CFD) simulations of the prementum to understand the relationship between the shape of the prehensile labial mask and its hydrodynamic properties. Our results suggest that both types are highly streamlined and generate a low-pressure area, likely leading to an effect analogous to compensatory suction feeding. While little is known about such effects in arthropods, this is a well-studied strategy in various vertebrates, to mitigate the formation of a bow wave which could alarm or even displace prey in front of the predator. The hydrodynamics of fast prey capturing movements might be an interesting concept for biomimetics, like technical application in small scale underwater grasping devices.

Morphology
Oral presentation

Failure prevention mechanisms in taenioglossan radulae of African gastropods (Paludomidae) are related to the species ecological niche

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The molluscan radula, a thin membrane with embedded rows of teeth, is the structure for mechanical food processing. For proper functioning, structural failure, resulting from high local stress when interacting with the preferred food, must be either avoided or reduced. In this case study on four gastropod species from Lake Tanganyika, we tested the underlying principles for failure reduction of the radula. The selected Paludomidae are of high interest for evolutionary biologists, since they represent different trophic specialisations to distinct feeding substrates. As their radulae are non-mineralized, chitinous, and rather soft, a high degree of structural failure was expected, but not observed. To gain insight into failure-preventing mechanisms, we analysed teeth's mechanical properties and showed that hardness and elasticity are either gradually or homogeneously distributed along each tooth. We additionally observed the behaviour of the radula in a biomechanical experiment by applying load with a force transducer until structural failure occurred. As the experiments were carried out under dry and wet condition, the high influence of the water content on the mechanical behaviour and breaking forces was documented. Wet teeth resisted higher forces, because teeth and their underlying membrane were flexible, enabling teeth to either slip away or/and gain support from adjacent teeth. The hardness, elasticity, mechanical behaviour, and fracture forces can be related to the gastropod ecological niche and are here suggested as adaptations to the feeding substrates. Finally, we combined the mechanical property data with the 3D shape of teeth for every species in a finite-element-analysis and visualized stress and strain. By altering the sizes of the radular models and thus the load per volume we tested the influence of size on the stress and strain distribution. We found that all teeth of soft substrate feeders can resist lower forces/volume whereas teeth of rocky substrate feeders can resist higher forces/volume emphasizing the influence of tooth shape, arrangement, and material properties on the mechanical behaviour.

Physiology
Oral presentation

In search of a superhirudin – construction of recombinant leech salivary proteins and their functions

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Medicinal leeches have been used for centuries in a wide variety of therapeutic or medical applications. The more than 100 bioactive ingredients present in their saliva show a wide range of properties such as anti-coagulatory, anti-microbial or anti-inflammatory potencies. One of the most studied ingredients in leech saliva is the thrombin inhibitor hirudin, an anti-coagulant. Only recently, a new class of substances was detected in the saliva of the medical leeches, the hirudin-like factors (HLFs) which are structurally similar to the hirudins. While some of these factors are anti-coagulants, others have minor or no thrombin-inhibitory potency at all. Of those HLFs that were successfully expressed as recombinant proteins in bacteria, the HLFs 1, 3, 4, and 6 showed no or extremely low potency of thrombin inhibition while the HLFs 5 and 8 showed moderate effects. Site-directed mutagenesis of the genes encoding such factors revealed that exchange of certain amino acids in the N-terminus, the central globular domain or the C-terminus had substantial effects on the thrombin-inhibitory potency of the protein products. Thus, we set out to design genes using the sequences encoding these regions of different HLF types in search of a kind of “superhirudin”. Hybrid combinations were produced from hirudin variant 1 (HV1) and hirudin-like factor 1 (HLF1V). In addition, constructs were formed which had the N-termini of HLF3 or HLF6 while the rest of the molecule originated from HV1 or HLF1V. Subsequently, all factors were expressed in *E. coli*, purified and tested for anti-coagulatory potency using the thrombin time assay. The results show that the activities of most new hybrid constructs are in the range or even below the activities of the initial factors HV1 and HLF1V. The only factor that has increased thrombin-inhibitory potency is composed of the N-terminus of HLF1V and the central globular domain as well as the C-terminus of HV1. This finding confirms the importance of the N-terminus in determining the ability of such molecules to inhibit thrombin.

Behavioral Biology
Oral presentation

Light influences the stridulatory behaviour of the bushcricket *Tettigonia viridissima* (Tettigoniidae, Orthoptera)

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Seasonal and circadian temporal niches are important for effective communication. The intraspecific acoustic communication of tettigoniids underlies a circadian rhythm. Males of *Tettigonia viridissima* produce their calling song by wing stridulation mainly during early night in order to attract females. In an experimental setup with controlled light-dark regimes and temperature, they stridulate for about 7 h in the dark phase. In constant light, the rhythm is lost, but the total duration per 24 h is maintained. In constant darkness, the activity rhythm is shifted in time, reflecting the internal biological clock of the animals. Long-term recordings in the field show that stridulation usually starts at sunset during the whole season. The shorter duration of stridulation in the field (about 4 h) is probably caused by decreasing temperatures at night. The light dependency of the communication behaviour raises the question of the influence of artificial light at night on the stridulation. *T. viridissima* occurs in urban areas, as well as in rural areas. Experimental exposure of caged animals to different habitats, including close to streetlights show that onset and duration of stridulation is not affected by artificial light at night. Sudden light flashes during the night can interrupt the calling behaviour or even end it. Interestingly, light flashes also prolong total stridulation duration per night. It remains to be seen, whether artificial light at night influence female behaviour and, ultimately, reproduction.

Physiology
Oral presentation

Matched growth of metabolic demand and tracheal air supply in larvae of a large wood boring beetle: support for symmorphism rather than the fractal network theory

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There are several competing evolutionary hypotheses claiming to explain variation in the scaling of respiratory tubes or gas exchange structures of insects with ontogeny. To date, few studies have undertaken a thorough quantitative assessment of alternative hypotheses based on temporally-replicated three-dimensional empirical data. Here, we explore and test competing hypotheses using µCT scan data of tracheal structures (at 15 µm resolution) and estimates of metabolic rates at rest, in developing larvae of the cerambycid beetle *Cacosceles newmannii* across a wide range of body size. Our results show that between two of the major alternative hypotheses proposed to date, symmorphosis is supported while the fractal network theory is rejected, as both tracheal system volume and area scaled more than would be predicted based on the latter. These results suggest that gas influx is probably set by Murray's law - i.e. that physiological flow networks have been optimized, through evolution and natural selection, so that flow is achieved with the least possible biological work - in larvae of *C. newmannii*. Further work is needed however, to understand gas efflux and the relative importance of tissue costs or trade-offs in both processes, especially since the present results suggest hyperallometry in the scaling of supply structures with ontogeny, indicating a significant excess capacity for oxygen supply. As an overdimensioned air supply system may be costly in terms of energy expenditure, oxygen toxicity or space restrictions, there are probably balancing factors requiring such a capacity that are not linked to direct tissue oxygen demand and that have not been thoroughly elucidated to date.

Morphology
Oral presentation

The diversity of aphid lions over time – a quantitative comparison

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Aphid lions are the larval stages of some lineages within Neuroptera, the group of lacewings. More precisely aphid lions are representatives of Chrysopidae (green-lacewings) or Hemerobiidae (brown-lacewings). The name 'aphid lion' originates from their ecological function as specialised predators on aphids. Accordingly, they play also an economic role as biological pest control. Aphid lions have, mostly, elongated spindle-shaped bodies, and are equipped with a pair of venom injecting stylets, as most lacewing larvae. The stylets are mouthparts and are used for sucking on the prey. A major difference to other well known larvae of lacewings, such as those of antlions and owlflies, aphid lions have simple curved stylets without any teeth. Fossils that have been interpreted as aphid lions are known preserved in ambers of various ages including: Cretaceous (130 and 100 million years ago), Eocene (about 40 million years ago) and Miocene (about 15 million years ago). Here, 58 new aphid lion specimens are reported from 100 million years old amber. The shapes of head and stylets were compared quantitatively over the different time slices. With the newly described fossils and specimens from the literature, a total of 361 specimens could be included into the analysis. The results indicate that the diversity of head shapes in Chrysopidae remains more or less unchanged over time, while in the diversity of the head shapes in Hemerobiidae increases. In many other ingroups of Neuroptera, a distinct decrease in diversity of head shapes in larval stages was observed over time. This demonstrates that the diversity of lacewings did not simply decrease over time, as generally assumed; at least some lineages diversified since the Cretaceous.

Developmental Biology
Oral presentation

Dissecting the mechanism underlying the evolution of head development in *Drosophila*

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The Mendelian genetics concept relies on simple genotype-phenotype relationships with few genes having major effects on the phenotype. However, many traits evolve by a combination of variation in many genomic loci with minor phenotypic effects. Therefore, it is challenging to reveal individual genes underlying natural variation in quantitative traits. Most genes do not act individually, but they are interconnected in gene regulatory networks (GRNs). Revealing variable nodes and modules within GRN, thus has the potential to gain mechanistic insights into phenotypic evolution. The formation of the insect compound eye is determined by a complex GRN involving more than 5,000 genes and natural variation in eye size is pervasive in *Drosophila*. To reveal the molecular basis of this variation, I study eye development in *Drosophila melanogaster* and *D. mauritiana*. It has been shown that variation in expression of the GATA transcription factor Pannier (Pnr) affects many target genes and remodels the GRN significantly. However, genetic tests suggested that the causative genomic changes lie upstream of the pnr locus. I integrated several unbiased genome wide datasets, such as developmental gene expression (RNAseq), chromatin accessibility (ATACseq) and quantitative trait loci mapping to reveal candidate genes. Those genes were tested for their functional involvement in eye development applying an RNA interference screen and phenotypically relevant candidates were used to reconstruct a core GRN with 20 crucial genes. Based on this network I could propose a developmental hypothesis that I am currently testing applying functional assays. Overall, my work shows that a GRN-centric approach is highly powerful to reveal the mechanism underlying the evolution of complex organ development.

Evolutionary Biology
Oral presentation

Leafcutter ant queens' ovaries show fewer transcriptomic changes with age than the brains and fatbodies do

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Evolutionary theory of ageing suggests that one reason for senescence is the preferential allocation of resources into reproduction, leaving little for body maintenance. This leads to a physiological decline and eventual death. Such a life-history strategy of high fecundity combined with a short lifespan can be found across many taxa. In the social insects, such as ants, that have highly reproductive queens and non-reproductive workers, such a trade-off between fecundity and longevity seems absent. The highly fecund queen typically outlives her workers for years if not decades. Brain, fatbody, and ovaries are all physiologically crucial tissues linking various aspects of sociality, fecundity and longevity in social insects. In this study, we were able to obtain brain, fatbody, and ovaries from young (max 2 years) and old queens (up to 15 years) of the Panamanian leaf cutter ant, *Acromyrmex echinatior*. Transcriptomic analyses showed that age affected the three tissues very differently. Out of 12,290 genes found across all tissues and age groups, only five genes were differentially expressed with age in the ovaries, whereas genes in the fatbody and brain varied much more with age. In long-lived *A. echinatior* queens, the cost of stable ovarian function appears to be borne by the brain and fatbody, which invest more in regulatory and metabolic processes. Our study underscores that, in order to disentangle genes associated with fecundity and longevity, we may need better understand the specific roles of tissues and to explore how they act in synergy.

Ecology
Oral presentation

Phylogenetic isolation of host tree reduces resource tracking by ectophagous herbivores and their parasitoids

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Parasites use movements and sensory capabilities in foraging strategies that enable them to track host-resources. Such resource tracking may be reduced by spatial isolation of hosts due to limited movements and sensory information. However, even spatially proximate hosts can be difficult to track, such as host trees in a forest canopy. We hypothesised that when host-trees in a forest are phylogenetically isolated i.e. surrounded by phylogenetically distant neighbours, specialized herbivorous insects which parasite on trees might find it difficult to track resources due to masking of host odours or reduced movement. We studied tracking of resource quantity and quality by guilds of herbivorous insects and their parasitoids on individual oak trees that differed in their degree of phylogenetic isolation. For four years, we determined the abundance of guilds of herbivorous insects, the extent of herbivory, and potentially important leaf parameters. We also reared the sampled ectophagous caterpillars to determine parasitism. We found that phylogenetic isolation reduced the tracking of resource quantity by ectophagous caterpillars and their parasitoids. Tracking of resource quality by ectophagous caterpillars as well as resource tracking by endophagous herbivores was not evident and not affected by phylogenetic isolation. Our results suggest that for phylogenetically isolated hosts the degree of herbivory is less predictable which may select for increased reliance on induced defences.

Evolutionary Biology
Oral presentation

Adaptation in a changing world: disentangling genetic adaptation and phenotypic plasticity in a common garden experiment with the invasive New Zealand Mud Snail, *Potamopyrgus antipodarum*

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Climate change is affecting the entire biota of our planet and organisms are either forced to adapt or to move to new, suitable habitats. Adaptation can be accomplished either genetically or through phenotypic plasticity. In order to understand and predict adaptive responses, adaptive evolution and plasticity have to be disentangled in common garden experiments. Invasive species are particularly well-suited models to study adaptation as the habitats they invade are by definition novel. Therefore, we investigated the adaptive potential of invasive populations of a fresh- and brackish water snail, the New Zealand Mud Snail *Potamopyrgus antipodarum* (NZMS). The NZMS has reached Europe in the mid 19th century and has since then spread across the continent. Invasive populations reproduce clonally and only two mitochondrial lineages have established in Europe. The NZMS is characterized by an extreme morphological variability which has been shown to be fitness relevant. In our experiment we reared snails from 11 populations from Germany, Spain and Portugal at three different temperatures, 15, 19 and 23 °C. We investigated shell morphology in the framework of geometric morphometrics and also measured shell size. Based on previous work we expected that size is considerably more plastic than shape and that snails should become more similar to each other in the common garden. Furthermore, size and temperature were expected to correlate. We were particularly interested if the NZMS has accumulated already detectable genetic variation over the roughly 180 to 360 generations it is present in Europe. Our first two general expectations were confirmed, however, with remarkable differences between the mitochondrial lineages. In contrast, size did not react linearly to the temperature gradient and patterns differed across populations. These differences between populations may be indicative of genetic differentiation, suggesting adaptation already within a short period of time.

Morphology
Oral presentation

Breaking behaviour of the paramere used for traumatic insemination in the bedbug *Cimex lectularius* (Insecta: Hemiptera)

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The bed bug family Cimicidae is well-known for traumatic insemination, and males pierce females with their paramere and transfer sperm through it. The shape of parameres are diversified among species in the family, and in some genera the paramere is elongated, looking less resistant against lateral deflection and breakage. To understand the mechanical background enabling the evolution of prevailing and highly diversified parameres in the family, we studied the penetration mechanics with a particular focus on breaking behaviour of the paramere of the common bed bug, *Cimex lectularius*. For this purpose, we analysed geometry and material distribution along the paramere using confocal laser scanning microscopy. The paramere is likely homogeneously sclerotized except for a flexible basal wing-like structure, which can interlock with an anal sclerite during mating. The entire paramere is slightly twisted, the tip region is circular in cross-section, and the geometry of the rest is rather complex. We also conducted axial buckling experiments in wet and dry conditions. Wet parameres were mainly buckled, while dried parameres were broken off. The forces causing these critical failures were significantly higher with dried parameres (13.3 mN [dried] vs 10.7 mN [wet] in average). In both cases, the forces were higher than the forces necessary for piecing the female abdomen (ca. 2.35 mN) previously studied, but we also found that males can potentially produce the force in a range being able to break the paramere. Moreover, during our observation of mating behaviour, kicking parameres by females was also observed. Based on the structural and experimental results, we will discuss the functioning of the paramere in this species.

Physiology
Oral presentation

Carbonic anhydrase activity underlying a novel carbon concentration mechanism in calcifying cells of the sea urchin larva

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Carbonic anhydrases (CA) mediate the reversible hydration of CO2 to HCO3- and are a fundamental component of biological calcifying systems. While their presence has been widely described in calcifying tissues and cells, the exact mechanistic basis of their contribution to the calcification process remains less clear. We examined the role of cytosolic and a membrane bound extracellular CA in calcifying primary mesenchyme cells (PMCs) of the sea urchin larva. Transcriptomic and in situ hybridization results demonstrated the presence of a cytosolic CA (Cara2) in PMCs. Intracellular pH measurements in combination with CO2 pulse experiments demonstrated dose-dependent inhibition of Cara2 activity in PMCs by acetazolamide (AZM). The second carbonic anhydrase (Cara7) that is exclusively expressed by actively calcifying PMCs is equipped with a GPI-Anchor suggesting its membrane bound extracellular localization. A Cara7 specific antibody underlines its localization in the plasma membrane of PMCs and knock-down of this enzyme reduces the formation of specific skeletal segments. H+-selective electrode measurements were used to measure in-vivo Cara7 activity at the cell surface of PMCs demonstrating reduced CO2 hydration rates in the presence of AZM or in knock-down larvae. Finally, intracellular pH measurements in combination with the ammonia pulse method demonstrated reductions in HCO3- accumulation during inhibition and knock-down of Cara7. We conclude that the extracellular Cara7 enables PMCs to catalyze the hydration of metabolic CO2 at the cell surface that is subsequently transported back into the cell as HCO3-. This recapture of metabolic CO2 helps to maintain a high intracellular dissolved inorganic carbon (DIC) pool that is required during active mineralization.

Ecology
Oral presentation

Fitness consequences of pre- and post-mating selection in the field cricket *Gryllus bimaculatus*

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Sexual selection operates pre-mating via male-male competition (i.e., males compete for breeding territories and access to mates) and female choice (i.e., females preferentially mate with certain partners), as well as post-mating via sperm competition (i.e., sperm of multiple males compete for fertilization of eggs) and cryptic female choice (i.e., females bias fertilization towards certain males). The relationship between these episodes of selection, whether they act in concert, reinforcing each other or trade-off, acting in opposing ways, is central for understanding the role sexual selection plays in evolutionary processes. Understanding how each episode alone contributes to fitness may allow disentangling their effects and shedding light on their relative role. Using the field cricket *Gryllus bimaculatus* we investigated the fitness outcomes of matings occurring exclusively with i) pre-mating selection, by allowing males to fight against other males, court, and females to choose, with the successful pair breeding monogamously; ii) post-mating selection, by allowing females to mate multiply with 3 consecutive males, avoiding pre-mating interactions; and iii) no sexual selection, by enforcing monogamy. We then measured female survival and fitness by measuring offspring numbers, survival and growth rates. Our results will help us understand whether pre-mating mechanisms of female choice and male-male competition are more important than the post-mating processes cryptic female choice and sperm competition in determining reproductive outputs.

Morphology
Oral presentation

Fluid feeding in millipedes - a complex example of convergent evolution in millipedes and insects

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Fluid feeding by means of a sucking pump allows the exploitation of liquid food sources and evolved several times independently across the Arthropoda. Here, we report the first record of a sucking pump in millipedes (Diplopoda). We describe a previously unknown sucking pump mechanism in several colobognathan millipedes, utilizing high resolution X-ray µCT imaging, histology, scanning electron microscopy and 3D reconstructions. We studied the head morphology of nine enigmatic colobognathan species covering all six families within the taxa Polyzoniida, Siphonocryptida and Siphonophorida. All groups share highly modified mandibles, which are probably used to scrape off particles or to penetrate surfaces to make liquid food available by a protrusion-retraction movement similar to the maxillary movement in insects. Saliva released from externally opening glands might aid in suspension or external digestion of particles, which are transported into the intestine by a combination of capillary action and active pumping. In the head of all species, we discovered a pumping chamber, which acts as positive-displacement pump and is strikingly similar to that of various suctorial insects, showing fine structural convergences, such as (1) a rigid ventral wall, (2) a flexible dorsal wall with (3) large dilator muscles, (4) a posterior sphincter muscle, and (5) a variable set of compressor muscles. Based on its morphology we propose that the sucking pump of these millipedes works similar to that of bugs and butterflies. The apparently convergent evolution of this complex morphology in several unrelated arthropod lineages shows how feeding advantages, in this case the exploitation of liquid food, can lead to similar biomechanical solutions.

Evolutionary Biology
Oral presentation

Counting days for lunar time-keeping and the evolutionary origins of circalunar clocks

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Organisms are adapted to regular environmental cycles through various endogenous time-keeping mechanisms. While the circadian clock is well understood at the molecular level, the mechanisms of other clocks remain elusive. Many marine organisms possess a circalunar clock, which anticipates lunar phase and times reproduction accordingly. We investigated the circalunar clock mechanism in the marine midge *Clunio marinus*. In order to explore the role of the circadian clock in circalunar time measurement we employed a classic chronobiological experiment. We monitored the free-running circalunar emergence rhythm (i.e. without lunar time cues) under different manipulated daylengths (22h – 28h). From 22 to 26-h days, the free-running period of the circalunar rhythm increased linearly with daylength, indicating that lunar timing involves the counting of days. In 28-h days the circalunar rhythm was lost, probably because the circadian clock could no longer synchronise to the aberrant daylength. This would imply, that *Clunio*’s circalunar clock counts endogenous circadian clock cycles. Additionally, we analysed unpublished data by the late D. Neumann on the re-setting of the circalunar clock in *Clunio tsushimensis* with moonlight pulses. We found an immediate and linear resetting of the circalunar rhythm, consistent with a circadian cycle counter. Counting days is one of three possible circalunar clock mechanisms proposed by Bünning & Müller (1961). Based on a thorough re-evaluation of literature on other species, we gathered evidence for all three mechanisms. We propose that circalunar clocks evolved multiple times and are based on different physiological mechanisms.

Developmental Biology
Oral presentation

Natural variation in compound eye size in *Drosophila melanogaster* – A potential role of apoptosis in defining organ size

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Extensive intraspecific variation in ommatidia number in *Drosophila melanogaster* makes it a perfect model to reveal the developmental and molecular mechanisms underlying complex trait evolution using a micro-evo-devo approach. To identify genetic variants and genes underlying differences in ommatidia number between 162 strains of the *Drosophila* Genetics Reference Panel (DGRP) GWAS analysis was performed. A functional validation screen of the three genes containing most associated single nucleotide polymorphisms (mbl, trim9, CG15498) confirmed their potential involvement in eye size regulation. To learn more about potential cellular and developmental mechanisms, I further analyzed trim9, a gene encoding a RING domain E3 ubiquitin ligase. Knockdown of this gene in the eye-antennal imaginal disc (EAD) resulted in severe reduction or the entire absence of compound eyes. Moreover, my data strongly suggests that the number of apoptotic cells increased upon trim9 knockdown, implying that Trim9 may be a negative regulator of apoptosis in the developing EAD. Therefore, natural variation in expression of trim9 could account for the differences in ommatidia number observed between the different strains of *D.melanogaster* by regulating programmed cell death in the EAD. Intriguingly, the role of apoptosis in ommatidia number variation in fruit flies has not been observed yet. This work, therefore, presents an exciting new view on morphological evolution.

Ecology
Oral presentation

Eco-morphological diversification of parrots (Aves: Psittacidae: Arinae) along a tropical elevational gradient

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The New World parrots are a species-rich group of birds widely distributed in the Neotropics, where they inhabit various habitats across an extensive altitudinal range from lowlands to the treeline. Previous analyses of the parrots’ altitudinal distributions have found interesting, yet not fully understood, patterns of species (co-)occurrences across different altitudinal gradients. While some species are confined to relatively narrow altitudinal belts, others occur almost all along the whole gradient. At the same time, it has been projected that climate change may result in altered compositions of bird communities, with some species being pushed to the limits of their existence because of altitudinal decoupling of birds and their food plants. Therefore, our study aims to understand eco-morphological variation, interspecific competition, and associated lifestyles of an authentic community of 26 parrot species along a 3500 meters elevation gradient in the Manú National Park, south-east Peru. For this purpose, we assessed morphometrics of 305 museum specimens (10 parameters per specimen) and correlated these measurements with data on phylogeny, altitude, and species ecology using multivariate statistics. Finally, we tried to elucidate the evolutionary diversification of the parrots in the light of regional ecological adaptations. Our multivariate analyses document distinct morphological groups of parrots (i.e., large long-tailed, large short-tailed, small long-tailed, and small short-tailed) that are well-separated from each other in the multidimensional trait space. However, these size groups are not entirely correlated with phylogeny. Moreover, the measurements of wing shape, bill dimension, and tarsus size are more strongly correlated with altitude, indicating that they are more likely to be considered adaptive, i.e., ecologically-driven characters. Consequently, we conclude that the altitudinal distribution of parrots reflects a complex pattern of functional morphology, habitat characteristics, and resource competition, with altitude being an essential factor promoting morphological divergence at relatively resource-poor higher elevations. In comparison, at lower elevations, different morphological groups of parrots can coexist.

Behavioral Biology
Oral presentation

Physiological responses to energetic challenges in wild macaques

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Energy availability is an important determinant of an individual's life history traits such as age of maturation, reproductive rate, or longevity. The advance of non-invasive methods using fecal and urine samples to measure energetic markers such as thyroid hormones (T3), regulating an individual's metabolic rate, and glucocorticoids (GC), reflective of an individual's energy mobilization, allows investigating metabolic strategies of individuals in wild populations. Here, we combine behavioral (~3000 focal hours), physiological (~400 urine samples for T3 and GC analyses), life history (reproductive state), and environmental (phenology, temperature) data on 42 Assamese macaque females living in their natural habitat at Phu Khieo Wildlife Sanctuary in Thailand, to investigate how females cope with seasonally occurring fluctuations in energy expenditure and energy intake. We found that variation in energy intake, ambient temperature, and female reproductive state affected both hormones in partly contrasting, yet predicted directions. Specifically, T3 metabolite levels decreased with decreasing energy intake, reflective of a downregulation of metabolic rate and thus an energy-saving strategy, whereas GC levels increased with reduced food intake potentially indicating allocation of energy away from storage and into other functions. GC levels (but not T3) also increased in response to low ambient temperatures indicating energy mobilization to react to cold stress. Lastly, as predicted, reproduction, particularly gestation, was associated with increases in both hormone levels reflecting increased energy expenditure. We will discuss these findings in light of the species' breeding strategy in relation to seasonally fluctuating resources which is a mix of traits associated with income and capital breeding.

Evolutionary Biology
Oral presentation

A chemical key to biological invasion – A comparative analysis of antipredator defences induced by fish bile salts in the zooplankton species *Daphnia lumholtzi*

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The zooplankton species *Daphnia lumholtzi* is notoriously famous for spectacular morphological structures featuring very long head and tail spines, and for having a strong potential to invade new habitats. Originating from tropical and subtropical lakes of Africa, Asia, and Australia, *D. lumholtzi* successfully invaded lakes in North and South America, and eventually might also be able to invade european lakes. One important factor for the invasion success of *D. lumholtzi* is their effective defence against fish predation based on phenotypically plastic morphological changes. In response to chemical cues released by fish predators, animals can extend their head and tail spines, which serve as an effective protection against fish predation. We report the chemical identity of the fish-derived chemical signal (kairomone) that induces this defensive response. We used non-targeted bioassay-guided fractionation (LC-MS) of incubation water of the common roach (*Rutilus rutilus*) to identify the bile salt 5α-cyprinol sulfate, the most frequent bile salt in cyprinid fish, as the kairomone. We confirmed this finding by bioassays, in which *D. lumholtzi* was exposed to purified 5α-cyprinol sulfate from carp (*Cyprinus carpio*) bile and showed that 10 pM 5α-cyprinol sulfate induces significantly elongated helmets and spines. We used a comparative approach and investigated if *D. lumholtzi* responds with similar morphological defences to fish species that do not synthesize 5α-cyprinol sulfate. If *D. lumholtzi* would show similar defences, this would point at another, yet unknown kairomone. If *D. lumholtzi* would not respond with defensive morphological changes, this would suggest that the invasive success of *D. lumholtzi* requires the presence of cyprinid fish.

Physiology
Oral presentation

The influence of oxygen regime on energy metabolism and biological activities of *Mya arenaria*

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Coastal benthic organisms are often exposed to oxygen deficiency (hypoxia) which diminishes aerobic ATP production and can impair energy-dependent functions such as bioirrigation and bioturbation. We exposed the soft-shell clam, *Mya arenaria*, a widely distributed bioturbator, for 21 days to constant hypoxia (~20% air saturation), cyclic hypoxia (~10-50% air saturation) and normoxia (~100% air saturation), and assessed their bioirrigation and digging performance, energy reserves (lipids, carbohydrates), metabolism and oxidative stress biomarkers. Lipids were an important energy fuel for clams acclimated to constant hypoxia, while clams acclimated to cyclic hypoxia used glycogen. Enzyme activities at the phosphoenolpyruvate branch point indicated that the clams acclimated to constant hypoxia strongly relied on aerobic metabolism whereas the clams kept under cyclic hypoxia were more dependent on anaerobic pathways during the hypoxic phase of the oxygen cycle. Reliance on anaerobic glycolysis was supported by accumulation of succinate during the hypoxic phase of the cyclic hypoxia followed by the succinate oxidation during recovery. Reliance on aerobic metabolism was associated with oxidative injury to proteins (in constant hypoxia) and lipids (during the recovery phase of cyclic hypoxia). Clams acclimated to constant and cyclic hypoxia dug slower than their normoxic counterparts. Bioirrigation capacity decreased in clams acclimated to constant hypoxia. Our results indicate that acclimation to constant or cyclic hypoxia impede bioturbation and bioirrigation capacity of *Mya arenaria* and therefore might affect their ecological function in coastal ecosystem.

Behavioral Biology
Oral presentation

Spatial learning in a swimming tunnel reveals the navigation strategies and the usage of visual and electric information in the weakly electric fish *Apteronotus albifrons*

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Organisms ranging from invertebrates to vertebrates are endowed with individual navigation capabilities based on different navigation strategies which have evolved, because successful navigation skills enhance the animals' probability of survival. This study investigated the navigation strategies of black ghost knifefish including the fish's usage of different senses during this process. In general information from several modalities contributes to a more complex perception than the cues from a single sense, so that an individual's interaction with the environment is more adaptive to its conditions. Therefore, the hypothesis was that the fish's performance would be better in tests in which two types of sensory information and or only electric information were presented than only visual one, because it is a nocturnal weakly electric fish and its vision is controversially discussed. To approach these questions, black ghost knifefish were trained to learn the position of a target in an arena in which the walls provided a balanced amount of visual and electric information during training and manipulated sensory information during experiments. Video-recordings were taken during pretests and experiments to analyse different elements of the individual's target-oriented behaviour during solving the spatial task. The major findings were that the tested fish was deviating from the trained rewarding point by about 1.2 %, 6.7 %, 16.9 % and 23.9 % in conditions in which only visual, only electric, visual and electric, or no sensory information were available to the individual. Against the expectations, the fish's performance was the best in the test in which only visual cues were presented than in the one in which only electric information or both modalities were available to the individual. These results suggest that the black ghost knifefish is able to learn a distance and to use allocentric navigation in a near range.

Evolutionary Biology
Oral presentation

Speciation and cytoplasmic incompatibility in *Lariophagus distinguendus*: a novel phenotype for *Spiroplasma*

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In symbioses of bacterial endosymbionts and arthropod hosts, mechanisms employed by bacteria manipulating the hosts' reproduction can act as isolating barriers and have been shown to promote speciation processes. Cytoplasmic incompatibility, an incompatibility between the sperm of infected males and the eggs of uninfected females, is one of these mechanisms. It prevents the formation of diploid zygotes, which, in haplodiploid organisms like parasitoid wasps, leads to the emergence of only haploid male offspring, if any. The pteromalid wasp *Lariophagus distinguendus* (Förster, 1841), a parasitoid of coleopteran larvae, has been shown to consist of a species complex of several distinct species, which are separated by different barriers. One barrier, consisting of the absence of female offspring in crosses between two *L. distinguendus* species, was identified as endosymbiont-induced CI since antibiotic treatment restored the female offspring. We found this endosymbiont to be *Spiroplasma*, which had not been known to cause CI before. Furthermore, we identified CI as the only reproductive barrier between two genetically distinct wasp strains, which indicates that *Spiroplasma* promotes the speciation process in *L. distinguendus*.

Evolutionary Biology
Oral presentation

Sibling cooperation in a genus with interspecific variation in offspring dependence

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The widely spread evolutionary strategy of parental care is considered an important driver of social evolution. While offspring were long thought to primarily interact competitively, recent studies revealed the potential importance of sibling cooperation. Theories suggest that the degree of cooperation in offspring interactions depends on the degree of offspring dependence on parental care: offspring unable to forage on their own should compete more, whereas more independent juveniles may increase the degree of cooperation. In this study, we tested the occurrence of sibling cooperation in the absence of post-hatching care in several burying beetle species exhibiting varying degrees of offspring dependence. To this end, we measured larval growth rate and survival in presence and absence of pre-hatching care using different brood sizes. We found that sibling cooperation cannot be exclusively explained by offspring dependence on parental care. While larval cooperation occurred across species in the absence of care, we found that only species with more independent larvae cooperated when receiving pre-hatching care. Our results suggest that some forms of sibling cooperation were present in an early ancestor of silphids both with and without parental care. Overall, these findings give important insights in the transition from facultative to obligate family life.

Morphology
Oral presentation

Biomechanics of the intralamellar joint in the caudal lamellae of a damselfly larva (Insecta: Odonata)

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The larvae of Odonata are limnic predators capable of respirating and swimming underwater using three fin-like structures, the so-called caudal lamellae. Several aquatic species use similar structures like fins as drive for locomotion but larvae of *Erythromma najas* - the red eyed damselfly - additionally shows a special joint within their 'fins' – the caudal intralamellar joint. The joint is located more or less in the middle of the lamellae and contains thorn-like setae on one side serving as stoppers in one direction for the bending movement. Here we demonstrate that disabling the caudal intralamellar joint, in a manipulation experiment, reduces the average swimming velocity by 16 % in comparison to the unmanipulated - natural - joint system condition. Our results indicate that the caudal intralamellar joint contributes to a higher average swimming velocity of the larvae, similar to the compliant fin in aquatic animals, such as tuna. Literature data show that the thrust in these latter animals is maximised by a multi-joint system containing rigid and flexible elements, resulting in higher vorticity, propulsive and side forces while swimming. For the first time, our study reveals a similar biomechanical system in insects and offers novel insights in underwater insect locomotion.

Developmental Biology
Oral presentation

Conserved and divergent aspects of clawless function in distal leg patterning in the spider *Parasteatoda tepidariorum*

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The distal portion of the arthropod leg usually ends in a claw-like structure, and this distal element might therefore represent an ancestral component of the arthropod limb. Research in the fly *Drosophila melanogaster* has identified a number of genes required for distal leg patterning, with the homeobox gene clawless (cll) being required for the formation of the claw. We have identified two homologs of cll in the spider *Parasteatoda tepidariorum*, termed cll1 and cll2, and both genes are expressed in the distal portion of the legs. We have studied the function of cll1 using RNA interference. We show that in third nymphal instars the tarsus is malformed or missing after cll1 RNAi, but surprisingly a claw is always present. Only in stronger phenocopies that do not survive beyond the second nymphal instar, the entire distal leg portion distal to the metatarsus is lacking. This suggests that the role of cll in the distal leg is generally conserved, but differs in the extent of the effect, because in spiders the entire distal end is affected, whereas in *D. melanogaster* only the claw is affected. These divergent aspects of cll functions might be caused by differences in cll regulation between insects and spider, because the genes aristaless (al) and Lim1 that interact with cll in *D. melanogaster*, are not co-expressed with cll1 or cll2 in *P. tepidariorum*, and are thus unlikely to regulate cll in this spider.

Evolutionary Biology
Oral presentation

Seminal fluid-mediated manipulation of post-mating behaviour in a simultaneous hermaphrodite

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Seminal fluid proteins (SFPs) are uniquely positioned to mediate post-mating sexual selection and sexual conflict. They may be especially important in simultaneous hermaphrodites, in which individuals will often agree to receive sperm in order to be able to donate it, shifting the arena of sexual selection to post-mating reproductive interactions. Nevertheless, as in separate-sexed organisms, identifying individual SFPs responsible for specific post-mating effects is difficult, owing to the complexity, rapid evolution, and functional redundancy of seminal fluid. We sought to identify SFPs that influence one striking post-mating behaviour of the simultaneously hermaphroditic flatworm *Macrostomum lignano*, the so-called ‘suck behaviour‘, in which worms respond to ejaculate receipt by placing their pharynx over their female genital opening and seemingly attempt to remove sperm and/or other ejaculate components. We hypothesized that sucking is counter to the sperm donor’s interests, potentially selecting for SFPs that reduce the suck propensity of mating partners. We tested this using a combination of quantitative genetics and RNA interference (RNAi) knockdown. As predicted, we found negative genetic correlations between the expression levels of six (out of 58) seminal fluid transcripts and partner suck propensity. RNAi knockdown confirmed that two of these transcripts, designated suckless-1 and suckless-2, indeed caused mating partners to suck less often. We suggest that these proteins are male counter-adaptations to recipient suck behaviour, which itself is likely a female counter-adaptation in the ongoing evolutionary conflict to (re)gain control over ejaculate fate after mating in this hermaphroditic organism.

Morphology
Oral presentation

A glimpse into Cretaceous ant cephalic anatomy – the head of †*Gerontoformica* from Burmese amber (Hymenoptera, Formicidae)

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Cretaceous amber from Myanmar has revealed hitherto undreamt-of wealth of information about the evolution of many present-day insect lineages. In Formicidae, a host of fossils belonging to the stem group of the family have been discovered in recent years, many of them with morphological features unlike any species alive today. Here, we report the finding of an exceptionally well-preserved worker specimen of †*Gerontoformica* in burmese amber, belonging to the presumably generalized Sphecomyrminae. The fossil contains well preserved internal soft tissue, allowing us to present the first three-dimensional reconstruction of internal anatomy of a cretaceous insect based on µCT scanning microscopy. This includes a nearly complete muscle set, the digestive tract, several glands and the brain including optic neuropils and mushroom bodies. Through comparison with the published literature on recent ant species as well as newly generated µCT scan data of apoid and vespoid outgroup taxa, we analyse the morphological ground plan of the ant head. Notable discoveries include: the mandibles of *Gerontoformica* conform highly with the ancestral aculeate pattern and we present a hypothesis for the evolution of the modern “triangular” ant mandible; the set of muscles that could be reconstructed is highly similar to that of recent ants; optic neuropiles and antennal neuropils are equally well developed and the antennal pedicel is already developed as in the recent geniculate ant antenna, potentially indicating improved use of the antenna for communication relative to the non-eusocial outgroup taxa.

Evolutionary Biology
Oral presentation

The Evolutionary Significance of Horizontal Gene Transfer in Ants

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Bacteria have profoundly influenced animal evolution either as parasites, commensals, or beneficial symbionts. In addition, bacteria have been important sources for new genetic material via horizontal gene transfer (HGT). Specifically in insects, the impact of HGTs on the evolution of phenotypic innovations and environmental adaptations is well documented. However, the extent of HGTs in ants, one of the most successful insect families, remains largely unknown. In this study, we systematically search for HGT in over 160 ant genomes from 12 subfamilies, which were sequenced by the Global Ant Genomics Alliance (GAGA). Among several hundred HGT candidates that contain potentially functional genes, we find convergent transfers of a *Wolbachia*-derived ankyrin repeat protein, an antibacterial lysozyme conserved in several Crematogastrini, and several species-specific HGTs of metabolic genes. In general, we find that HGTs in ants come predominantly from intracellular endosymbionts, likely due to their intimate association with their eukaryotic hosts and germline. Our study builds the foundation for understanding how HGTs affected the evolution of an ecologically dominant and diverse insect family and may furthermore help to understand the evolutionary significance of HGTs in general.

Evolutionary Biology
Oral presentation

Differential gene expression in Zebra Finch *Taeniopygia guttata* brain and testes in response to experimentally manipulated sperm competition risk

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Sperm competition risk (SCR) is one of the main dimensions of the social niche of individual males. The aim of this study was to investigate how males plastically adjust their reproductive phenotype in response to variation in sperm competition. Specifically, we aimed to determine how changes in the transcriptomic profile underlie plastic phenotypic responses in male Zebra Finches *Taeniopygia guttata*.We therefore included tissues implicated in the regulation of both pre- and post-mating competitiveness. In addition, we correlated the gene expression profiles of individuals with their hormone profiles (e.g. testosterone) and key behavioural traits (e.g. aggression towards competitors). Our experimental design consisted of a comparison of two treatment levels – single breeding pairs (no SCR) vs. two breeding pairs per breeding cage (SCR). In total 60 males (30 per social treatment level) were sacrificed and overall 173 RNA samples from testis (n = 59) and two brain areas, tectum (n = 57) and pallium (n = 57), were sequenced successfully. Based on these individual transcriptomes, we identified differential expression for multiple genes as well as gene co-expression modules that differed between social treatment groups, particularly in the pallium brain region and testis. A Gene Ontology (GO) enrichment analysis showed that the identified modules were related to metabolic processes in the brain. Additionally, we found a number of modules that were related to male aggressiveness in both testis and the two brain tissues. In conclusion, experimental manipulation of sperm competition risk leads to the modification of multiple gene expression pathways, particularly in the pallium and testes, which was also related to changes in hormone profiles and behaviours.

Physiology
Oral presentation

Mimicry of honeybee sugar taste in *Xenopus* oocytes

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Plant sugars derived from plant nectar glands are the main source of carbohydrates for honeybees. It is therefore highly important for honeybees to perceive and evaluate sugars. When it comes to taste, however, honeybees display a rather poor set of receptors. They express only three annotated and partly characterized sugar receptors (AmGR1, AmGR2 and AmGR3). AmGR1 seems to detect different sugars including sucrose and glucose, while AmGR3 is assumedly a pure fructose receptor. AmGR2 appears to act solely as co-receptor. To further elucidate the function of honeybees' gustatory sugar receptors we characterized the function of AmGr1, AmGr2 and AmGr3 by heterologous expression in *Xenopus laevis* oocytes and elucidated their sugar-induced cation transport characteristics through two-electrode voltage-clamp technique (TEVC). Thereby we found that honeybee sugar receptors represent ligand/sugar-gated and hyperpolarisation-induced non-selective cation channels. Moreover, co-expression experiments suggest that the sugar specificity and desensitisation-behaviour of AmGr1 is influenced by heteromerization with its co-receptor AmGr2. In contrast, AmGr3 seem to function as a fructose-specific homotetramer only. To link the electrophysiological data derived from oocyte measurements to the in vivo situation in bees, we finally compared behavioural studies of CRISPR/Cas9-generated *Apis mellifera* knock-mutants with the electrical response of oocytes that express different ensembles of AmGrs; thus, we mimicked the repertoire of sugar receptors of WT and KO bees in the heterologous expression system of *Xenopus* oocytes and could confirm the importance of AmGr1 and AmGr3 for the sugar taste of honeybees.

Behavioral Biology
Oral presentation

Rhythmicity of foraging activity in leaf-cutting ants: Influence of molecular and environmental factors

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South American leaf-cutting ants show changes in their foraging activity patterns throughout the day and year. Also, workers transition from in-nest tasks to out-of-nest foraging with age. Here, we tested, in the laboratory, how activity patterns differ with age and are affected by environmental factors (light and temperature). Further, we analyzed the influence of molecular processes, i.e., the expression of the foraging gene, linked to social behaviour in social insects. First, a colony of *Acromyrmex lundii* leaf-cutting ants could forage under simulated spring and summer conditions and activity patterns on the foraging trail were recorded. Some foragers were then collected and the alfor gene expression of their brains was analyzed using qPCR. Other foragers were placed in activity monitors and their solitary activity patterns recorded at constant temperatures of 25°C, either under a light/dark cycle or in complete darkness. We found that workers shift their daily foraging activity from daytime foraging in the spring to nighttime foraging in the summer, when daylight temperatures are high. However, all foragers, irrespective of season, showed similar activity patterns with a high peak during the day and no longer during the night in the monitors, when influence of high daylight temperatures was missing. Young workers showed surprisingly rhythmic activity patterns. The qPCR analysis did not reveal any differences in foraging gene expression with age or task. Light proved to be an important time cue for leaf-cutting ants to set their biological clock to a 24 h rhythm. However, unlike other ants such as *Camponotus*, leaf-cutting ants do not show entrained activity rhythms once climatic factors change. Rather, they seem to have a highly plastic foraging behavior, allowing them to rapidly adjust colony foraging patterns to best suited environmental conditions.

Evolutionary Biology
Oral presentation

Juvenile ecology drives adult head shape evolution in earwigs and stoneflies

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Complex life cycles where discrete life phases are separated by metamorphosis are found in about 80% of all animal species, including all winged insects (Hexapoda: Pterygota). The prevalence of complex life cycles is often explained by the adaptive decoupling hypothesis. This states that discrete life phases can independently evolve according to their phase-specific selection pressures, leading to a low degree of between-phase correlations of traits. However, it is yet unknown to what extent adaptive decoupling is realized in hemimetabolous insects, where metamorphosis takes place within only a single moult. To quantify the correlation between ecological traits and morphology in these insects, we studied the adult head shape of 219 species of the closely related orders of earwigs (Dermaptera) and stoneflies (Plecoptera) using 3D geometric morphometrics and multivariate statistics. Ecological information on juveniles and adults was extracted from 960 literature sources. We show that, despite the drastic ecological change in the life-history of stoneflies (aquatic nymphs vs. terrestrial adults) and the resulting presumed antagonistic selection pressures, juvenile food preference is the main driver of adult head shape, while adult food preference has no significant impact. In earwigs, on the other hand, nymphs and adults generally share an ecological niche, and adult head shape is equally adapted to both juvenile and adult ecology. Our results suggest that stronger niche shifts during ontogeny do not necessarily lead to lower trait correlations between life phases. Instead, the final moult in hemimetabolous insects does not seem to facilitate high degrees of adaptive decoupling across metamorphosis, so that adult shape evolution is constrained by juvenile ecology.

Behavioral Biology
Oral presentation

Family social condition affects the outcome of parent-offspring conflict

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Theory predicts that parents and offspring show a disagreement over the allocation of resources and parental investment. Although this conflict between parents and offspring has been intensively studied, for most species it is presently unknown whether the conflict outcome is closer to the parents' or offspring's optimum and if the presence of a second parent affects this outcome. To address these questions, we used the burying beetle *Nicrophorus vespilloides* as a model system, which provides elaborate parental care. We first of all established that a parent-offspring conflict over the production of second brood exists. Next, we manipulated the initial brood size in uni- and biparental families to examine how many offspring are necessary to repress maternal egg production and maintain parental care in the current brood. Additionally, we forced parents to invest in a second brood by removing their first brood. We found that parents continued to invest in current offspring, even at brood sizes in which the reproductive output would have been higher if they had discontinued their care and produced a replacement brood. This result suggests that the outcome of the conflict is closer to the offspring's than the parents' optimum. However, as biparental females laid a second egg clutch more frequently and produced more larvae than single caring females, our results also indicate that in biparental families the outcome of the parent-offspring conflict is shifted towards the parent's optimum. Consequently, our study provides some evidence that offspring can influence maternal investment decisions, but this capability is negatively affected by the presence of a second parent.

Morphology
Oral presentation

Structures and forces involved in Phasmid hatching

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Biomechanical investigations can help to shed light on the principles and demands of biological processes. The diverse Phasmida egg shapes have not yet been investigated regarding the biomechanics of their hatching process, despite clear functional implications of shape, seeing as different species employ various egg-laying strategies. Furthermore, Phasmida have relatively long developmental times compared to many other insect species, e. g. 80-90 days in *C. morosus*. During this time, the eggs need to provide sufficient protection from various biotic and abiotic stresses and thus require a durable outer protective layer. Previous studies have shown a complex ultrastructure of the Phasmid eggshells, which consists of several distinct layers. Some of these layers include calcium crystals – presumably “reinforcing” the structure. However, hatching insects usually have a low degree of sclerotisation, which should limit the muscular forces they are able to produce to “break open” the eggshell from the inside. Phasmida embryos circumvent this using a distinct opening hatch (operculum) to leave their egg. To achieve that, the forces required to open this hatch from the inside should be relatively low; at the same time, the operculum must not be a structural weak spot for potential external predators. Focusing on the model species *C. morosus*, we investigate how the eggshell and the operculum interact mechanically to allow for these apparently contradicting properties. In order to address this question, a variety of techniques including 3D microCT data of the operculum’s zipper-like ultrastructure and fracture tests are employed. Effects of egg-age and environmental humidity conditions on the mechanical properties of the egg (e. g. load to failure) are considered.

Evolutionary Biology
Oral presentation

Signatures of positive selection in the evolution of mutualistic insect endosymbionts

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Insects are the most diverse and abundant group of animals on earth. Throughout their evolutionary history, insects repeatedly established obligate mutualistic symbioses with endosymbiotic bacteria, allowing the emergence of evolutionary innovations and novel adaptive traits in the insect host. Compared to closely related free-living bacteria, obligately mutualistic endosymbionts typically have highly reduced genomes, consistent with relaxed selection on sets of genes and genomic functions irrelevant for an intracellular lifestyle. However, the transition to obligate mutualistic symbiosis should also invoke strong positive selection on certain traits and genes. To study signatures of positive selection in mutualistic endosymbionts, we focused on the evolution of the *Sodalis*-allied clade (Gammaproteobacteria: Enterobacterales), comprising important insect endosymbionts from diverse hosts, e.g., ants, mealybugs, psyllids, and flies. To investigate adaptative changes allowing their extreme lifestyle inside insect cells we used phylogenetic and comparative genomic analyses to retrace the molecular evolutionary history of these endosymbionts. We found remarkably strong signatures of positive selection at the ancestral branch that could reflect the necessary adaptive genetic changes underlying the ecological transition towards intracellular mutualism. Particularly, genes coding for proteins involved in cell wall synthesis, tRNA metabolism and DNA recombination were among the genes most significantly affected by positive selection. We propose that these functions might have played a crucial role in the evolution of mechanisms to evade the host immune system and the extreme degradation of endosymbiont genomes, respectively.

Systematics, Biogeography & Diversity
Oral presentation

Discovery of a cryptic species among samples of one of the most common European vespid wasps — *Polistes dominula*

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The vespid wasp *Polistes dominula* (Christ, 1791) is an established model for sociobiological research and for understanding neozoic invasions. Previous investigations revealed that it carries two distinct mitochondrial (mt) haplotypes. However, it has remained unclear whether samples carrying different mt haplotypes are reproductively isolated from each other. Using an integrative taxonomic approach, we show that *P. dominula* sampled at locations in Southern Germany, where wasps carrying the two mt haplotypes occur in sympatry, differ in more than 10,000 allelic SNPs in their nuclear genomes and in their cuticular hydrocarbon (CHC) profiles from each other. We conclude that *P. dominula* constitutes two biological species. By examining allele states of nuclear markers in the published draft genome of *P. dominula*, we were able to unambiguously assign the genome to one of the two species. *P. dominula* has been described as a species with remarkable diversity in ecological, behavioral, and phenotypic traits. We expect our results to show that many of these traits are not as variable as previously assumed but represent species-specific differences between the two species.

Ecology
Oral presentation

Ecology of predator-induced morphological defense traits in *Daphnia longispina*

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Inducible defenses against predators are widespread among plants and animals. For example, some *Daphnia* species form neckteeth against predatory larvae of the dipteran genus *Chaoborus*. Though thoroughly studied in *D. pulex*, knowledge about neckteeth in other *Daphnia* species is limited. The occurrence of this trait in the *D. longispina* species complex is only sporadically reported and the specific shape of neckteeth or the occurrence of other morphological defense traits is scarcely known in this widespread group. Here, we explored neckteeth occurrence in a large number of *D. longispina* populations across Scandinavia and studied neckteeth formation and other morphological defense traits on three *D. longispina* clones in the laboratory. In the study region, neckteeth on juvenile *D. longispina s. str.* were observed frequently in permanent ponds, but only when *Chaoborus* spp. larvae were present. In the laboratory experiments, all three *D. longispina* clones developed neckteeth (very similar to *D. pulex*) in response to *Chaoborus* kairomone exposure. The *D. longispina* clones also developed a longer tail spine, wider body, and larger neckteeth pedestal in response to predation threat, likely as a defense against the gape-limited predator. The intensity of neckteeth expression also depended on the clone studied and the concentration of *Chaoborus* kairomone. Our results demonstrate that neckteeth on *D. longispina* can be common in nature and that *D. longispina* can also induce other morphological defenses against predators. The similarity of neckteeth in *D. longispina* and *D. pulex* imposes yet unresolved questions on the evolutionary origin in these distantly related *Daphnia* groups.

Morphology
Oral presentation

Visualization of insect exo- and endocuticle using X-ray microtomography

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The insect exoskeleton is considered to be one of the most versatile and complex composite biological materials. Previous studies have shown that the biomechanical properties of cuticle can vary strongly due to sample condition, age, test orientation etc. In insects, the exoskeleton can be differentiated into two main layers: exocuticle (outer layer) and endocuticle (inner layer). For many biomechanical research questions it would be very beneficial to be able to selectively characterise the geometry (thickness, ratio, etc.) of these layers. However, most conventional preparation methods (cross-sections, histological staining, SEM) require complex and destructive sample preparation, which provides only two-dimensional information. Here, we present a novel, simple staining method using X-ray microtomography to distinguish between exo- and endocuticle in a 3D environment without sample destruction. Our method allows an easy and direct measurement of exo- and endocuticle and their respective geometric features. We illustrate the power of our method using locust (*Locusta migratoria*) hindleg tibia, a well characterised biomechanical sample. Applying our method to microCT scans of insect cuticle will help to understand the biomechanical role of exo- and endocuticle within an insect exoskeleton and will allow us to understand its composition and morphological features in more detail.

Physiology
Oral presentation

Effects of salinity acclimation on mitochondrial resilience to hypoxia/reoxygenation stress in the Pacific oyster, *Crassostrea gigas*

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Coastal environments commonly experience fluctuations in salinity and hypoxia/reoxygenation (H/R) stress that can negatively affect mitochondrial functions of marine organisms. Marine intertidal bivalves are adapted to fluctuating oxygen and salinity, yet the underlying molecular mechanisms that sustain mitochondrial integrity and function under these conditions are not yet well understood. We hypothesised that mitochondria of the hypoxia-tolerant Pacific oyster *Crassostrea gigas* can maintain respiration and avoid excessive production of reactive oxygen species (ROS) during H/R stress under normal salinity (33) whereas hypoosmotic stress will sensitize mitochondria to H/R stress. We determined respiration and ROS production in mitochondria of oysters acclimated to high (33) or low (15) salinity, and exposed to either normoxic conditions (control; 21% O2) or to short-term hypoxia (24 h at <0.01% O2) and subsequent reoxygenation (1.5 h at 21% O2). Further, we exposed isolated mitochondria to anoxia in vitro to assess their ability to recover from acute (~10 min) oxygen deficiency (<0.01% O2). Acclimation to low salinity stimulated mitochondrial respiration, especially in OXPHOS state and enhanced ROS production and oxygen consumption during post hypoxic recovery in vitro. Enhanced mitochondrial function at low salinity might reflect the estuarine origin of this species but it comes at a cost of elevated ROS production. These findings shed light on the survival in coastal waters experiencing salinity stress due to freshwater-runoff, precipitation and freshening of surface waters.

Developmental Biology
Oral presentation

Single-cell transcriptome dynamics throughout the life cycle of *Nematostella vectensis*

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The sea anemone *Nematostella vectensis* belongs to the phylum Cnidaria, which is known for remarkable regenerative capacities and the absence of senescence. Cnidarians consist of two germ layers which both form differentiated cells, which have to be continuously replaced throughout their long life spans. Recent advances in single-cell RNA-seq technology have given an overview of cell type diversity, but it is still unclear how the complexity of cell types arises during development. To this end, we have generated a time series of single-cell transcriptomes throughout the life cycle of *Nematostella*, spanning diverse stages from blastula to juvenile polyps. This dataset allows us to study cell trajectories from differentiation during embryonic development to homeostasis in the adult animal and reveals similar molecular mechanisms, thus providing new insights into the population structure of *Nematostella*. Furthermore, we report a highly resolved differentiation trajectory of cnidocytes, the phylum-defining stinging cells, which we validate with in vivo characterizations of transgenic lines.

Evolutionary Biology
Oral presentation

The emergence of ecotypes in a parasitoid wasp: A case of incipient sympatric speciation in Hymenoptera?

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To understand which reproductive barriers initiate speciation is a major question in evolutionary research. Despite their high species numbers and specific biology, there are only few studies on speciation in Hymenoptera. This study aims to identify very early reproductive barriers in a local, sympatric population of *Nasonia vitripennis* (Walker 1836), a hymenopterous parasitoid of fly pupae. We studied ecological barriers, sexual barriers, and the reduction in F1-female offspring as a postmating barrier, as well as the population structure using microsatellites. We found considerable inbreeding within female strains and a population structure with either three or five subpopulation clusters defined by microsatellites. In addition, there are two ecotypes, one parasitizing fly pupae in bird nests and the other on carrion. The nest ecotype is mainly formed from one of the microsatellite clusters, the two or four remaining microsatellite clusters form the carrion ecotype. There was slight sexual isolation and a reduction in F1-female offspring between inbreeding strains from the same microsatellite clusters and the same ecotypes. Strains from different microsatellite clusters are separated by a reduction in F1-female offspring. Ecotypes are separated only by ecological barriers. This is the first demonstration of very early reproductive barriers within a sympatric population of Hymenoptera. It demonstrates that sexual and premating barriers can precede ecological separation. This indicates the complexity of ecotype formation and highlights the general need for more studies within homogenous populations for the identification of the earliest barriers in the speciation process.

Neurobiology
Oral presentation

Analysis of the neural substrate for visual motion processing in cursorial and stationary hunting spiders

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Some animal species have evolved different types of eyes that are specialized for specific tasks. A prime example for this are spiders (Araneae), which possess eight pairs of eyes, of which one pair (the principal eyes) are used for object discrimination, while the three other pairs (the secondary eyes) are used for movement detection. We investigated the brain neuropils that process information from the secondary eyes in four spider species differing in lifestyle and in the size and arrangement of their eyes: two cursorial hunters *Marpissa muscosa* (Salticidae) and *Pardosa amentata* (Lycosidae), and two stationary, web-building hunters *Argiope bruennichi* (Araneidae) and *Parasteatoda tepidariorum* (Theridiidae). We predicted that the differences in primary sensory input between the different species would be mirrored by differences in those brain areas that process the incoming information. Using Bodian silver impregnations, immunohistochemistry, microCT and dye backfills, we investigated the structure and volume of the visual neuropils and higher-order neuropils, as well as their connectivity, including projections to the ventral nerve cord. We show that the neural substrate for movement detection differs in neuropil number, arrangement, relative volume and connectivity between the investigated spider taxa. While the cursorial hunters possess prominent mushroom bodies that send projections toward the leg neuropils, these are much reduced or absent in the stationary hunting spiders. Our results indicate that the spider mushroom bodies may play a major role in visual motion processing, and show that depending on lifestyle, strong differences exist in the visual systems of spider species.

Physiology
Oral presentation

Conserved molecular pathways underlie intercellular lipid transport during sea anemone vitellogenesis

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The evolution of systemic nutrient transport in animals, e.g. by circulatory systems, is poorly understood. Sea anemones (Anthozoa, Cnidaria) consist of only two epithelia, belong to the phylogenetic sister group to bilaterians, and develop oocytes within the extra-cellular matrix between two epithelia. Yolk formation (vitellogenesis) in anthozoans thus constitutes an experimental framework to study and compare the molecular and cellular features of inter-cellular nutrient transport between cnidarians and bilaterians. With that aim, we studied nutrient uptake and transport, with a focus on lipids, during vitellogenesis in the sea anemone *Nematostella vectensis*. Fluorescent bead uptake experiments reveal the somatic gonad epithelium as one of three highly specialised endocytic regions within the inner epithelium. Furthermore, fatty acid pulse-chase experiments show fast (<2 hours) trans-epithelial transport of fatty acids from the gastric cavity into growing oocytes. Gene expression studies suggest that a conserved pair of Vitellogenin ligand/Very low-density lipoprotein receptor (VLDLR) likely underlies lipid uptake into growing oocytes. In order to study if systemic lipid transport occurs in sea anemones, we generated a genomic knock-in reporter line of the *Nematostella* ApolipoproteinB protein, whose orthologs are the main lipoproteins in insect and vertebrate blood systems. Preliminary results indicate a role for ApoB lipoproteins during spermatogenesis, while a more systemic role is currently investigated. Altogether, we uncovered conserved genes and cellular mechanisms involved in lipid transport in *Nematostella* vitellogenesis, highlighting striking similarities to systemic lipoprotein transport via circulatory systems in bilaterians.

Neurobiology
Oral presentation

Comparison of chemosensory pathways in Arachnida – insights from a neuroanatomical and behavioral approach

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The chemical sense is an essential and integral modality in many forms of live. In most arthropods, the primary chemosensory organs are associated with the second head segment. However, Arachnida – belonging to the most basal euarthropod clade Chelicerata – do not possess dedicated chemosensory appendages associated with the second head neuromere, but evolved such organs in locations different from the euarthropod antennae. In whip scorpions, for instance, the 1st walking legs have transformed into antenniform legs, and scorpions possess so-called pectines as dedicated pairs of chemosensory appendages associated to the 2nd mesosomal segment. Detailed knowledge of the neuroanatomy as well as functional aspects of these sensory organs is rather scarce, especially in comparison to the other euarthropod clades. In this presentation, I will summarize the neuroanatomical appearance of chemosensory pathways in several representatives of Arachnida, including pseudoscorpions, whip scorpions, sun spiders and scorpions. In general, these pathways are associated with different structures and thus have evolved convergently. Nevertheless, they possess several striking similarities, like glomerular shape of the primary chemosensory neuropil and similar projection patterns towards higher integration centers. Further, I will present results from behavioral assays, that suggest that at least scorpions are able to detect not only nearfield substrate-borne chemosensory cues but also volatile stimuli from prey and conspecifics. These findings re-shape the general opinion that volatile stimuli play an inferior role in the detection of chemosensory cues in Arachnida.

Neurobiology
Oral presentation

Visually-guided proboscis movements fine-tune probing on flower patterns in the hummingbird hawkmoth

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Visually guided reaching is a crucial ability for most mammals, and requires detecting a target's position in 3D space, enacting control commands to the limbs and adjusting the ongoing movement via visual and motor feedback to minimize errors. In insects, limb movements to visually selected targets are often stereotypical motor sequences that are triggered, but not guided, by visual inputs. In some species of grasshopper and fly, parameters of the motor programme, for example the amplitude of a leg stroke, can be adjusted via visual distance perception. Here, we provide the first quantitative description of an insect's appendage movement that is continuously updated according to the relative position of the animal to the visual target: the proboscis movements of the hummingbird hawkmoth (*M. stellatarum*). These agile fliers hover in front of flowers while probing them with their proboscis to find the nectary. We filmed hawkmoths probing artificial flowers with prominent visual patterns at high speed, to quantify movements of their body and proboscis, identified by marker-free tracking of the proboscis, head and thorax positions. We show that the hawkmoths could detect the general orientation of flower patterns down to their visual resolution limits, although their probing precision was less accurate. Using a model predicting proboscis position based on the animals' tracked body position, but randomised proboscis movements, we show that flight control provided the major contribution to targeting the proboscis on the pattern. By restricting the animal's flight manoeuvres, we were able to delineate the contribution of proboscis movements to visual targeting: with restricted flight movements, the relative proportion of frontal and lateral proboscis movements was adjusted to maximise contact with the pattern. We therefore conclude that flight movements provide the coarse targeting of the proboscis to visual flower patterns, while proboscis movements fine-tuning the targeting to improve the probing precision.

Physiology
Oral presentation

Brown algae, *Eisenai bicyclis*, extract increases lifespan in *Drosophila* by interfering with S6K in the fat body

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Life and health prolonging effects of natural products are highly interesting and numerous anti-aging compounds have been identified from Algae, which are well-known for their health-promoting effects. Nonetheless, the underlying molecular mechanisms of their life and health-promoting positive features are only partially understood. Here, we showed that aqueous brown algae extracts (*Eisenia bicyclis*) extend the life of the fruit fly *Drosophila melanogaster* substantially if used as nutritional additives to conventional food. This life-prolonging effect is considerably enhanced under stress conditions, such as high-fat dieting or drought. Tor-deficient flies did not display the increase in longevity, indicating that functional TOR signaling is pivotal to reveal the positive effects of furbelow extracts on this important trait. In addition to extending lifespan, the brown algae extract is able to rescue deleterious effects of a high sugar diet which indicates that *E. bicyclis* might be considered as an anti-diabetic food.

Systematics, Biogeography & Diversity
Oral presentation

Lack of support for Deuterostomia prompts reinterpretation of the first Bilateria

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(The bilaterally symmetric animals (Bilateria) are considered to comprise two monophyletic groups, Protostomia (Ecdysozoa and the Lophotrochozoa) and Deuterostomia (Chordata and the Xenambulacraria). Recent molecular phylogenetic studies have not consistently supported deuterostome monophyly. Here, we compare support for Protostomia and Deuterostomia using multiple, independent phylogenomic datasets. As expected, Protostomia is always strongly supported, especially by longer and higher-quality genes. Support for Deuterostomia, however, is always equivocal and barely higher than support for paraphyletic alternatives. Conditions that cause tree reconstruction errors—inadequate models, short internal branches, faster evolving genes, and unequal branch lengths—coincide with support for monophyletic deuterostomes. Simulation experiments show that support for Deuterostomia can be explained by systematic error. The branch between bilaterian and deuterostome common ancestors is, at best, very short, supporting the idea that the bilaterian ancestor may have been deuterostome-like. Our findings have important implications for the understanding of early animal evolution.

Morphology
Oral presentation

Influence of water films and surface energy of the substrate on the attachment performance of Phasmatodea with different adhesive surface microstructures (AMS)

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Phasmatodea (stick and leaf insects) are exclusive herbivores. As they settle in a broad range of habitats, they need to attach to and walk on a wide variety of substrates. These substrates can vary in roughness, surface energy, and curvature. Especially the surface energy of the surfaces of the food plants preferred by different stick insect species can differ a lot. Although considerable experimental research was carried out on different aspects of stick insect attachment, including measurements of single attachment pads on surfaces with different properties, the influence of humidity-induced water films on the attachment performance remains unclear. In this study, we investigated the adhesion and traction forces in three species of stick insects with different adhesive microstructures (AMS) (smooth, nubby and hexagonal ones) on their euplantulae on three substrates with different surface energy and with the presence/absence of water. The hexagonal patterned euplantulae were hypothesized to attach stronger under wet conditions based on previous experimental studies performed on artificial samples. The attachment forces of all three species were influenced by the surface energy and the presence of water. All three species showed higher pull-off and traction forces on dry surfaces if compared to the surfaces covered with a water film. However, the extent to which the surface properties influenced attachment was different depending on the species. This result can be explained by the specific AMS or/and the overall dimensions of the projected attachment pad surface. Nonetheless, all three species were able to produce enough attachment force to hold themselves on the experimental surfaces (their safety factor, which is attachment force divided by the weight force, was > 1).

Evolutionary Biology
Oral presentation

The evolution of inbreeding preference in cichlid fishes

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Costs and benefits of in- and outbreeding define the limits for the evolution of inbreeding avoidance and preference. Theory predicts that the costs of inbreeding, i.e. strength of inbreeding depression can depend on the inbreeding history of a population. Benefits of inbreeding can result from the reduced sexual conflict over mating and brood care between related individuals due to kin selection. *Pelvicachromis taeniatus* is a biparental cichlid fish with mutual mate choice and ornamentation. Fish originating from a highly inbred African population showed kin-mating preference. Accordingly, the *Pelvicachromis* species group is predestinated for the examination of the causes and consequences of inbreeding and outbreeding. Different experiments with *P. taeniatus* revealed better cooperation between related parents compared to unrelated parents at different phases of parental care indicating benefits from mating with kin. Further studies revealed variation in inbreeding preference in *P. taeniatus*, e.g. high quality individuals showed stronger kin preferences than low quality individuals did. Quality-related inbreeding may contribute to maintain genetic variation in an inbreeding system. The examination of inbreeding preference and inbreeding depression in an outbred population of *Pelvicachromis pulcher*, a closely related species to *P. taeniatus*, revealed no evidence for inbreeding preference, but in contrast evidence for inbreeding avoidance and depression. Our results suggest variation in the cost of inbreeding in this species group that is associated with according in- or outbreeding preference. Further species and population comparisons are required to disentangle the causal relationship between the inbreeding history of a population, the strength of inbreeding depression and kin mating preferences.

Developmental Biology
Oral presentation

The neuroblast timer gene nubbin exhibits functional redundancy with gap genes to regulate segment identity in *Tribolium*

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The neuroblast timer genes hunchback, Krüppel, nubbin, and castor are expressed in temporal sequence in neural stem cells, and in corresponding spatial sequence along the *Drosophila* blastoderm. As canonical gap genes, hunchback and Krüppel play a crucial role in insect segmentation, but the roles of nubbin and castor in this process remain ambiguous. We have investigated the expression and functions of nubbin and castor during segmentation in the beetle *Tribolium*. We show that Tc-hunchback, Tc-Krüppel, Tc-nubbin and Tc-castor are expressed sequentially in the segment addition zone, and that Tc-nubbin regulates segment identity redundantly with two previously described gap/gap-like genes, Tc-giant and Tc-knirps. Simultaneous knockdown of Tc-nubbin, Tc-giant and Tc-knirps results in the formation of ectopic legs on abdominal segments. This homeotic transformation is caused by loss of abdominal Hox gene expression, likely due to expanded Tc-Krüppel expression. Our findings support the theory that the neuroblast timer series was co-opted for use in insect segment patterning, and contribute to our growing understanding of the evolution and function of the gap gene network outside of *Drosophila*.

Morphology
Oral presentation

Room for one more inside? Morphological adaptations of *Veneriserva pygoclava* Rossi 1984 (Dorvilleidae, Annelida) to a life inside another worm

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Endoparasitic annelids living inside another annelid host are known, particularly with regard to Oenonidae, but in general are poorly studied. Rossi (1984) described the dorvilleid *Veneriserva pygoclava* from Southern California, giving it the allusive genus name (Latin = Venus's servant), referring to their close association with *Aphrodita*. Little is known on fundamental questions on the biology of *Veneriserva pygoclava*. What is the mode of reproduction? How do they feed? How do they penetrate the host? We have studied multiple parasitized hosts and *V. pygoclava* specimens, using an integrative approach, combining µCT, histology and electron microscopy. 3D reconstructions from µCT data of a parasitized *Aphrodita*, show the exact position of the parasites in their natural condition within the host's coelomic cavity. Ultrastructural investigations of the parasites revealed interesting adaptations to their life-style such as; the complete reduction of a gut, despite the presence of a functional jaw apparatus and a modified epidermis putatively enabling nutrient uptake from the coelomic fluid. In addition to these, we also investigated the ultrastructure of spermatogenesis and oogenesis in *Veneriserva*. Sperm morphology indicated an external fertilization of eggs within the coelomic cavity of the host. Mature male and female parasites living inside the same mature host, and the presence of juvenile *Veneriserva* within juveniles of *Aphrodita* suggest an obligate form of parasitism with a very early penetration of the hosts. In addition to our detailed morphological investigation, we have conducted a molecular phylogenetic analysis showing the position of *Veneriserva* relative to other symbiotic/parasitic dorvilleids.

Systematics, Biogeography & Diversity
Oral presentation

Genomic approaches to characterize *Wolbachia* in arthropod communities of soil

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Wolbachia is a widespread, intracellular, endosymbiotic Alphaproteobacteria known to infect arthropods and several groups of filamentous nematodes. The most important effects of *Wolbachia* on hosts include manipulation of reproduction, vitamin supplementation, and pathogen restriction. Most of the phylogenetic analyses and co-phylogenies made so far for *Wolbachia* were based on the multilocus sequence typing system (MLST), which comprises 5 conserved housekeeping genes. However, while supergroups can be well-distinguished by this system, it often results in a lack of resolution of strains. Currently, there are 16 identified and classified supergroups of *Wolbachia*, from different hosts and habitats, including nematodes, hexapods, and other pancrustaceans, or arachnids. As an alternative for strain typing approaches sequencing and annotating draft genomes have been proposed. In this project, we aim to investigate the molecular diversity of arthropod communities from the soil environment. After screening for the presence of *Wolbachia*, we used Illumina-based short-read sequencing to generate draft genomes of *Wolbachia* from soil organisms. Using a newly established pipeline, the symbiontDivider, we retrieve *Wolbachia* reads and contigs from metagenome assembly of mixed hosts and symbionts and assemble and annotate draft genomes. Using phylogenomic approaches, we phylogenetically place the *Wolbachia* genome sequences, including putatively new supergroups. The diversity of *Wolbachia* in soil arthropods is discussed and we interpret the results in the light of the evolution of *Wolbachia*-arthropod symbiotic relationships.

Behavioral Biology
Oral presentation

Chemical variation and differences in aggressive behavior between haplometrotic and pleometrotic populations of the ant *Pogonomyrmex californicus*

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California harvester ants, *Pogonomyrmex californicus*, found new nests usually alone (haplometrosis), i.e. a single foundress queen starts digging and takes care of her own brood. Other queens are expelled and eventually killed if they try joining the nest. However, one *P. californicus* population was discovered where several queens cooperate in nest founding (pleometrosis) and share brood care for several years together. How these strikingly different behaviors are regulated and maintained remains enigmatic. We hypothesized that the aggression displayed by queens of haplometrotic populations may also be reflected by aggression levels of their workers. Since nestmate recognition and associated aggression has been demonstrated to be mostly mediated by cuticular hydrocarbons (CHCs), we analyzed CHC profiles using gas-chromatography coupled with mass spectrometry (GC-MS), and quantified worker aggression in behavioral assays. We found that CHC profiles between all castes were clearly discrete, most strikingly evident between queens from the two different founding strategies. Intriguingly, workers from pleometrotic colonies had twice as much CHCs (total mass) than haplometrotic workers. As hypothesized, workers from haplometrotic colonies were generally more aggressive than workers from pleometrotic colonies. Higher aggressive behavior against foreign workers as compared to nestmates was revealed in both populations. Our findings shed light on fixed phenotypic and behavioral characteristics differentiating these two founding strategies and bear important implications on *P. californicus* population dynamics. These results are further discussed in light of recent advances on the origin and maintenance of polygyny (nests with several queens) in social insects.

Systematics, Biogeography & Diversity
Oral presentation

Burrowing animals: composition and characteristics along a climate and ecological gradient

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Although the burrowing activity of single species at specific sites is well studied, a comprehensive inventory of burrowing animals along a climate gradient is not yet available. We compiled published information on all burrowing vertebrates and invertebrates along the climate and ecological gradient in Chile, including information about the dimensions and characteristics of their burrows. In addition, we empirically quantified the zoogeomorphic effects on hillslope mass transport at the animal community level and along the arid to humid-temperate climate gradient within the Chilean Coastal Cordillera (27-38°S latitude). We highlight the diverse and latitudinally varying number of burrowing vertebrates and invertebrates present in different biomes and discuss how burrowing activity changes over this gradient and is influenced by mean annual temperature, mean annual precipitation, slope aspect and latitudinal related incoming solar energy.

Physiology
Oral presentation

Effects of dietary protein content on immuno-metabolic resource allocation strategies in *Drosophila melanogaster*

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Dietary Restriction (DR) is one of the most reproducible ways for lifespan extension in a range of animals, but the consequentially reduced fecundity still lacks a proper evolutionary explanation. The most accepted theory is the disposable soma theory, which explains it as increased investment in somatic maintenance when facing nutrient shortage until the resumption of nutrients. However, immunity, an important somatic trait, shows ambiguous results in response to DR. Addressing this issue, we investigated the effects of DR on the range of pathways, directly and indirectly, contributing to *Drosophila melanogaster*'s immunity. To achieve this, we took diets varying in protein content to create a regimen covering normal, restricted and malnourished diets. We chose a bacterial infection treatment that can resolve the different diets in terms of fitness-related immune parameters such as survival rate and bacterial clearance. Surprisingly, here we saw no substantial differences in the induction of most important immunity-related genes in the whole animal body between the different diets. We did tissue-specific transcriptomic profiling of the two cell types that contribute the most to immunity in insects, i.e., fat body and hemocytes, after keeping the animals on different diets, with and without bacterial infection. At the tissue level as well, we see the same trend of almost equivalent induction of important immune regulators in the different diets post-infection. However, we see that some pathways that are probably indirectly contributing to the immune reaction and are induced in the control diet on bacterial infection (including but not limited to redox homeostasis, proteasomal machinery, lipid, carbohydrate and protein metabolism) are not regulated to the same extent in the diets with less protein. We also observe that the concerned pathways are also different in the different tissue types. Altogether, our study suggests that DR affects resource allocation in the immune response as well, but not in terms of the major immune contributors, rather the indirect cell maintenance strategies that are also essential for fighting the infection.

Systematics, Biogeography & Diversity
Oral presentation: Invited Talk

Molecular Barcodes for Identification of Nemerteans - A Piece of Cake or just one Piece of the Puzzle?

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DNA-barcoding for the identification of species holds great promise for fast and easy assessment of biodiversity. It thus represents a valuable tool to estimate existing species inventories and monitor their change in the future. The scientific public, notably ecologists and conservation biologists, would enormously benefit from quick, easy, and straightforward identification of species, especially in taxonomically challenging groups such as Nemertea (ribbon worms). Part of the challenge in nemertean species is their being nocturnal predators; most of the time hidden from the sight of the observer. On the other hand, their predatory lifestyle bears a currently underestimated ecological relevance by presumably drastically impacting their respective prey communities.

To conclude, currently the potential of molecular markers in nemertean taxonomy for the scientific public cannot be fully exploited. Morphological and life-history data remain pivotal to species identification and delimitation at present. To provide useful species identification based on molecular barcodes in the future, current scientific practice has to combine molecular data with ecological and traditional morphological methodology in an integrative taxonomic approach.

The talk reports on the usefulness and practicability of molecular barcoding for species identification in Nemertea by disentangling species complexes with several species newly discovered and exemplifies the shortcomings and potential pitfalls of this method, such as absence of reference data, past erroneous synonymizations, hybridization or polyploidy.

Nemertea are unsegmented, spiralian worms with only few distinct external morphological characters to be used for identification. Therefore, species identification and taxonomy in the past had been based on characters of internal anatomy, that recently have been assumed as too variable to be used for reliable identification to species level. Furthermore, it becomes more and more evident that species complexes are rampant in this group of worms.

Physiology
Oral presentation

The cyanotoxin cylindrospermopsin reduces cell proliferation rate and alters mitotic dynamics in cultures of immortalized human airway epithelial cells

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Cylindrospermopsin (CYN) is a cyanobacterial toxin that occurs worldwide in aquatic environments. Although acute toxicity is moderate, it is known for its delayed effects upon oral uptake in animals and humans. A less well studied route of CYN internalization is the inhalation of CYN-contaminated aerosols. We analysed potential effects of different CYN concentrations (1, 2.5 and 5 µmol/l) on cultures of immortalised human bronchial epithelial cells (16HBE14o-). Impedance, a proxi for cell attachment to the culture support, cell spreading, cell growth and cell proliferation, was measured using an Acea iCELLigence device. Cell division rate and metaphase duration were determined using time lapse movies (Nikon Biostation II) of CYN-exposed cell cultures. Our investigations revealed that exposure of cells to CYN concentrations of 1 µmol/l or higher led to a concentration- and time-dependent attenuation of impedance development as well as cell proliferation rate and an extension of the metaphase of the cell cycle. These effects may be mediated by CYN-induced alterations in the biosynthesis of components of the cell cycle checkpoints (cyclins, cyclin-dependent kinases) or alterations in the biomechanics of chromosome transport during ana- or telophases of mitosis (kinetochors, microtubuli etc.). Although the mechanisms behind the CYN-mediated effects are still unknown, these results indicate that exposure of airways in humans and animals to aerosolised CYN over longer periods may be harmful.

Ecology
Oral presentation

Resource intake of stingless bee colonies in a tropical ecosystem in Ecuador

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Stingless bees (Apidae: Meliponini) are a highly diverse group of social bees and represent one major pollinator group in tropical forests. Alarmingly, stingless bee diversity and pollination services are threatened by intense land-use changes and losses that tropical forests are experiencing. Despite their diversity, abundance, and their importance as pollinators, we still know little about their foraging behaviour, resource intake (i.e. pollen, nectar, and resin), or the floral sources visited for resource allocation. A better understanding of these factors is however essential for capturing the bees' role in tropical plant-pollinator networks and to improve conservation programs aimed at supporting these pollinators in altered ecosystems. Here we show species-specific differences in foraging activity, resource intake (pollen, nectar, and resin), sucrose concentration in collected nectar, and floral sources visited (obtained from collected pollen via DNAmetabarcoding) of eleven stingless bee colonies (seven different species) in two nature reserves in the Esmeraldas Province, Ecuador. We also show that the sometimes-underestimated percentage of collected resin (more or less than 20% of the total collected) plays an important role on the visited floral sources and foraging activity of these stingless bees.

Ecology
Oral presentation

Spatiotemporal Gradients of Transamazonian Forest Mite Assemblages and Diversities, Evaluated by Metabarcoding Technique

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Species communities constantly change with time and space and are influenced by variation in abiotic and biotic environmental factors. Huge tropical forests like Amazonia are suitable to investigate these changes and factors, without being too much affected by direct human impact. Although Acari are a dominant and highly diverse arthropod group in these tropical forests, only little is known about their fine scale species composition patterns and degree of overlap on tree barks and the corresponding litter, nor about the degree of species turnover on a large (here transamazonian) or fine scale. Using barkspray technique, we collected bark dwelling arthropods from 399 tree trunks (28 plots) in a tropical montane rainforest in Podocarpus National Park, Ecuador, along an elevational gradient (1000-3000 m) in 2007 to 2009. In 2011, 160 tree trunks (16 plots) were sampled in a lowland rainforest in Les Nouragues, French Guiana, and largely resampled in 2014 and 2017. Additionally, in 2014 the litter fauna of 120 tree bases (12 plots with 10 trees each) was experimentally sampled in a line transect (1100 m long) at 100m intervals, and compared to the respective bark fauna. In 2015, another 110 tree trunks (11 plots) were sampled in a lowland rainforest in Mitaraka, French Guiana. DNA barcodes for a total of 26,820 mite specimen were created. Quality filtered COI reads were clustered into 3773 Acari associated OTUs at 98% similarity. We compared the changes of Acari community composition along spatiotemporal and corticolous parameters using presence/absence- based similarity indices and NMDS for community composition. Chao2 diversity estimator predicted 2718 OTUs for Ecuador and 3329 for French Guiana. Roughly, the half of the calculated/expected Acari diversity was recorded, except for Mitaraka due to the campaigns´ low sampling effort in the rainy season. Predicted diversity of the bark fauna along the experimental line transect was no less rich than corresponding litter plots (1611 vs. 1463 OTUs). Similarity indices (Sørensen-Dice and Jaccard index) indicated relatively constant mite assemblages over a six-years period (time scale) at Les Nouragues, but changed over spatial parameters as horizontal distance or elevation. These distributional patterns were confirmed by plotwise NMDS ordinations. Our results show 1) spatial differences, both, elevation and distance, have a greater influence on Acari communities than time, 2) the habitat compartments bark and litter bear distinct communities, 3) corticolous mite communities are more heterogenous and strongly correlated with tree bark characteristics (and stochastics of colonisation?), whereas litter fauna is more homogenous but changing with spatial distance (betadiversity): "tree trunks are island in a sea of litter!"

Ecology
Oral presentation

Acclimation to low quality food: Intra- and interspecific differences in rotifers

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Dietary, biochemical constraints influence consumer performance and mediate trait variation within and between consumer species. To investigate inter- and intraspecific differences in fatty acid retention and conversion in freshwater rotifers, we provided strains of closely related rotifer species with dietary algae that differ in fatty acid composition. Rotifers grazed on dietary algae with different polyunsaturated fatty acid (PUFA) profiles, for five days before the diet was switched to a PUFA-free diet, which was offered for three additional days. We found inter- and intra-species differences in fatty acid composition of rotifers to the respective food sources and, in particular, highly specific acclimation responses to the PUFA-free diet. These differential responses suggest inter- but also intraspecific differences in physiological traits, such as PUFA retention, allocation, and bioconversion capacities, among the rotifers, most likely associated with differences in their dietary requirements. We suggest that dietary constraints may differentially affect traits among closely related species and among strains of a given species.

Ecology
Oral presentation: Invited Talk

Sensing predation - mechanisms underlying predator perception in the freshwater crustacean *Daphnia*

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Ecological communities are organized in trophic levels sharing manifold interactions forming complex food webs. Infochemicals have a significant impact on these interactions, e.g. by inducing defenses in prey. The micro-crustacean *Daphnia* is able to respond to predator-specific chemical cues indicating an increased predation risk. *Daphnia* shows plastic responses by adapting its morphology, behavior and physiology, increasing organism and population fitness. We study the molecular mechanisms of predator detection and elucidate the involved chemoreceptors, in line with the neuronal signaling cascades and the cellular adaptations in the vicinity of morphological defense expression. Using RNAi, we were able to determine the involvement of two chemo-co-receptors involved in chemoperception. With the help of immunohistochemistry, confocal imaging and morphometrics, we found neuronal plasticity in line with a rewiring of cell-cell connections in the central brain. With the help of an EdU cell proliferation assay, we determined that a substantial increase in cellular size finally leads to the formation of defensive morphological features. Our data contribute to the understanding of the sensory pathway involved in predator perception. Future work will address, predator specific chemoreceptors and further detail the neurotransmitter networks engaged in odor cording.

Physiology
Oral presentation

Functional characterization of ecdysteroid transporters from *Tribolium castaneum*

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Ecdysteroids are one of the major insect molting hormones. Ecdysone (E) is produced in the prothoracic gland and released into the hemolymph. According to the current view, E is uptaken by cells of the target tissues and converted into 20-Hydroxyecdysone (20E) by the cytochrome P450 enzyme Shade, a member of the Halloween protein family. In this study, we focused on ecdysteroid transporting membrane proteins in the red flour beetle, *Tribolium castaneum*. We identified two transporters, which are involved in the transport of both E and 20E. The ATP binding cassette (ABC) transporter G-8A (TcABCG-8A), which is highly expressed in larval fat body and pupal elytra and the Organic anion transporter (OATP) 4C1 (TcOATP4-C1), which is highly expressed in the pupal elytra, larval head and the larval fat body. Injection of dsRNA to knockdown TcABCG-8A function by RNAi in *T. castaneum* larvae resulted in developmental arrest, molting defects, premature development of an adult eye, and a 50% mortality. Similarly, injection of dsRNA for TcOAT-4C1 resulted in molting defects, premature development of adult eyes and a 80% mortality. These effects resembled phenotypes that were observed following RNAi for the two ecdysone receptors, TcECR-A and TcECR-B, as well as TcATET, a ABCG transporter discovered in *Drosophila melanogaster*, which is necessary for the loading of neurosecretory vesicles in the prothoracic gland. To dissect the function of these transporters in more detail, we quantified mRNA levels during larval-to-pupal development and analyzed the effects of TcABC-G8A silencing on the expression of TcE75, which is an early ecdysone-induced gene. Furthermore, we investigated the effects of TcABCG-8A and TcOAT-4C1 knockdowns in the fat body by mass spectrometry and established a role in the conversion of E into 20E. In addition, we detected 20E in the hemolymph of the beetles. Direct injection of 20E into larvae showed accelerated progression of development, demonstrating the importance of distributing 20E via the hemolymph. These results suggest that different ecdysteroid transporters are involved in the uptake and release of E and 20E, and that 20E in the hemolymph has a role in regulating molting.

Behavioral Biology
Oral presentation

Appetitive olfactory learning suffers in ants when octopamine or dopamine receptors are blocked

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There is nothing stable in the world; those that can adapt to changes will prevail. When the profitability of food sources changes over time, it would be advantageous to quickly learn which ones are currently most rewarding. Individuals can do so by associating the food with other stimuli such as odours or colours. Associative learning relies on octopaminergic and dopaminergic neurons. It was long assumed that appetitive learning is governed by octopaminergic neurons, while dopamine is required for aversive learning. This view has been recently challenged: Both neurotransmitters seem to be involved in both types of memory in bees and flies. Here, we test which neurotransmitters are required for appetitive learning in ants. We trained *Lasius niger* ant workers to discriminate two mixtures of linear hydrocarbons and associate one of them with a sucrose reward. We found that they preferred the rewarded odour over the other. We then blocked octopamine and dopamine receptors pharmacologically and investigated how this affected the learning abilities of the ants. The ants that were treated with the octopamine receptor blocker did not learn at all. Blocking the dopamine receptors only receptor allowed the ants to learn, but they did not seem to commit the information to the long term memory. Our results show that appetitive learning depends on both octopamine and dopamine signalling in ants, indicating that memory formation is more complex than previously thought.

Behavioral Biology
Oral presentation

Mirror Self-Recognition in Pigeons: Beyond the Pass-or-Fail Criterion

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Spontaneous mirror self-recognition is seemingly limited to humans and few other species. Does this indicate the existence of an evolutionary ‘cognitive Rubicon’ that only a few privileged species can pass? Some findings question this all-or-nothing interpretation: Once trained for mirror self-recognition, monkeys start using mirrors to scrutinize their body. Also, without any training, monkeys don’t seem to see a stranger in the mirror but rather an uncanny individual. This evidence speaks in favour of a gradualist view of mirror self-recognition. We hypothesize that such a gradual process possibly consists of at least two independent aptitudes, the ability to detect synchronicity between self and foreign movement and the cognitive understanding that the mirror reflection is oneself. Pigeons are known to achieve the first but fail at the latter. We, therefore, expected them to treat their mirror image differently from an unknown pigeon, without being able to understand that the mirror reflects their own image. In this talk, I am going to show our results from a non-traditional mirror task through which we gain a better understanding of their position on the gradualist scale of mirror self-recognition and further experiment ideas to expand the used methodology. In addition, I am going to demonstrate the importance of quantitatively measuring bird behaviours by means of leveraging supervised machine learning techniques for behavioural categorization.

Evolutionary Biology
Oral presentation

Building behaviour does not drive rates of phenotypic evolution in spiders

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Do animals set the course for the evolution of their lineage when manipulating their environment? This heavily disputed question is empirically unexplored but critical to interpret phenotypic diversity. Here, we tested if the macro-evolutionary rates of body morphology correlate with the use of built artefacts in a mega-diverse clade comprised of builders and non-builders – spiders. By separating the inferred building-dependent rates from background effects, we found that variation in the evolution of morphology is poorly explained by artefact use. Thus natural selection acting directly on body morphology rather than indirectly via construction behaviour is the dominant driver of phenotypic diversity.

Ecology
Oral presentation

Hidden friends or foes? A gregarine shifts insect responses to sublethal insecticide residues

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In a complex environment, insects are not only subjected to individual challenges, but multiple factors may act in concert and affect their fitness. For example, naturally occurring parasites, such as gregarines, but also anthropogenic pesticide pollution are two commonly occurring challenges. However, knowledge on the impacts of gregarine infection alone or in combination with exposure to sublethal insecticide concentrations on (non-) target insects is limited. Thus, we investigated the effects of gregarine infection on larval food consumption and life-history traits of the leaf beetle *Phaedon cochleariae* and examined whether gregarines may modulate leaf beetle responses to sublethal insecticide concentrations. Our laboratory experiments revealed that food consumption was unaffected by these challenges. In contrast, the development of the beetles was prolonged by gregarine infection, whereas exposure to a sublethal insecticide concentration led to a reduced male body mass and altered female reproduction. When facing both challenges, the survival probability of the insects was lowest. Additionally, we found that insecticide exposure led to an increased gregarine burden in larvae and adult individuals. To conclude, both gregarines and sublethal insecticide exposure alter the fitness of the leaf beetle and may also influence the population dynamics of other (non)-target insects. Therefore, the effects of different challenges acting alone or in combination should be considered in ecological risk assessment to counteract global insect declines.

Ecology
Oral presentation

Worldwide diversity of egg, embryos, hatchlings, and juveniles of deep-sea dumbo octopuses (Cephalopoda: Cirrata)

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The finned or dumbo octopuses (Cephalopoda: Cirrata) constitute a taxon of eight-armed cephalopods known to occur in deep-sea habitats around the World. Due to their lifestyle and vertical distribution in the marine realm, cirrates are difficult to observe in situ. This applies to the adults, but even more so to early life stages such as eggs, embryos, hatchlings, or juveniles. Using historical as well as recently gathered data, we present the first comprehensive overview of various early life stages from a broad taxonomic range within the Cirrata. Apart from still as well as moving imagery obtained using remotely operated vehicles (ROVs) operating down to several thousand meters depth, we also provide novel morphological and anatomical data gathered using non-invasive imaging techniques including magentic resonance imaging (MRI) and contrast-enhanced micro-computed tomography (µCT). Our overview of the current knowledge on cirrate early life stages provides a solid fundament for future analyses on the life style and evolution of a still enigmatic group of extant deep-sea cephalopods.

Neurobiology
Poster: NB 01

Polarization- and light-sensitive neurons in the central brain of the cockroach *Rhyparobia maderae*

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Many insects are able to use celestial cues for spatial orientation. In addition to the perception of the sun position, the detection of the celestial polarization pattern, likewise, plays a key role in spatial orientation and navigation. Studies on various species showed that these celestial cues are encoded in the central complex, a brain area controlling goal-directed locomotion. The central complex is a group of neuropils in the center of the insect brain and consists of the protocerebral bridge (PB), the upper (CBU) and lower division of the central body (CBL) and paired noduli (Honkanen et al. 2019, J Exp Biol 222:jeb188854). The Madeira cockroach *Rhyparobia maderae* is a nocturnal insect that, in addition to visual cues, strongly relies on antennal information for spatial orientation. The animal is a well-studied model organism in research on circadian rhythms. Despite its nocturnal lifestyle, Loesel and Homberg (2001, J Comp Neurol 439:193–207) identified two polarization-sensitive neurons associated with the circadian clock, the accessory medulla. Based on these data we investigated polarization- and light sensitive neurons in the central brain of the cockroach. Through intracellular recordings followed by tracer injections we identified several cell types that responded to navigational signals such as blue polarized light, unpolarized UV light, or a green light spot simulating the sun. Neurons with projections in the optic lobes showed responses to UV light and blue polarized light. Two types of central-complex neurons were sensitive to the angle of polarization of zenithal light, suggesting that the central complex of the cockroach is involved in sky compass orientation, as shown in other insects.

Neurobiology
Poster: NB 02

Motor pattern in a discrimination task

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It has already been documented that weakly electric fish *Gnathonemus petersii* is capable of discriminating size, shape and material of objects, and that when solving a perceptual task they tend to show specific kinematic sequences. Previously our research group found that a stereotyped behavior —centering— is mediated by electric parallax. This suggests that a back-and-forth movement could potentially be performed by the fish in order to elicit electric parallax for depth perception. So far there have not been reports of weakly electric fish actively performing such a motor pattern to extract (depth) information under experimental conditions. Nevertheless, although we have not recorded va-et-vient movements exhibited by the fish, we have seen apparent small alterations of their motor pattern, like changes in speed while passing along objects laterally before making a decision in a two-alternative forced-choice discrimination paradigm. In such experiments, relative size and distance information is required to correctly solve the task. Fish seemingly decreased the swimming speed in one condition where it significantly chose the S- that was placed closest to the inner corridor. Such changes in speed suggest variations as well in sampling density. Multiple testing conditions are now taking place and the effect of the electromotor behavior on the sensory input and electric parallax is being quantified.

Behavioral Biology
Poster: Behav 01

The role of chemicals in sexual communication in *Aphidius ervi*

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Chemical communication is a vital mechanism for many insect species. *Aphidius ervi* Haliday (Hymenoptera: Braconidae) is a parasitoid wasp species specialized on aphids as hosts. In our study, we intend to gain more knowledge on courtship behaviour in relation to chemical communication in *A. ervi*. Specific antennomers were previously shown to have integumentary glands and a role in secreting chemical compounds from the micropores on these antennomers. Male and female wasps initiate courtship by positioning their antennae in parallel and smearing them together. This is followed by mounting and copulation, if mutual mate acceptance is achieved. In order to investigate the role of these chemicals in *A. ervi* courtship, behavioural trials were conducted with intact and antennal-ablated individuals in different combinations. By establishing an ethogram and characterizing the involved chemicals, we aim for a better understanding of the chemical mechanisms initiated mating behavior. We already detected striking differences in the chemical profiles between male and female *A. ervi* with females possessing significantly higher amounts of dienes. Conversely, *Lysiphlebus fabarum*, a closely related species, lacks dienes and this finding coincides with the loss of one desaturase gene in that species. Intriguingly, *Drosophila melanogaster*, a distant Dipteran species, uses dienes as a sexual pheromone in females. Understanding the role of dienes in *A. ervi*'s sexual communication might provide us an evolutionary overview of a compound class that has a similar role in two species that were parted approximately 327 million years ago.

Evolutionary Biology
Poster: EvoBio 01

Brain evolution in selected extant and extinct Artiodactyla clades: morphological and size changes in microevolution and macroevolution

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Artiodactyls have the most complex brains after primates. Comparative studies of extant versus fossil forms contribute to our understanding of how the brain evolved to the diverse states known today. We present three new Pleistocene endocasts: that of a new “Palaeolama”, of *Camelops hesternus*, the giant camelid, and that of a wild aurochs (*Bos primigenius*). Camelidae were the first artiodactylan lineage to increase neocortical complexity in the Eocene. Our examinations are the first glimpse into their Pleistocene condition. We describe this peak in brain complexity before reaching that of modern taxa, and the neocortical changes suggesting developments in information processing. Comparing living camelids, we find differences between wild and domestic forms that are of phylogenetic significance for *Camelops*. Mirroring the majority of wild-domestic comparisons, the aurochs brain is much larger than that of modern cattle. Breeds of the latter differ in degree of brain reduction, correlated with behavioral and metabolic variables. Correlations of brain size and behavior are possible among other artiodactyls, due to reliable methods for predicting endocranial volume, and the directed behavioral selection among some breeds. Variation in brain form is not only a function domestication, but of multiple other parameters, and we share those findings here.

Ecology
Poster: Ecol 01

Don’t let fluctuations push you around - How brackish invertebrates function in variability

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Aquatic organisms in coastal areas and estuaries experience variable abiotic conditions in their natural environments. Existing temperature patterns are projected to undergo massive changes due to global change. But not only thermal means are changing, also frequencies and amplitudes of temperature variability are being altered. These temperature changes shift the long-term performance of ectotherms, driven by short-term metabolic responses. Ingestion rates serve as approximations for metabolic activities and largely shape the energy availability of brackish invertebrates. Running experiments target to acquire knowledge about vulnerabilities and adaptation processes of a local mysid from the Baltic Sea, *Neomysis integer*, by examining ingestion rates in different constant and fluctuating temperature regimes. In our study, we aim to disentangle fluctuation effects and contribute to the research in the context of non-linear averaging (Jensen’s Inequality) in order to project organisms’ performance in a changing world of variability.

Behavioral Biology
Poster: Behav 02

Immediate effect of light on eclosion behaviour

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Light signals can shape the daily timing of behaviour in two ways. On the one hand they synchronize the endogenous (circadian) clock to appropriately adjust an organism to the 24h environmental period and on the other hand they can also obscure ("mask") the circadian output by directly modulating this behaviour. Therefore, these immediate light effects, which are independent of the circadian clock, are also called "masking effects". In *Drosophila melanogaster*, the immediate light effects are mediated by the eyes and most evident as a response to light in one of the well described behavioural rhythms of the fly – the emergence rhythm of the adult insect from the pupa, called eclosion. Eclosion is gated by the circadian clock to the early day to prevent desiccation and enhance survival rate. A light stimulus induces a rapid increase in the eclosion rate and is referred to as the lights-on response (LOn) (1). Light information is received by the compound eye, which consists of about 800 ommatidia. Each ommatidial unit is equipped with six outer (R1-6) and two inner (R7, R8) photoreceptor cells, which express different rhodopsins. While the outer photoreceptor cells express the blue-green sensitive Rh1 visual pigment, the inner ones can be subdivided into pale (UV-sens. Rh3 in R7p; blue-sens. Rh5 in R8p) and yellow (UV-sens. Rh4 in R7y; green-red sens. Rh6 in R8y). Besides the compound eyes, flies contain three simple dorsal eyes called ocelli, which consist of only one photoreceptor type (UV-sens. Rh2). As it has been shown that each rhodopsin has its own spectral sensitivity (2), we addressed the rhodopsins individually using monochromatic light of certain wavelengths and demonstrated that activation of a single rhodopsin appears to be sufficient to elicit a LOn. (1) McNabb, S.L., Truman, J.W. Light and peptidergic eclosion hormone neurons stimulate a rapid eclosion response that masks circadian emergence in *Drosophila*. J. Exp. Biol. 211 (14): 2263-2274 (2020). (2) Sharkey, C.R., Blanco, J., Leibowitz, M.M. et al. The spectral sensitivity of *Drosophila* photoreceptors. Sci Rep 10, 18242 (2020).

Neurobiology
Poster: NB 03

Parallel spatial processing in hawkmoth vision

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Many animals strongly rely on their visual sense, which provides information about the natural world with particularly high dimensionality. But the breadth of information also increases the need for sensory filtering and for categorizing visual signals at an early stage. To process the complex input with limited neural capacities, one strategy is to spatially segregate visual inputs. We investigate such filtering strategies both across and within the same region of the visual field in the hummingbird hawkmoth *Macroglossum stellatarum*. We recently demonstrated that the same visual stimulus elicits different flight behaviours, when viewed in the dorsal or ventral half of their visual field (Bigge et al. 2021:j.cub.2021.02.022). To study stimulus segregation in the same input region, we investigate the potential for parallel spatial processing in the first visual neuropil of the hummingbird hawkmoth brain, the lamina. The lamina receives information directly from the photoreceptors. Different contrast, luminance, colour or temporal properties are transmitted downstream by its main relay neurons: lamina monopolar cells (LMCs). We previously showed that one type of LMC in *M. stellatarum* performs spatial summation by integrating visual information via its lateral dendrites, that reach into neighbouring visual units or cartridges (Stöckl et al. 2020: sciadv.aaz8645). To characterize the potential for spatial integration, revealed by the dendritic profiles of the other LMC types, we obtain a full 3D-scan of one lamina cartridge via serial block-face scanning electron microscopy (SBF-SEM). Our first results surprisingly revealed a higher number of LMCs than previously described. We identified 5 LMCs, 7 short visual fibres (Svf) terminating in the lamina and 2 long visual fibres (Lvf). Based on the anatomical locations of the neurons in the cartridge, and their lateral extensions, we suggest a preliminary classification of the different LMCs, taking into account homologies with other insect groups.

Physiology
Poster: Phy 01

Insights into the structural features of hemocytin from the red flour beetle, *Tribolium castaneum*

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To prevent and fight infections, insects can rely only on their innate immune reactions because they lack an acquired immune system. The mechanisms of the insect immune system include melanization, ROS formation, phagocytosis, hemocyte coagulation and anti-microbial peptides. A possible key component of insects' innate immune system is hemocytin, which is produced in hemocytes and is a homolgous to the mammalian von Willebrand factor. In contrast to the mammalian homolog, its function is not restricted to act as a mechano-sensistive coagulation factor in the hemolymph but hemocytin is also able to encapsulate foreign substances and thus is a part of the immune system. *Bombyx mori* hemocytin gene expression is upregulated in response to fungal infections, which leads to the agglutination and encapsulation of the fungal cells. Moreover, hemocytin also recognizes and adheres to bacteria. Among insects, the hemocytin of *B. mori* has mainly been investigated so far, whereas barely is known about the hemocytin function in other insects. Therefore, we decided to examine hemocytin in the red flour beetle, *Tribolium castaneum*, a pest species and important insect model. To start, we compared amino acid sequences and structural domains of the *Tribolium* hemocytin with the mammalian von Willebrand factor and *Bombyx* hemocytin. Besides sharing common domains such as the D domain, they also exhibit structural differences. For example, *Tribolium* hemocytin includes a chitin-binding domain, which is missing in the *Bombyx* hemocytin and may play a central role in detecting and combating fungal infections. We will have a closer look at the structural and sequential properties of the hemocytin of *T. castaneum* in comparison to other hemocytins.

Morphology
Poster: Morph 01

Phenotypic variability in body morphology of some eumalacostracan larvae – a quantitative comparison of laboratory and wild caught material

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Morphological identification of planktic crustacean larvae is required in many scientific contexts, such as ecology or taxonomy. Due to a still low availability of genetic sequences for many ingroups of Eumalacostraca, this task is still more feasible by morphological methods. A sound understanding of eumalacostracan larval morphology is therefore necessary. It is well known, at least based on anecdotes, that there is quite some phenotypic variability in eumalacostrancan larvae. We investigated four eumalacostracan ingroups; Galatheidae (type of squat lobsters), Hippoidea (“false” sand crabs), Raninidae (frog crabs) and Stomatopoda (mantis shrimps) for aspects of variability. All four groups develop through spiny planktic larval forms. Using 3D outline shape analysis of the shields, we compared specimens from the wild with laboratory-reared specimens. We found that the phylogenetic differences in the data sets of Hippoidea and Raninidae are too strong concealing possible phenotypic variability. However, in Galatheidae and Stomatopoda, a difference in shield morphology can be found between wild-caught and laboratory-reared specimens. This difference is likely caused by phenotypic variability. The exact environmental signals causing this phenotypic variability are still unknown, but some candidates can be discussed.

Developmental Biology
Poster: Dev 01

Epigenetic modification during diapause development in *Daphnia magna* embryos

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Organisms have evolved different strategies to overcome periods of adverse environmental conditions. For example, diapause, which is a genetically programmed phase of suspended animation and occurs during specific developmental stages. In general, diapause is characterized by arrested ontogenesis, decreased metabolic activity, and increased stress resistance. These hallmarks may be a result of differential gene expression. There is growing evidence that development-related genes are downregulated while diapause-related genes are upregulated during diapause. This raises the question as to what mechanisms govern gene expression during diapause. Epigenetic processes control gene expression patterns without alternations in the DNA sequence and have been suggested to play a role in diapause regulation. Upon these processes, histone modifications are one of the best-studied. Here changes in chromatin structure control gene transcription. We investigated the role of histone modifications during diapause development in the waterflea *Daphnia magna*. We analyzed expression patterns of four genes controlling histone acetylation (kat2a, kat6b) and methylation (suv4 and metk), at different stages of *D. magna* diapause destined embryos using quantitative PCR. Our results demonstrated that kat6b, suv4 and metk decreased during diapause. During resurrection the expression level of these three genes increased indicating that they probably play a subordinate role in diapause but a more significant role in active development. In contrast, kat2a is constantly expressed even during diapause, which may suggest its involvement in diapause maintenance. The distinct expression patterns of the four genes may indicate the modification status of histone sites, which may reflect the transcription status throughout diapause development.

Developmental Biology
Poster: Dev 02

Genome editing strategies to mark homologous neurons between insect species

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Insects are the biggest phylum in the animal kingdom and therefore represent a very large diversity of species. This diversity can also be found in their brains despite the general composition and function of brain neuropils being rather conserved. The neuropils vary in shape and size but also in their developmental timing (heterochrony) in accordance with the adaptations of the species to its ecological niche. Marking homologous neuron populations between different insect species could visualise these differences of brain regions and make it possible to analyse them in a detailed way. Here I present my approaches to use genome editing to mark homologous neurons in the species *Drosophila melanogaster* and *Tribolium castaneum* with the goal to study and compare central complex development throughout development in these two species.

Evolutionary Biology
Poster: EvoBio 02

Developing search filters for literature reviews: A case study with non-human primates

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Literature reviews aim to synthesize available research on a particular topic to help summarize scientific research and identify gaps in the field. Developing search filters for literature reviews identify scientific publications of interest in a replicable manner can be difficult and time consuming. Here, we describe the process of creating comprehensive search filters for literature reviews involving animal taxa and discuss considerations that should be accounted for during filter creation. We present search filters for detecting studies with non-human primates (NHP), which we created for three different bibliographic sources (PubMed, PsycINFO, and Web of Science). Combining these NHP search filters with a topic search (here studies measuring cortisol) revealed more than twice as many scientific publications than search filters a novice would typically create. To aid other researchers interested in conducting literature reviews on NHPs (or sub-taxa), we have made our search filters accessible and easily adjustable via filterNHP (https://filternhp.dpz.eu), a web-based application and R package. We hope to promote the use of filterNHP as well as inspire the development of such tools for other animal taxa. Literature reviews stemming from thoughtfully developed search filters can help inform conservation and public policy efforts, determine how robust scientific observations are, and guide future research.

Developmental Biology
Poster: Dev 03

Two heat shock protein 70 members during diapause and stress in the freshwater Crustacean *Daphnia magna*

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Environmental conditions in natural habitats are never stable and can quickly switch from being favorable to being harsh and detrimental. To cope with this, many animals have evolved a special developmental phase, called dormancy, in which development and metabolism are largely suppressed. Diapause is a pre-programmed and endogenously mediated form of dormancy, it is usually accompanied by enhanced stress tolerance toward adverse environmental factors. Stress tolerance during diapause is discussed to be achieved via a variety of physiological and biochemical mechanisms. For instance, heat shock proteins 70 (Hsp70), which are often produced in response to various types of stress, have been suggested to play a role in many diapausing species. Considering the diversity of the Hsp70 family, different Hsp70 members may have different functions during diapause. *Daphnia* diapausing embryos are highly resistant to harsh conditions, e.g., extreme temperatures. We here investigated whether different Hsp70 members (Dmhsp70-A and Dmhsp70-B) have distinct roles in diapause regulation, and whether Hsp70s are involved in stress resistance in *D. magna* diapausing embryos. We found that Dmhsp70-A may inhibit the embryonic development, while Dmhsp70-B may participate in normal cellular activities. The gene product of Dmhsp70-B performed a heat-shock-like nuclear accumulation upon diapause entrance, which may protect the DNA and intranuclear proteins from denaturation during diapause. Moreover, heat and cold shock did not induce significant changes in the expression of these two Hsp70 members during diapause. Our study underlines the distinctive roles that different Hsp70 members play in *D. magna* diapause destined embryos.

Developmental Biology
Poster: Dev 04

Optimising efficiency of the CRISPR/Cas9 system in *Tribolium castaneum* by germ line-specific Cas9 expression

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The breakthrough discovery of the CRISPR/Cas9 system has significantly increased the experimental possibilities of genome editing. It has successfully been applied in many model organisms, such as the red flour beetle *Tribolium castaneum*, a valuable insect model organism. Different methods to supply the Cas9 protein have been evaluated concerning their consistency and efficiency. Compared to embryonic injections of Cas9, the in vivo expression of Cas9 in the germline substantially increases germline mutation rate, while somatic cells remain unaffected leading to an increased viability. However, thus far no *Tribolium* line expressing Cas9 in the germline has been generated. To develop such a tool, orthologues of the *Drosophila* germ line markers tudor and vasa were identified. We aim at developing two transgenic lines with germline specific Cas9 expression, by placing the expression of Cas9 under similar regulatory control as tudor and vasa. To generate them, potential regulatory regions of tudor are placed upstream of Cas9 while the vasa Cas9 enhancer trap construct is knocked into the locus of vasa, so endogenous regulation takes up. In addition, we want to characterise a *Tribolium* line, which expresses Cas9 in vivo driven by Wnt8/D enhancers. Despite not being germline exclusive Wnt8/D is active in the posterior pole of the blastoderm embryo, where the germline arises. We are planning an in-situ hybridization of Cas9 and want to assess optimal settings for embryonic injections when utilizing the Wnt8/D-Cas9 *Tribolium* line. Ultimately, by improving the consistency and specificity of the CRISPR/Cas9 system, we want to enhance the molecular toolkit in *Tribolium*.

Physiology
Poster: Phy 02

Using CRISPR/Cas9 to differentiate the function of honeybee (*Apis mellifera*) sugar receptors

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Honeybees (*Apis mellifera*) depend on flowers, their main source for proteins in pollen and carbohydrates in nectar. Thus it is remarkable that they only possess ten gustatory receptors (Grs), which they use to evaluate their food for quality and edibility, whereas the fruit fly (with 69 genes) or the mosquito (with 75 genes) have a much broader set. Only three of these gustatory receptors actually detect sugars (AmGr1, AmGr2 and AmGr3), but it is known that honeybees can detect a wide variety of carbohydrates (such as sucrose, fructose, glucose, maltose, melicitose and trehalose). Characterization of these receptors in a cell system suggested that AmG3 is a specific fructose receptor, AmGr1 can detect different sugars including sucrose and glucose and AmGr2 is considered a co-receptor. We used the CRISPR/Cas9 approach to characterize all three gustatory receptors in vivo. We microinjected honeybee eggs with specific sgRNA and Cas9 enzyme and raised worker bees carrying a double nonsense mutation in one of the three sugar receptor genes. Testing their sugar responsiveness using the proboscis extension reflex, we show that AmGr3 mutants are insensitive to fructose, but not sucrose. Whereas AmGr2 mutants did not show any differences compared to wild type bees, AmGr1 mutants showed a reduced response to sucrose and glucose, but not fructose. This indicates that CRISPR/Cas9 is a strong molecular tool for honeybee research, allowing functional analysis of receptors in live bees combined with behavioural studies.

Neurobiology
Poster: NB 04

Campaniform Sensilla Influence Interleg and Intraleg Coordination in *Drosophila melanogaster*

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Locomotion is a crucial component of animal survival that must be adaptable to be consistently successful. This adaptability is necessary for walking insects to overcome complex and changing terrains. During walking, sensory organs monitor motor output and provide dynamic feedback, both modifying and reinforcing, onto central network components. Campaniform sensilla (CS), cuticular sensory organs found on the majority of insect limb segments, encode highly dynamic strains that occur in the cuticle. In *Drosophila melanogaster*, leg CS research remains limited, and it is unclear how different CS and whole CS fields encode specific strains or which are necessary and sufficient to alter motor programs. The genetic tractability of *D. melanogaster* provides the opportunity to study these organs and their complex network interactions without the limitation of only using mechanical manipulations. We tested how CS subsets within two leg fields influence leg movements and coordination using transient optogenetic manipulations in intact walking and standing flies. This demonstrated the involvement of small CS subsets for these behaviors, highlighting their importance for both kinematic and temporal coordination. Inhibiting varying CS subsets leads to alterations in interleg and intraleg coordination, while activation of the same subsets was sufficient for eliciting limb movements that changed joint angles in multiple limb segments. Interestingly, the effects of both inhibition and activation show that different leg types respond differently to CS feedback. Our work underlines the function of different constellations of CS in walking and postural control and depicts the importance of individual CS within a field.

Behavioral Biology
Poster: Behav 03

Individual consistency in the cognitive abilities of honey bees across elemental and non-elemental learning paradigms

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Since the first discovery that the individual performance of humans in a variety of cognitive tasks is positively correlated, the study of general intelligence or g factor has been extensively studied in humans. There is now increasing evidence for the existence of a general intelligence in a wide range of vertebrate species and factors underlying those individual differences in cognitive ability. However, the study of correlated performances in cognitive abilities of individuals and consistent individual differences has been mainly ignored in invertebrate species. The honeybee is a powerful model organism for the study of various elemental and non-elemental forms of learning and cognition. Thereby a lot of studies reported that honeybees exhibit appreciable variation in their performance in several learning tasks. However, it remained unclear if this variation in learning performance is due to different extrinsic factors or rather represents an intrinsic characteristic of an individual honeybee. In the present study it was examined if honeybees show consistent individual differences in their learning ability over time and across learning tasks of different complexity and cognitive requirements. In a first experiment the bees were subjected to elemental visual discrimination tasks for three consecutive days. The results show that the individual bees' performance remained stable over time. In a second experiment we tested the bees in an elemental discrimination task and a non-elemental concept learning task. Again, the performances of individual bees in both tasks were positively correlated. In a third experiment bees were tested in a reversal learning and negative patterning protocol, two forms of non-elemental learning. The reversal learning consists of an elemental learning phase in which one stimulus is associated with a reward (A+) and a second stimulus is not rewarded (B-) and a non-elemental reversal learning phase where the reward contingencies of the learning phase are reversed. The learning phase assesses the bees' discrimination ability, and the reversal learning phase evaluates cognitive flexibility. In the negative patterning paradigm two single stimuli are rewarded (C+ and D+) while their compound is not reinforced (CD-), it represents a form of pure non-elemental learning and assesses the bees´ ability for configural processing. The results show that the bees´ performance was positively correlated across both phases of reversal learning as well as across the learning phase and negative patterning. However, when comparing the two non-elemental paradigms, i.e. the reversal learning phase and negative patterning there was neither a correlation nor a trade-off in the individual performances. Demonstrating correlated cognitive performances of individual honeybees challenge the classical view of invertebrates being merely "reflex machines" which only stereotypically respond to stimuli. Furthermore, such findings stretch the importance of considering individual differences as important factor accounting for variability in the cognitive abilities of invertebrates. However, our results point against a "general factor" in the cognitive ability of individual honeybees and rather support the view of independent cognitive modules within the honeybee brain that underlie the success in certain cognitive abilities but not in others.

Evolutionary Biology
Poster: EvoBio 03

Polygenic adaptation from standing genetic variation allows rapid ecotype formation

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Clunio marinus is a known model for lunar-rhythmic reproduction. The Atlantic ecotype synchronizes the reproduction to spring low tides around the full moon and new moon days, and on these days oviposits on exposed algae. The Baltic ecotype's habitat is constantly submerged because of the lack of tides there. As result the Baltic ecotype lost the lunar rhythmicity, concentrating emergence to every day after dusk. Two sympatric populations of the Atlantic and Baltic ecotype at one location near Bergen (Norway) are reproductively separated by few hours on days of overlapping emergence. By resequencing 168 whole genomes from seven populations of both ecotypes we found that there is generally geographic isolation between sites. However, the two sympatrically co-occurring ecotypes from Bergen showed ongoing gene flow. We also detected a single introgression event from the Baltic Sea into both Bergen populations. The data suggest that all Northern European populations originate from a single colonization event after the last glacial maximum. Finally, the lunar-arrhythmic ecotypes likely evolved from standing genetic variation, followed by a re-assortment of ecologically favorable alleles in the new habitats. We then investigated ecotype-associated variants and identified a prominent region on chromosome 1 containing strong signals of ecotype-association and differentiation. A set of 1,400 genes is affected by strongly ecotype-associated SNPs. Many of these genes are prominently involved in time-keeping and behavior, nervous system and pre-pupal development, as well as ecological adaptations to the Baltic Sea. Our study shows that the ecotype formation can occur rapidly despite gene flow and by re-assortment of existent and possibly co-adapted alleles.

Behavioral Biology
Poster: Behav 04

Distance estimation in weakly electric fish, *G. petersii*

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Weakly electric fish, in our case *Gnathonemus petersii*, forage at night and return to their hideouts. Whether the fish can utilize path integration in performing this navigation in absence of visual information is still unclear. One crucial element for this is the ability to determine both the distance and direction the fish travelled from its shelter in order to compute the shortest route back. In our study we try to elucidate if *G. petersii* can measure the distance travelled. We use two channels, one for training and one for test. Fish are trained in darkness to find and dig larva hidden under glass beads at a certain distance from their starting point. They are tested in the second channel in absence of food to determine the distance where they search or dig for the expected food. Tests are conducted from three different start positions in the channel, including the training release position. The preliminary results indicate that *G. petersii* can estimate the distance travelled.

Physiology
Poster: Phy 03

Bacteria-induced NO production in Locust hemocytes

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The innate immune system of several insect species has been shown to respond to an infection with different defensive approaches, including melanization and synthesis and release of cytotoxic nitric oxide (NO) by the insect immune cells, the hemocytes. NO also functions as a signaling molecule in the mammalian immune system, and in the nervous system of both mammalians and insects, which raises the possibility of NO-based neuro-immune interactions. In the present study, nitric oxide production was indirectly measured in adult and first instar locusts (*Locusta migratoria*) after an infection, using an antibody against the by-product of NO synthesis, L-citrulline. For this purpose, locusts were injected with heat-inactivated gram-negative (*E. coli*) or gram-positive bacteria (*Staphylococcus aureus*, *Streptococcus suis*), or the bacterial cell wall component muramyl dipeptide (MDP). After 6 and 24 hours post injection, abdomens of first instar locusts were dissected, and primary cell cultures of adult hemocytes were prepared. L-citrulline immunofluorescence was assessed qualitatively in first instar abdomens, and quantitatively in hemocyte cell cultures. A strong increase of hemocyte NO production as well as an increased number of melanized hemocyte aggregates in the abdomens was observed after treatment with *E. coli* and *S. suis*, whereas *S. aureus* injection only slightly increased NO production and MDP had no effect. Citulline-immunoreactive hemocytes and aggregates were found both dorsally, close to the heart and ventrally, adjacent to the central nervous system. Based on this, a possible influence of hemocyte-mediated NO production on the nervous system can be investigated in future experiments, using e.g. antibodies against cGMP, the second messenger in the canonical NO signaling pathway.

Neurobiology
Poster: NB 05

Elevated pCO2 affects neuronal plasticity underlying predator perception in the freshwater crustacean *Daphnia longicephala*

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With industrialization atmospheric CO2 increased substantially during the past decades. This has been shown to have significant effects on different ecosystems. For example, increased atmospheric CO2 dissolves in aquatic habitats and has a negative impact on olfactory and visual senses thereby changing species interactions. In some cases, elevated levels of pCO2 thereby reduce predator induced defense expression, as in the case of the water flea *Daphnia*. *Daphnia* is thereby less defended and more prone to predation. However, the effect of pCO2 on the neuronal and cellular mechanisms involved in defense expression are not understood. We studied this in the freshwater crustacean *Daphnia longicephala*. When exposed to predators, *D. longicephala* develop defensive crests, which are associated with neuronal plasticity, where the brain volume increases together with a rewiring of the inhibitory neuronal connections. When exposed to elevated levels of pCO2 this neuronal plasticity is impaired, so that there is no brain volume increase, and we find a reduced number of inhibitory neuronal connections in comparison to the ambient treatment. Our results demonstrate the first functional impact of how elevated pCO2 levels affect species interactions on the neuronal level.

Neurobiology
Poster: NB 06

One appendage - two behaviors

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Behavioral flexibility of pectoral appendages is a common feature throughout the animal kingdom. One fish group that shows specialized pectoral behaviors are hatchet fish. Their hypertrophied abductor muscles enable them to explosively leave the water in response to a potential threat. We show that the hatchet fish also displays an additional, previously undocumented behavior, which we termed fin flickering, that likely serves a postural function. In contrast to the escape behavior, fin flickering is characterized by a smaller amplitude and more variable duration of pectoral fin motion. How can such widely different behaviors be mediated by the same set of motoneurons? Retrograde tracing of the nerves innervating the pectoral fin muscles revealed a widespread spatial distribution and a set of differently sized motoneurons, the latter being associated with different behaviors in other systems. Gap junction passable tracers did not reveal trans-synaptic labeling, even though gap junctions are known to occur between moto- and pre-motoneurons in the hatchet fish pectoral system. While the pre-motoneuronal network of escape responses is associated with the Mauthner escape system, and has been detailed previously, this system is, however, not able to generate fin flickering behavior. This suggests that additional neuronal populations are involved in pectoral control. Our data thus suggests that the observed pectoral fin abductive behavior dualism is likely associated to differences in motoneuron size and pre-motoneuronal control, instead of altered pre-motoneuronal activity. As large motoneurons likely only contribute to escape behavior, we expect to find prominent differences in the action potential firing behavior and membrane properties of differently sized motoneurons.

Systematics, Biogeography & Diversity
Poster: Syst 01

Optimization of DNA barcoding methods to study beetle diversity in the Leipzig floodplain forest

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With over 350,000 described species, Coleoptera represent the largest order of insects worldwide. With their great species richness and the presence of many cryptic species, many families of beetles pose a challenge for morphologically determination and require expert knowledge. Without this expertise, biodiversity is often vastly underestimated in morphological taxonomic studies. Molecular methods, such as DNA barcoding, offer a solution for this problem. Here, we present an optimized molecular approach for beetle determination using DNA barcoding and metabarcoding. For DNA barcoding, the extraction and amplification method were adapted to obtain DNA from one or several legs of each beetle species. This method is used to establish a genetic reference database and serves as a basis for a non-destructive metabarcoding approach without the destruction of the specimen. This offers advantages especially in the study of cryptic species or type material, because after genetic examination more attention can be paid to morphological differences. Our study is part of the Leipzig canopy crane (LCC) project and provides, among very few projects worldwide, the possibility to explore canopy diversity of beetles. Together with the investigation of the understorey, comprehensive biodiversity studies across the whole forest ecosystem can be now conducted. By optimizing previous molecular methods, our project contributes greatly to the rapid and reliable determination of the beetles and thus to answering important questions of ecology and biodiversity. Furthermore, we contribute greatly to the compilation of reference databases, which are crucial for DNA barcoding studies, and to the further investigation of cryptic species in beetles.

Ecology
Poster: Ecol 02

Detecting and protecting the endangered leather beetle *Osmoderma eremita* (Juchtenkäfer)

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The Russian leather beetle *Osmoderma eremita* is one of Europe's endangered species of insects inhabiting tree hollows. His presence was found to be beneficiary for the species richness of old agriculture trees and more and more effort is put into preserving this species and its habitat in Europe. As it is the case with many other xylobiontic species, much of his lifestyle and behavior still remains unknown. Circadian rhythms dominate the activity of almost any organism, but how does this cryptic lifeform cope with the lack of day light? Does the leatherbeetle use other environmental cues to entrain its rate of activity or does he live a life without any influence from outside rhythms? We addressed these questions in a field study using laser vibrometry. Six different statistic models were tested to compare vibratoric activity of the beetles and their larvae with ambient temperature and the velocity of the wind. Results show that these beetles are able to synchronize their activity to the sparsely available sunlight, instead of entraining to other cues. Furthermore, we analyzed the acoustic signal composition of trees inhabited by russian leather beetles. This information provides the possibility to identify beetle infested trees via laser vibrometry.

Neurobiology
Poster: NB 07

Neuromodulator diversity of local olfactory interneurons and regionalization of olfactory glomeruli in crustaceans

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In malacostracan crustaceans, the primary olfactory centers (olfactory lobes) in the brain consist of an array of fields of dense synaptic neuropil, the olfactory glomeruli (review Harzsch & Krieger, 2018, Prog. Neurobiol. 161:23-60). These fundamental units of olfactory processing are sites where axons from olfactory sensory neurons synapse with local olfactory interneurons and olfactory projection neurons. In higher crustaceans, glomeruli are elongate and are regionalized into functional compartments along their long axis, the cap, subcap and base regions, each with a distinct neurochemistry. This study sets out to understand the neurochemical basis of glomerular regionalisation in two crustacean representatives that in previous studies we had found to feature highly complex central olfactory systems, the hermit crabs *Coenobita clypeatus* and *Pagurus bernhardus*. To that end, we explored the neurochemical diversity of local olfactory interneurons using antisera against serotonin, allatostatin, and RFamide in combination with anti-synapsin immunohistochemistry. These interneurons can be broadly subdivided into two morphological classes, one of which primarily targets the cap and subcap regions of the glomeruli (“rim” interneurons), and a second class which primarily invades the base of the glomeruli from inside of the lobe (“core” interneurons). Our data provide evidence for 1.) a small-scale subdivision of crustacean olfactory glomeruli into regional compartments, and 2.) for distinct differences in the innervation pattern of local olfactory interneurons even between closely related crustacean species. This study was supported by DFG grants Ha 2540/13-1 (SH), Ha 5871/5-1 (BSH), and the Max Planck Society.

Morphology
Poster: Morph 02

The larval diversity of spoon- and thread-winged lacewings

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Neuroptera is an ingroup of the superdiverse group Insecta, more precisely of its large ingroup Holometabola, and is closely related to Coleoptera, the group of beetles. Despite still unresolved conflicts on the internal relationships of Neuroptera, a still stable ingroup is Myrmeleontiformia, represented by the antlion-like forms. Among these are spoon-winged lacewings (Nemopterinae) and thread-winged lacewings (Crocinae), together forming the group Nemopteridae with 150 currently known species (Nemopterinae: 100, Crocinae: 50). Nemopteridae has a disjunct distribution, with extant representatives being native to Africa, South America, Australia and the southern parts of Eurasia, living mostly in deserts or other dry areas. As in most other lacewings, their larvae are highly specialised predators. Larvae of Nemopterinae and Crocinae, though being sistergoups, differ recognisably in shape. In Nemopterinae, the larvae have short and stout mouthparts (stylets) and a very broad trunk. In Crocinae, the larvae have a long neck between head and prothorax, preventing the body from getting harmed by animals they prey upon. While many myrmeleontiformian larvae have prominent teeth on their venom-injecting mouthparts (stylets), these are mostly absent in larvae of Nemopteridae. When looking back in time, i.e., when studying the fossil record, there are relatively few fossils known resembling larvae of spoon-winged or thread-winged lacewings, namely from 100 million-year-old Myanmar amber. We review all known occurences of extant and fossil larvae interpreted as representatives of Nemopteridae. We furthermore report some new fossil larvae from this group and provide a comparison of the morphological diversity of these larvae through time based on a morphometric approach.

Morphology
Poster: Morph 03

Quantitative comparisons of whip spiders reveal that their morphology was less static in evolution than generally assumed

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Whip spiders, close relative of web-spinning spiders, are quite impressive animals of the group Amblypygi. The second pair of appendages forms massive prey-grasping structures, the third pair of appendages forms antenniform feelers. Amblypygi is not a very species-rich group, but has survived for quite some time, seemingly unchanged. The oldest unambiguous whip spider fossils (some doubtful fragments have been dated to an age of 385 million years) are known from 300 million-year-old ironstone nodules and similarly old preservation types. Younger occurrences are known from 110 million-year-old limestones and especially from amber of various ages: several specimens are known from 100 million-year-old Kachin amber, a single adult female and her brood from 50 million-year-old Cambay amber, and again several specimens are known from 15 million-year-old Dominican amber. We review all known occurrences of fossil whip spiders and provide a quantitative comparison of their morphology over time. This comparison reveals a recognisable change over time: walking and grasping appendages become longer (on average), being longest in the modern fauna. The finding emphasises the use of quantitative comparisons also in groups with seemingly unchanged morphologies over long time periods. This is especially promising for a group like Amblypygi in which qualitative comparisons are often challenging as, for example, specimens preserved in ironstone nodules provide a quite different level of details compared to specimens in amber (although both provide a 3D type of information). Quantitative morphology offers a comparative frame here.

Morphology
Poster: Morph 04

Astonishingly diverse lacewing larvae in amber demonstrate now extinct extreme morphologies

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Lacewings, the beautiful representatives of the group Neuroptera, appear sometimes forgotten due to the overwhelming presence of other groups such as those of beetles (Coleoptera), moths (Lepidoptera), flies (Diptera), and wasps (Hymenoptera). While the modern fauna does hence not provide a huge diversity of lacewings, this seems to have been different in the past. This is especially exemplified by the larval forms of lacewings. These are characterised by a specialisation of the mouthparts: each upper and lower jaw form a so-called stylet, often injecting venom and saliva into their prey and allowing the larvae to suck out the dissolved inner parts. Already modern-day forms are quite intriguing such as the pit-building larvae of antlions, the for gardeners quite useful aphid lions (larvae of green and brown lacewings), the parasitic larvae of mantis lacewings, or the long-necked antlions (larvae of thread-winged lacewings). Yet, despite the already impressive form diversity of modern-day lacewing larvae, 100 million years ago even stranger appearing larval forms existed. Examples of such larvae include animals with over-sized body parts or with combinations of characters today only known in quite divergent lineages. Oversized mouthparts include stylets that can reach up to one third of the overall body length, but also palps that resemble the antennae. Oversized legs outperform any other larvae of Insecta and even most adults. Also protrusions on the back of different fossil larvae, used to carry a camouflaging cloak, are several times the length of similar structures in modern animals. We present a variety of such unusual larvae (LEON) that demonstrate the diversity of lacewing larvae in the past and also the “capabilities” of larvae of the group Insecta in general.

Evolutionary Biology
Poster: EvoBio 04

The vampire amoebae: widespread yet poorly known microbial predators

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The vampire amoebae (Vampyrellida, Rhizaria) comprise naked, filose amoebae of a remarkable genetic and phenotypic diversity that inhabit a variety of aquatic and terrestrial ecosystems. However, the actual diversity, ecological roles and geographic distribution of these intricate protozoa are still fragmentarily known. In this talk, I review the phylogenetic position and the known diversity of the Vampyrellida, introduce the currently characterised family-level clades, and give an ecological overview. Special attention will be drawn to the diversity of morphotypes, cell motility and, in particular, feeding strategies, as most vampyrellids show stunning feeding strategies to prey on relatively large eukaryotic prey. Open questions and some new discoveries will be presented as well, e.g. so far unrecognised cell biological aspects of engulfing vampyrellids (Leptophryidae), and the deepest-branching vampyrellid family that was very recently described. Finally, I will present our future plans to further explore this exciting order of microbial predators in a new and collaborative project of the 'Taxon-omics' Priority Programme (German Research Foundation).

Ecology
Poster: Ecol 03

Local differences of *Daphnia* in sensitivity to light pollution and fish kairomones

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Biological systems are more and more affected by increasing anthropogenic disturbances. Since natural systems are mainly controlled by light, anthropogenic disturbance by artificial light at night (ALAN) may have a major impact on ecosystems. Recently researchers interests in studying the effects of ALAN in aquatic systems increased. Here we examined whether ALAN is affecting the growth responses of zooplankton species such as the cladoceran *Daphnia magna* originating from different locations along a North – South gradient. As the effects of ALAN might be modulated by additional stressors such as the presence of predators, we additionally exposed the animals to fish kairomones. The experiments were conducted in a cross sectional study design with animals that had either been exposed or not exposed to ALAN and additionally exposed or not exposed to fish kairomones. In the case of ALAN we tested both a long-term and a short-term exposure. As response variables somatic growth and reproduction rates of animals were recorded. The *Daphnia* clones showed different growth responses when exposed to ALAN but the effect by the additional stressor fish kairomone was minor. It appeared that clones originating from northern latitudes were more sensitive to ALAN-exposure than southern ones suggesting a local adaptation, which is under further discussion.

Neurobiology
Poster: NB 08

Functional assessment of putative chemo co-receptors IR25a and IR93a of predator perception in *Daphnia*

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The freshwater crustacean *Daphnia* is well known to adapt to an increased predation risk, through the expression of predator specific inducible defenses. Some of these defensive strategies can be seen in form of morphological adaptations, like the formation of spines, thorns or neckteeth, increasing the individual's fitness. The expression of these inducible defenses are initiated by predator specific chemical cues. However, the mechanisms of chemoreception in *Daphnia* have only been studied to a limited extent and especially the involved chemoreceptors remain unknown. Ionotropic receptors (IRs) are discussed as a central element of chemoreception in crustaceans. In silico, two putative co-receptors have been suggested, i.e. IR25a and IR93a, that together with dedicated tuning receptors form a functional chemoreceptor. We here tested the involvement of IR25a and IR93a in predator perception in three *Daphnia* species (*D. magna*, *D. longicephala* and *D. lumholtzi*) responding to three different predator cues (*Triops*, *Notonecta*, and *Gasterosteus*). With the help of RNA-interference (RNAi) we knocked down IR25a and IR93a. Knock down animals did not express defensive features indicating that the animals lose their sense of smell. We confirmed knock-down of the target gene using quantitative PCR. This study provides a first functional proof of both chemo co-receptors being involved in predator perception and probably chemo perception per se.

Neurobiology
Poster: NB 09

The organization of the central and lateral complex in the brain of the cockroach *Rhyparobia maderae*

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Many insects use the position of the sun or the polarization pattern of the sky to navigate in diverse environments. The central complex (CX), a group of neuropils in the center of the insect brain, plays a key role in these navigational tasks. The CX consists of the protocerebral bridge (PB) and the upper (CBU) and lower division of the central body (CBL) and a pair of globular-shaped noduli. The most prominent input and output area of the CX is the lateral complex (LX). These structures have been analyzed in several insect species including a locust, bees, beetles, the fruit fly, and the monarch butterfly (Honkanen et al 2019, J Exp Biol 222:jeb188854). To investigate the organization of the CX in an insect that, in addition to visual cues, strongly relies on antennal information for spatial orientation, we investigated the structure of the CX in the cockroach *Rhyparobia maderae* at the level of individual dye-filled neurons. In addition, subcompartments of CX and LX neuropiles were reconstructed through immunostainings and arborization patterns of CX neurons. The neuronal organization of the CX in *R. maderae* differs in several aspects from that in other well-studied insects. Most strikingly, the CBL consists of intercalated systems of 8 cones and 9 wedges. The anterior lip, a brain area closely associated with the CX, is particularly large in the cockroach, considerably smaller in the locust, and completely absent in flies. The LX of the cockroach is highly compartmentalized. In addition to a large bulb, small distinct bulb-like regions receive axonal terminals of columnar neurons from the CBL and CBU.

Neurobiology
Poster: NB 10

Tuning properties of wide field motion-sensitive neurons in the bumblebee

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A moving animal experiences a displacement of the retinal image caused by its own movement providing information about wide field motion (Gibson, 1950, Am. J. Psychol.). Such optic flow cues serve to estimate different parameters like flight speed (David, 1982, J. Comp. Physiol. A) or distance (Esch and Burns, 1995, Naturwissenschaften) and play an important role in flight control and stabilization. Therefore, insects use different components of motion information such as frequency or velocity. Here we want to investigate the tuning properties of motion sensitive neurons in the central brain of the bumblebee *Bombus terrestis*. To do so we do extracellular tetrode recordings in tethered animals while presenting moving stripe patterns at different temporal frequencies. We record activity from neurons responding to wide field visual motion stimuli. Characterization of first results show a tuning towards a single temporal frequency that differs between individual units. To further investigate tuning properties of these neurons, and to differentiate between frequency- and velocity-tuned units, grating with different spatial frequencies will be presented in future experiments.

Physiology
Poster: Phy 04

Targeted expression of a constitutively active EGFR allele in the respiratory system of *Drosophila melanogaster* induces lung cancer like phenotypes

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Mutations in the Epidermal Growth Factor Receptor (EGFR) pathway are among the most common causes of lung cancer, particularly non-small cell lung cancer (NSCLC). In this study, we have focused on modelling cancer-like phenotype by expressing constitutively active EGFR (EGFRCA) in the tracheal system of *Drosophila*. The ectopic expression of EGFRCA throughout the airway system using a binary expression control system causes severe phenotypes like epithelial thickening, hyperplasia, and metaplasia, which often cause death in the early larval stage. Whereas the targeted expression of EGFRCA in tracheal Inka cells, ecdysis-triggering hormones (ETH) producing cells, did not result in significant phenotypes in the larval stages, it caused 100% lethality in the pupal stage. The cellular level analysis of the pupal trachea displayed possible tumour-like morphological changes like severe regional hyperplasia and hypertropia and thickened epithelium at the branching points of the primary branches in dorsal trunks, where Inka cells are normally located. The complete lethality in the pupal stage points towards the dysfunction of Inka cells, where the ETH production, and thereby the eclosion hormone (EH) secretion, is drastically suppressed or even totally terminated. It implies that the EGFRCA-induced changes in these cells interfere substantially with their normal role during the process of pupation. As the phenotypes observed in both pan-tracheal and Inka cell driver lines are highly significant and easily monitorable, they can be efficiently used for straightforward drug-screening approaches and drug-resistance experiments.

Developmental Biology
Poster: Dev 05

Generation and analysis of *Tribolium castaneum* imaging lines to study neuroendocrine development

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The red flour beetle *Tribolium castaneum* serves as an alternative insect model especially regarding head, brain, and nervous system development. Its genome is fully sequenced, and many transgenic tools are applicable. We want to investigate the emergence and development of neuroendocrine cell types marked by specific genes. Expression analysis for most genes is restricted to RNA in situ hybridization, which is only feasible in some tissues and stages. Therefore, we analyze enhancer trap lines originating from the GEKU insertional mutagenesis screen with respect to their suitability to study neuroendocrine development. Further, we use CRISPR/Cas9 to generate transgenic lines with insertions in desired regions that express fluorescent reporters recapitulating the expression of the gene of interest (GOI). We employ different approaches to create those fluorescent lines. Using non-homologous end joining (NHEJ) we inserted an mCherry reporter into the chx-locus and are currently analyzing the expression pattern. A more precise approach applies homology directed repair (HDR). We detail the generation of a bicistronic line via HDR, labelling the gene PC1/3, which is crucial in the processing of peptide hormone precursors and causes a severe growth phenotype when knocked down. The stop codon of the PC1/3 is removed using CRISPR cleavage sites and a GFP reporter is inserted in frame. Thus, the fluorescent protein uses the same promoter as the GOI and is transcribed without interruption, both are only separated in a second step using the 2A peptide. With these different strategies it will be possible to investigate expression patterns in time and space at different developmental stages and to gain valuable insight into the development of neuroendocrine cells and organs.

Neurobiology
Poster: NB 11

Neurotransmitters and Neuropeptides in the central complex of two non-pterygote hexapods

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While the organization of the insect brain has been studied considerably well in advanced winged species, basal wingless taxa have been less extensively explored. These include the entognathous Protura (coneheads), Collembola (springtails) and Diplura (two-pronged bristletails) and the ectognathous Archaeognatha (jumping bristletails). To further explore the ground pattern of hexapod brain organization, we have analyzed the brain of the collembolan species *Orchesella flavescens* and the dipluran species *Campodea augens* by immunolabeling, using antisera against the neuropeptides Lom-tachykinin II, Dip-allatostatin and myoinhibitory peptide, as well as antisera against the GABA synthesizing enzyme glutamate decarboxylase, synapsin, and the protein kinase DCO. Particular attention was paid on the presence and internal organization of the central complex, a brain area with a key role in goal directed navigation. Large central bodies subdivided into upper and lower divisions were present in both species. Columnar neurons immunostained for myoinhibitory peptide in *O. flavescens* and Lom-tachykinin II in *C. augens* innervated the upper division of the central body via four pairs of fiber bundles, the w, x, y and z bundles, that formed a chiasma posterior to the central body. Axonal projections could be traced to a confined area in the lateral complex likely homologous to the gall in pterygote insects. Paired antennal lobes with glomerular internal organization were prominent, but brain areas similar to mushroom bodies could not be identified in either species so far. The results show striking similarities with the neurochemical organization of the central complex in pterygote insects, suggesting that the chemical architecture of this brain area is highly conserved throughout the hexapods.

Ecology
Poster: Ecol 04

Flavobaterial symbionts support cuticle biosynthesis and adaptation to stress across beetle families

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Glyphosate is widely used as a herbicide, but recent studies begin to reveal its detrimental side effects on animals by targeting the shikimate pathway of associated gut microorganisms. However, its impact on nutritional endosymbionts in insects remains poorly understood. Here, we sequenced the tiny, shikimate pathway encoding symbiont genome of the sawtoothed grain beetle *Oryzaephilus surinamensis*. Decreased titers of the aromatic amino acid tyrosine in symbiont-depleted beetles underscore the symbionts' ability to synthesize prephenate as the precursor for host tyrosine synthesis and its importance for cuticle sclerotization and melanization. Glyphosate exposure inhibited symbiont establishment during host development and abolished the mutualistic benefit on cuticle synthesis in adults, which could be partially rescued by dietary tyrosine supplementation. Furthermore, phylogenetic analyses indicate that the shikimate pathways of many nutritional endosymbionts likewise contain a glyphosate sensitive 5-enolpyruvylshikimate-3-phosphate synthase. These findings highlight the importance of symbiont-mediated tyrosine supplementation for cuticle biosynthesis in insects, but also paint an alarming scenario regarding the use of glyphosate in light of recent declines in insect populations.

Ecology
Poster: Ecol 05

Migration under clock control? Light perception via cryptochrome 2 (cry2) and diel vertical migration in *Daphnia*

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The circadian clock is an endogenous system found in most taxa. Its rhythm regulates activities like sleep, body temperature, neural activity, or behaviour. Rhythmicity is often tuned by exogenous factors including light and thereby synchronizes the organism’s clock with the environment. Changes in light regimes are perceived through cry2 which functions as a photoreceptor in clock neurons. The freshwater crustacean *Daphnia* is able to plastically respond to environmental challenges, including the presence of visually hunting predators like fish. Fish presence can induce diel vertical migration, so that *Daphnia* migrate to deeper & darker water strata during the day. At night *Daphnia* migrates to upper nutrient-rich water strata. Therefore, fish presence seems to induce a switch from phototaxis to antitaxis, which may furthermore be correlated with circadian rhythms. Using a bioassay composed of water columns, we tested depth selection behaviour in control and fish exposed *D. magna*. The control animals show positive phototaxis, as they accumulate in the upper light exposed area of the water column. The fish- exposed animals show negative phototactic activity, as they migrate to the dark bottom of the column. This behaviour is daytime dependent and probably endogenous, so that migration away from light starts even before the dark period. We then knocked down cry2 using RNA interference. Upon gene knock-down we observe that both fish exposed and control animals, are evenly distributed in the water column. This indicates that cry2 functions as a central element in light perception and depth selection. As cry2 is a central element that tunes the circadian clock, we will test the involvement of clock genes in controlling depth selection behaviour in *D. magna* in future experiments.

Neurobiology
Poster: NB 12

Bigger brains are better: Shedding new light on neuroplasticity in the honeybee using expansion microscopy

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Throughout adult life, honeybee (*Apis mellifera*) workers display a remarkable behavioral plasticity. While progressing through different colony tasks with increasing age, they experience an ever-changing sensory environment with varying cognitive demands. Genuine traces of this high flexibility can even be found in the insect brain. Particularly, higher brain centers such as the mushroom bodies (MBs), prominent centers for learning, memory and sensory integration, are prone to structural changes in relation to age, experience and environmental cues. Most distinctively, structural plasticity can be found at the level of small synaptic microcircuits (microglomeruli; MGs) within the MB calyces, where sensory information from primary sensory neuropils is conveyed to MB intrinsic Kenyon cells (KCs). Conventional immunolabeling using fluorophore-conjugated antibodies combined with confocal laser scanning microscopy have proven to be invaluable tools to investigate structural neuronal plasticity at the level of MG. However, when trying to grasp the subcellular architecture of MG and the underlying plasticity, we are often confronted with constraints posed by the diffraction limit of conventional microscopy systems. A recently introduced technique, protein-retention expansion microscopy, is able to overcome this limitation via an isotropic physical expansion of conventionally immunostained tissue, enhancing the effective resolution to ~60 nm. For the first time, we have now established the expansion microscopy (ExM) protocol in a social insect species, the honeybee, to gain new insight into ultrastructural details of synaptic architecture. Here, we demonstrate the use of ExM for different antibody immunostainings, neuronal tracings from fluorescent dye injections and quantitative analyses, and thus establish a basis for future analyses of plasticity in synaptic microcircuits in social insects. Supported by a DFG grant to CG (GR3305/2-1) and the University of Würzburg.

Morphology
Poster: Morph 05

Absence asymmetry in the internal male genitalia of Austrophasmatidae, Mantophasmatodea

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Asymmetries are a widespread phenomenon in otherwise strictly bilaterally symmetric organisms. Investigation of such asymmetric structures can help us gather insights into fundamental evolutionary processes such as the selection for morphological novelties caused by behavioural changes. In insects, asymmetric genitalia have evolved in almost every order, and usually it’s the sclerotized parts and most conspicuous male phallic organs that are known to exhibit asymmetries. While external copulatory organs in insects have often been subject to investigations concerning asymmetries and the evolution thereof, internal reproductive structures have received far less attention. Here we describe the internal and external male genitalia of three species of Austrophasmatidae, Mantophasmatodea, using µCt imaging and light microscopy. We confirm that male heelwalkers exhibit asymmetries in the external genitalia and associated structures, represented by asymmetric phallic lobes and cerci. Moreover, we found an extreme asymmetry within the internal male genitalia: in all adult males investigated so far, the seminal vesicle, a dilatation of the vas deferens, was only developed at the right side of the male while completely missing on the left side. Nevertheless, both bilaterally arranged testes were well-developed and functional. If this holds true for all heelwalker species, this absence asymmetry constitutes another autapomorphy for the insect order Mantophasmatodea. The false-male-above mating position exhibited by Mantophasmatodea (the male sits above the female, bending his abdomen around the right side of the female, his genitalia contacting the female from below) and especially the concomitant long copulation duration of ca. 3 days might select for the asymmetries found in male external and internal genital structures.

Physiology
Poster: Phy 05

Metabolic changes upon smoke exposure and manipulation of the Nrf2 antioxidant pathway in *Drosophila melanogaster*

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COPD is a summary of different chronic lung diseases. Chronic inflammation, often combined with emphysema, leads to a loss in the expiratory volume. COPD is the third leading cause of death and only the symptoms can be alleviated. Therefore, it is mandatory to intensify the research of respiratory diseases aiming to understand the underlying molecular basis. To model COPD in *Drosophila*, larvae and adults, were exposed to cigarette smoke, which is the main reason for the disease in humans. CS exposure increases oxidative stress which is believed to be a key driving mechanism in the pathophysiology of COPD. One main cause of oxidative stress seems to be the reduced expression of the transcription factor nuclear factor erythroid 2-related factor 2 (Nrf2) which is negatively regulated by Keap1. In this work keap1 transcription was verifiably decreased via CRISPR in the trachea and the influence regarding development, lifespan and metabolism was analyzed. While smoke exposure showed no significant changes in the development and keap1 silencing only decreased the developmental rate slightly, a combination of both led to a highly decreased developmental rate. The lifespan is the gold standard for analyzing the influence of treatments in flies. It was shown that smoke exposed flies died significantly faster than control flies. A combination with keap1 silencing could rescue the lifetime of the smoked flies. A hypoxia sensitivity test indicates if epithelial cells in the trachea are still working. It was shown that CS exposure caused a higher mortality after low oxygen treatment while keap1 silencing led to an extremely decreased mortality, which means that these flies were less sensitive to hypoxia. Additionally, it was shown, that the fat content of flies after CS exposure was reduced significantly. Also the triglyceride amount in keap1 silenced flies was reduced. But interestingly a reduction of fat in CS exposed flies could be inversed in combination with keap1 silencing. Comparing younger and older flies showed that older flies tend to store more fat, but longtime CS exposure inversed this effect.

Neurobiology
Poster: NB 13

Neuromodulator diversity in the central olfactory pathway of *Parhyale hawaiensis* (Dana, 1895)

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To gain insights into the evolution of olfactory core circuits, our collaborative study investigates the olfactory pathway of on representative of crustaceans (our group) and hexapods (MPI for Chemical Ecology Jena). The amphipod crustacean *Parhyale hawaiensis* (Dana, 1853) is of similar size to many hexapods (1 cm) and its brain structure was previously analyzed by our group [1]. The primary olfactory centers (olfactory lobes, OL) in the malacostracan brain are subdivided into olfactory glomeruli, synapse-dense regions consisting of interacting afferents, local interneurons and projection neurons [2]. The wiring pattern of the glomeruli of crustaceans and hexapods are suggested to be homologous because of the pattern of connectivity of afferents, local interneurons, and projection neurons [3, 4]. The glomeruli receive input from the afferents of olfactory sensory neurons (OSN) which are associated with specialized sensilla on the first antennae, the aesthetascs. We used immunohistochemistry against the neurotransmitters serotonin, RFamide, allatostatin, histamine and orcokinin to describe the morphology of local olfactory interneurons that innervate the olfactory glomeruli. All glomeruli were equally innervated by interneurons with all five neurotransmitters. Allatostatin showed a distinct innervation of the cap of the glomeruli, the region receiving input from the afferents of the OSNs. Labeling synaptic proteins provided the basis for 3D reconstructions of the glomeruli by manual segmentation. Based on these analyses, we measured the volume and number of the glomeruli. Both parameters turned out to be highly variable among a population of adult male animals contrasting glomerular number in insects, which is fixed between individuals of one species.

Evolutionary Biology
Poster: EvoBio 05

The role of fas genes for desiccation resistance in the jewel wasp *Nasonia vitripennis*

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Depending on the humidity in the environment, insects are particularly prone to water loss through evaporation. Smaller insects tend to be more affected by the risk of losing water because with decreasing body size the correlated surface for evaporation increases. One mechanism for desiccation resistance is the waxy lipid layer on their epicuticle. One of the main components of this lipid layer are cuticular hydrocarbons (CHCs). CHC biosynthesis is majorly governed by a specific type of fatty acid synthesis (fas genes) genes, so far mainly studied in *Drosophila melanogaster*. There, it was shown that knockdowns of fas genes can dramatically reduce desiccation resistance. For a broader understanding of the role of fas genes in desiccation resistance, studies in other insect taxa are necessary. For genetic studies in Hymenoptera *Nasonia vitripennis* is a well-suited model organism. In *N. vitripennis*, orthologues to the fas genes of *Drosophila* were found, which I knocked down for my desiccation assays to investigate whether their desiccation resistance changed. The results of this research can help to get a broader understanding of the role of fas genes for desiccation resistance in insects.

Evolutionary Biology
Poster: EvoBio 06

On the origin and evolution of striated muscle cells: Insights into muscle cell transcriptomes from the scyphozoan species *Aurelia aurita*

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In the Bilateria, muscles mostly develop from the mesoderm. By contrast, in the diploblastic Cnidaria, muscles arise either in the inner or the outer layer. Like in Bilateria, cnidarians can form smooth or striated muscles. But in Cnidaria striated muscles are exclusively formed during development of the jellyfish in medusozoans and have not yet been discovered in sessile polyps, including those from medusozoans and anthozoans. However, the developmental origin and evolutionary relationship of those striated muscles is still obscure. Notably, modes of medusa development differ between hydrozoans, where medusae are formed by a lateral budding process and scyphozoans, where medusae are formed by an axial segmentation process, called strobilation. Hence, it is not even clear, whether striated muscles of medusozoans are homologous or convergent. In order to gain understanding on the evolution of morphological convergence our goal was to shed light on the origin of striated muscles in the cosmopolitan scyphozoan species *Aurelia aurita* and identify the muscle cell transcriptomes to be able to compare them between different cnidarian species. Therefore, we generated single-cell RNAseq libraries from distinct stages of the *Aurelia* life-cycle, which cover the transition from the sessile polyp to the free-swimming medusa as well as the juvenile medusa of the hydrozoan species *Clytia hemisphaerica*. Further, we validated the single-cell data via in situ hybridizations as well as immunohistochemistry to show the spatial location of striated muscles in the animals. We will present molecular similarities and differences between *Aurelia* and *Clytia* striated muscle cells and compare them with striated muscles of Bilateria.

Ecology
Poster: Ecol 06

Attractivity of native and non-native *Acer* and *Tilia* species for bees

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In urban areas, city trees provide important habitats and food resources for bees. Extreme weather conditions reduce the vitality of native tree species. Therefore, the question arises whether closely related, non-native tree species with higher stress tolerances could be considered as alternatives and whether they provide food sources and habitats for the same diversity and abundance of bees. In this study, ten different species of *Acer* (N = 45; species: 3 native, 7 non-native) and *Tilia* trees (N = 45; species: 2 native, 8 non-native) were examined. Visual observation, net catches and window flight traps were applied to determine the abundance and diversity of bees (honey bees and wild bees) within the tree crown and flowers. Overall, 39 wild bee species were observed in *Acer* sp. and 36 species in *Tilia* sp. 58.9 % (*Acer* sp.) and 47.2 % (*Tilia* sp.) of wild bee species were detected in both native and non-native trees. Furthermore, bees were found at least as often in flight traps of non-native trees as in those of their native relatives. However, in some non-native trees fewer bees were detected on flowers compared to native, closely related trees. This result might rather be driven by bee population dynamics, phenology and resource quantity than by resource quality. The results indicate that closely related native and non-native trees were mainly visited by the same bee species. Especially with regard to climate change, the high stress tolerance towards weather extremes of non-native, closely related tree species can make a useful complement to urban tree species composition and contribute to urban biodiversity.

Behavioral Biology
Poster: Behav 05

Do weakly electric fish use optic or electric flow information to control their position?

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Weakly electric fish forage in the night and hide in shelters during the day. A centered position within the shelter is maintained with high precision even when it is moving. To track the velocity of the shelter and keep a fixed distance from it, fish could rely on hydrodynamics, vision, and their elaborated electric sense, but the underlying mechanisms are not yet clear. In many flying animals, centering behavior is accomplished by balancing optic flow information on both sides of the body. Weakly electric fish were found to rely on electric flow cues in shelter tracking paradigms, but the contribution of optic flow has not been addressed thus far. Indeed, the use of optic flow in orienting behaviors in fish is currently controversial. Here, we investigate if and how the shelter tracking behavior of the weakly electric fish *Apteronotus albifrons* is affected by electric and optic flow information. Specifically, we equip a shelter's walls with electric, optic or combined gratings and move them along the fish with imbalanced velocities. We quantify the animal's position with respect to the shelter's midline and find that *A. albifrons* centers closer to the faster moving plate in electric and optic conditions alike. The fish also adjust their velocity to the closer pattern, thereby reducing the sensory flow on that side, indicating a similar strategy as in flying insects. Next, we test centering behavior in navigation experiments (also see Abstract by Nia Papadopoulou) where the generation of electric or optic flow solely depends on the fish's self-motion. By comparing results from both experiments, we aim to elucidate if weakly electric fish are able to use optic and electric flow and to understand how they integrate multiple senses to control essential behaviors.

Physiology
Poster: Phy 06

Transcriptomic analysis of neuronal cells transfected with putative neuroprotective genes from the hooded seal (*Cystophora cristata*)

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The brain of the hooded seal (*Cystophora cristata*) has a remarkable tolerance to low oxygen levels (hypoxia). It can endure conditions of extreme hypoxia, which would lead to neuronal death in other mammals. S100B and clusterin (apolipoprotein J) were found to be enriched in a previous transcriptomic analysis of the cortex of the hooded seal, compared to the ferret (*Mustela putorius furo*), a closely related terrestrial carnivore. The genes had protective effects on neuronal cell cultures, which might have been promoted by increased expression, but their mechanism and role in hypoxia and oxidative stress are largely unknown. S100B is a calcium binding protein and may function in neurite extension, astrocytosis and axonal proliferation. Clusterin is a secreted chaperone that can under some stress conditions also be found in the cell cytosol. It has been suggested to be involved in several basic biological events such as cell death, tumor progression, and neurodegenerative disorders. To elucidate their importance in facilitating the observed hypoxia tolerance a transcriptomic analysis was conducted on neuronal cells transfected with S100B and two isoforms of clusterin (soluble and nucleus clusterin). Cells were exposed to hypoxia and oxidative stress and differential gene expression analysis performed. Treatment as well as cell line affected gene expression. Responsible pathways and upstream regulators were identified via Gene Ontology (GO) and Qiagen Ingenuity Pathway Analysis (IPA). Significant GO terms included nervous system development (GO:0007399), neurogenesis (GO:0022008) and generation of neurons (GO:0048699), while significant canonical pathways in IPA included Axonal Guidance Signaling and NGF signaling.

Neurobiology
Poster: NB 14

Location and odor-induced differential expression of chemo-coreceptors in the water flea *Daphnia longicephala*

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Prey species often have the capacity to defend from predators by expressing defensive traits. These inducible defenses are formed when the predation risk is high. The predation risk is indicated through predator specific chemical cues. Chemical perception is therefore a major task for prey species as only the correct interpretation of the predator can reduce their predation risk. However, The underlying molecular mechanisms including chemosensation are not well understood. In silico a set of ionotropic receptors (IRs) has been identified and are discussed to be involved in chemoreception in crustaceans. Upon these, the IR93a and the IR25a are discussed to be coreceptors that together with tuning receptors form functional chemoreceptors. We here studied chemoperception in *Daphnia longicephala* with the aim to identify the location of these putative chemo-coreceptors. Furthermore, we tested for predator induced differential gene expression of these receptors. We exposed *D. longicephala* to the predator *Notonecta* to initiate defense expression. Controls were performed likewise, but in the absence of predators. Subsequently, we extracted RNA for quantitative PCR using primers amplifying IR25a and IR93a. We find a significantly higher amount of both IRs in the antennules in comparison to body and antennae irrespective of the treatment. This indicates that chemoreceptors are predominantly located on the antennules and to a limited extend also within the body. There are no chemoreceptors on the antennae. Receptor expression on the antennules is not static, but is significantly increased by predator exposure. We conclude, that both chemo-coreceptors when co-expressed with distinctive tuning receptors appear to be located on the antennules and are involved in predator perception.

Ecology
Poster: Ecol 07

Sex differences in sand goby feeding ecology during breeding season

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The trophic role of small benthic fish in the Wadden Sea has rarely been studied in ecosystem research, despite being a major food source for many taxa e.g. porpoises and predatory fish, including commercially relevant species. Even less is known about seasonal and sex-specific differences in fish feeding ecology. The sand goby (*Pomatoschistus minutus*) is one of the most abundant fish species along the coast of the North Sea and its extensive paternal care and nest defence during their single breeding season has been well studied. However, despite their high abundance, little data has been collected on their feeding ecology. For this study *P. minutus* were caught in the area of the Amrum Bank (German North Sea) in November 2019 and May 2020. All individuals were dissected and measured. The stomach contents were weighed and items identified. Our aim was to (i) reveal the trophic role of the sand goby by identifying its prey, (ii) to study seasonal variation in its feeding ecology, and (iii) to look into potential dietary differences between males and females. We show that sex and season affect the diet of *P. minutus*. There were no dietary differences between males and females in the autumn. In May, during the breeding season, males have less food in their stomachs and a different selection of taxa in their diet. The effects on the feeding ecology can be caused by different behaviour and feeding opportunities of female and male sand gobies during reproduction and male parental care. This study is among the first studies addressing gender-specific differences in the diet. We confirm that *P. minutus* is a second consumer which suggests its important role in the coastal marine food web and conclude that it´s time for ecosystem research to start considering sex differences.

Morphology
Poster: Morph 06

A unique tarsal spinning organ in glomeridesmid millipedes (Diplopoda, Pentazonia, Glomeridesmida)

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The production of sticky threads from ‘spinnerets’ is known from various myriapod groups including some representatives of the millipedes (Diplopoda). In Diplopoda the thread-producing glands are mostly setae-like and positioned terminally on the telson, and the secretion product is typically used to build molting chambers or egg sacs. So far, no such secretions or organs have been documented for the subgroup Pentazonia. Here we describe for the first time thread-producing glands from the enigmatic Glomeridesmida. These putative spinning organs are single circular fields of small pores (sieve plates) positioned on the outer side of the tarsi of all walking legs of mature and juvenile individuals of both sexes. These pores are the openings of cuticular tubuli, which extend from the tarsus to a putative gland within the femur. In several specimens thin threads were observed to be extruded from the sieve plate. The tarsal sieve plates are present in all 21 investigated Glomeridesmida morphospecies, including Termitodesmidae and Glomeridesmidae from South East Asia, the Indian subcontinent, Oceania, and South America. These peculiar organs constitute an apomorphic character of the Glomeridesmida, as similar organs are absent in other Myriapoda. The function of the extruded threads in Glomeridesmida remains speculative, because observations of living specimens of the group are almost non-existing. We suggest that the secretion might be used for defense, to build molting chambers or to secure tunnels burrowed in the substrate.

Neurobiology
Poster: NB 15

Identification and distribution of RYamides in the circadian clock of the Madera cockroach

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Transplantation studies located the circadian clock of the Madera cockroach *Rhyparobia* (*Leucophaea*) *maderae* to the accessory medulla (AME), ventromedially to the medulla of the brain´s optic lobes. The AME receives photic entrainment from compound eye photoreceptors and orchestrates circadian rhythms in physiology and behavior synchronized to the external 24h light-dark cycles. About 240 neurons innervate the AME which are abundant of partly co-localized neuropeptides. The best studied neuropeptide of the insect circadian clock is pigment-dispersing factor that controls rest-activity cycles. However, the identity and functions of most other neuropeptides of the circadian clock are not known. In this study, we identified three novel neuropeptides which encoded by the ry-amide gene whose precise expression and function have not yet been determined in *R. maderae*. We identified the RYamide gene transcript by transcriptome analysis of the central nervous system and predicted three potential RYamides: RYamide-1 (pQQFYPGGRY-NH2), RYamide-2 (GSSTFWSGSRY-NH2), and RYamide-3 (NDRFFIGSRY-NH2). By applying direct tissue profiling using MALDI-TOF mass spectrometry (MS) and Q- Exactive Orbitrap MS of the AME, we obtained all predicted RYamides in the *R. maderae* circadian clock center. Using a polyclonal antiserum which recognize the C-terminal sequence RYamide, we described its spatial distribution within the cockroach brain. The results of our study provide novel and necessary input for subsequent physiological and behavioral experiments revealing the functional role of neuropeptides in the insect´s circadian clock network. [supported by DFG grands STE531/27-1 to MS, NE911/5-1 to SN].

Neurobiology
Poster: NB 16

Investigating the sun compass in monarch butterflies (*Danaus plexippus*)

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Every autumn, monarch butterflies migrate from North America to their overwintering sites in Central Mexico. To maintain their southward direction, these butterflies rely on celestial cues as orientation references. The position of the sun combined with additional skylight cues are integrated in the central complex, a region in the butterfly's brain that acts as an internal compass. However, the central complex does not solely guide the butterflies on their migration but also helps monarchs in their non-migratory form manoeuvre on foraging trips through their habitat. By comparing the activity of input neurons of the central complex between migratory and non-migratory butterflies, we investigated how a different lifestyle affects the coding of orientation information in the brain. During recording, we presented the animals with different simulated celestial cues and found that the encoding of the sun was narrower in migratory compared to non-migratory butterflies. This feature might reflect the need of the migratory monarchs to rely on a precise sun compass to keep their direction during their journey. Taken together, our study sheds light on the neural coding of celestial cues and provides insights into how a compass is adapted in migratory animals to successfully steer them to their destination.

Behavioral Biology
Poster: Behav 06

Rathmayer Prize 2021 *(Jugendforscht Wettbewerb 2021)*

Environmental factors induce thelytokous parthenogenesis in the worker caste of *Messor capitatus* ants

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Thelytokous parthenogenesis or thelytoky is a phenomenon not only known from solitary but also eusocial Hymenoptera. In recent years thelytoky has been discovered in more and more eusocial species and especially in ants it seems to be more widespread than originally thought. One such ant species is *Messor capitatus*, where worker thelytoky has been shown in orphaned colonies. This study examines the influence of biotic and abiotic environmental factors such as temperature on the reproduction of the worker caste through thelytokous parthenogenesis. For the first time it could be shown that in *Messor capitatus*-colonies thelytoky in laboratory workers can also occur in queenright colonies if the right environmental factors are given and newborn workers are spatially separated from the queen in a different chamber for a longer period of time. The comparison of worker thelytoky in queenless and queenright colonies then opens the opportunity to propose conclusions over the role and importance of queens in species where worker thelytoky has been shown.

Evolutionary Biology
Poster: EvoBio 07

Visual Ecology of Earwigs

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Insects view the world using compound eyes, consisting of tens to thousands of individual photoreception units called ommatidia. The acuity and sensitivity of compound eyes are determined by the sizes of the ommatidia and the angles between them (interommatidial angle), which vary across the eye such that there are certain specialised regions of high acuity (‘acute zones’) or high sensitivity (‘bright zones’). However, the distribution of such acute and bright zones, and their correlation with the ecology of the animal remain largely unknown in a large number of insect taxa. Here we calculate ommatidial sizes, interommatidial angles, and the size and direction of the visual field in 115 species across the whole phylogeny of Dermaptera to investigate how the distribution of the acute and bright zones across the compound eye is correlated to the feeding ecology and microhabitat of the insect. We show that predatory Dermaptera tend to have more dorsally distributed acute zones, facilitating prey capture. In addition, we report the presence of ‘bright zones’ in Dermaptera, which have previously only been known from certain Diptera and Hymenoptera. Such bright zones might facilitate the detection of prey, mates, and predators in the dark microhabitat of these mostly nocturnal insects. Our results demonstrate how the variation in acuity and sensitivity across the eye is driven by the feeding ecology and microhabitat of earwigs. We expect our analysis to act as a foundation for further studies investigating the acuity and sensitivity of compound eyes, and their correlation with ecology across all insects.

Systematics, Biogeography & Diversity
Poster: Syst 02

A drop in the ocean of deep-sea diversity: 3D-microanatomy of a novel Solenogastres (Mollusca, Aplacophora) from the Northwest Pacific

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With the goal of expanding knowledge of deep-sea diversity, the 2015 SokhoBio Expedition explored the benthos of the Sea of Okhotsk, a marginal sea of the Northwest Pacific, at overall 11 stations from 1,600 to 4,800 meter. During the expedition, overall 93 solenogaster molluscs were collected. Solenogastres are a small class of vermiform shell-less molluscs, with currently close to 300 described species. They are distributed from shallow waters down to the deep sea, and can be found in polar water as well as tropical coral reefs. Recent investigations of the solenogaster fauna of the deep Northwest Pacific have revealed a rich diversity, with more than 60 candidate species new to science. One of these novel lineages is represented by a single individual, which was sampled from the bottom of the Kurile Basin in 3,500 m depth. Based on first morphological investigations and molecular data, this singleton was identified as a member of the family Pruvotinidae Heath, 1911 (order Cavibelonia), with 35 species the second largest solenogaster family. In this study, we used computer-based, histological 3D-reconstructions of all major organ systems to explore the microanatomy of this novel species. The 5 mm long animal is mature, with several well developed oocytes in its gonopericardial system. The digestive system is characterized by small multicellular digestive glands and lack of radula. Several sensory structures are associated with the nervous system, like the anterior atrial sense organ and the dorsoterminal sensory organ. The investigated specimen most closely resembles the genera classified among the subfamily Eleutheromeniinae Salvini-Plawen, 1978 but with a unique combination of anatomical features (e.g. presence of epidermal papillae, common atrio-buccal opening, lack of radula and respiratory folds). As recent molecular-based studies have already pointed to polyphyletic Pruvotinidae, we currently refrain from establishing a new taxonomic unit until Pruvotinidae have been revised via an integrative approach, combining morphological, anatomical and molecular data.

Evolutionary Biology
Poster: EvoBio 08

Born with a silver spoon or suffering due to your parent's food habits?

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Animals must be able to adapt themselves and their offspring according to the environment in order to ensure high fitness. Parental cues during the early development can shape the offspring´s traits to thrive in the prevailing environment. Here, we test the parental influence of diet switch in the offspring of wild house mice on offspring personality and life history. We hypothesize either a match-mismatch situation, i.e. offspring of parents which experienced a food-switch perform worse than offspring of parents who didn´t experience a food switch, or a silver-spoon situation in which offspring of parents receiving a high-quality diet have an advantage. Mice were maintained under semi-natural conditions and fed with different quality diets *ad libitum*. Diets were switched in the parental generation and the offspring generation was tested for exploratory and risk-taking behaviors using the novel environment and open field tests. In addition, we record growth rates, number of offspring produced and male sexually selected traits. Initial results from the novel environment tests suggest no significant difference in the latency to leave the trap, exploration time and number of individuals that left the trap to explore. The standard quality food treatment showed higher variance compared to the high-quality food treatment individuals. The number of exploratory bouts were significantly higher in high quality control food treatment individuals. Further data analysis of other traits tested might produce conclusive results of the maternal effects due to food switch. Current exploration data suggests no elusive parental effect.

Developmental Biology
Poster: Dev 06

Differences in orthodenticle expression promote ommatidial size variation between *Drosophila* species

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The compound eyes of insects exhibit extensive variation in ommatidia number and size, which affects how they see and adapt to different environments and lifestyles. However, very little is known about the genetic and developmental bases underlying differences in compound eye size. We found that *Drosophila mauritiana* has larger eyes compared to *D. simulans* due to differences in ommatidia size. We identified an X-linked chromosomal region in *D. mauritiana* that results in larger eyes when introgressed into *D. simulans*. Using a combination of fine-scale mapping and gene expression analysis we further investigated positional candidate genes and found that orthodenticle (otd) is expressed earlier in *D. mauritiana* than in *D. simulans* during ommatidial maturation during eye development. We confirmed that this gene is required for the correct organisation and size of ommatidia in *D. melanogaster*. Using ATAC-seq, we have identified several candidate eye enhancers of otd as well as potential direct targets of this transcription factor that are differentially expressed between *D. mauritiana* and *D. simulans*. Taken together, our results suggest that differential timing of otd expression contributes to natural variation in ommatidia size between *D. mauritiana* and *D. simulans*, which provides new insights into the mechanisms underlying the regulation and evolution of compound eye size in insects.

Physiology
Poster: Phy 07

A protein-reduced diet alone or as part of a combination therapy rescues tumor-associated phenotypes of an intestinal cancer model

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Intestinal tumors are among the most common cancers worldwide, and like many other tumor entities, show an unsatisfactory prognosis necessitating the development of safe and highly effective therapies. In the present study, we established a model with intestinal over-proliferation by ectopically overexpressing a constitutively active EGFR allele in intestinal stem cells (ISC) of the fruit fly *Drosophila melanogaster*. In this model, over-proliferation resulted in a substantially reduced lifespan and epithelial changes in the midgut. We assessed the effects of pharmacological treatment with the EGFR tyrosinekinase-inhibitor afatinib (BIBW2992), the effects of dietary (protein) restriction (DR) and a combination of both on cell proliferation and survival. Treatment with afatinib substantially reduced cell proliferation and moderately but significantly increased lifespan. In transversal cuts a treatment with afatinib showed a strong effect on ISC phenotypes but no effects concerning the epithelial bilayer that is formed in this model due to overproliferation. DR partially reduced cell proliferation but restored lifespan to control levels and epithelial monolayer in midguts. The combination of afatinib and DR efficiently reduced cell proliferation and completely restored lifespan. The positive effects of both afatinib and DR on the gut epithelium, ISC phenotype improvement and epithelial monolayer restoration, are found in gut treated with a combinational approach. These results were obtained in experiments in which the tumor phenotype was induced at the start of treatment. To test this strategy in a real-life scenario, we induced the full tumor phenotype before starting treatment. We observed that afatinib and DR had similar effects on cell proliferation and lifespan as observed in the early treatment design at overproliferation onset. Combinational treatment has the potential to combine the positive effects on the proliferation phenotype by the specific inhibitor with the positive life extending effect of the diet to create a promising strategy in cancer treatment.

Ecology
Poster: Ecol 08

Effects of high fluctuating temperatures on the performance of *Daphnia magna* originating from different latitudes

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Depending on their geographical distribution ectothermic species can experience high and varying temperatures close to their thermal limits. Increasing temperatures due to climate change may have detrimental effects on the performance of ectotherms by exposing them partly to temperatures above the upper thermal limit. Using the planktonic crustacean *Daphnia magna* as a model organism, we measured life history traits (e.g. growth, reproduction) of clonal lineages originating from different latitudes in response to high mean temperatures (24 and 28°C) and different fluctuating regimes (no fluctuation, ±2.5 and ±5°C). Our aim was to assess whether fluctuations at high temperatures have detrimental effects on performance and whether we observe signs of local adaption or phenotypic plasticity towards heat tolerance. The responses to high temperature and fluctuations were mainly clone dependent. However, acclimation to 28°C generally increased juvenile growth rate compared to 24°C, whereas the effects of fluctuating temperatures on growth rate were more pronounced at 28°C. Also, the number of eggs of the first clutch was affected both by temperature and fluctuation regime. We also assessed heat tolerance by knockout time at lethal temperature exposure and found that animals acclimated at higher temperatures were more heat tolerant than animals acclimated at lower temperatures. Moreover, animals acclimated to fluctuation regimes were more heat tolerant than animals kept on constant temperatures. Our results suggest that both phenotypic plasticity and local adaptation contribute to heat tolerance.

Ecology
Poster: Ecol 09

First insights into consequences of nutrient co-limited phytoplankton communities on the growth of a rotifer

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Phytoplankton, and thus primary production, is frequently limited not only by nitrogen (N) and phosphorus (P), but also by both nutrients simultaneously. The latter case of nutrient co-limitation in primary producers is now widely acknowledged, yet we know little about the consequences of co-limited phytoplankton for the growth of primary consumers. To gain first insights in how the response of nutrient (co-)limited phytoplankton translates into consumer growth, the rotifer *Brachionus calyciflorus* has been raised on freshwater phytoplankton communities grown on media of various N and P concentrations and ratios in laboratory experiments. We conducted a full factorial experiment spanning 6 N and 6 P concentrations around the Redfield ratio and assessed patterns of nutrient co-limitation arising in a phytoplankton community composed of 6 species of different nutritional traits. We then fed rotifers with the communities grown on a respective nutrient treatment. We measured phytoplankton growth and community composition and related these measurements to rotifer abundance (population size) achieved after 7 days, taking recent co-limitation theory into account. Phytoplankton growth was often serially co-limited, i.e. primarily by N and secondarily by P after N demands have been met, and particular phytoplankton species were more dominant at non-limiting conditions. Rotifer abundance showed a similar response to that of phytoplankton along the N and P supply gradients, suggesting food quantity as a major driver affecting secondary production, but slight differences also indicate that food quality may play a role.

Developmental Biology
Poster: Dev 07

Characterising putative type II neuroblasts in the *Tribolium* embryo

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The morphological diversity of insect brains goes back to a similar basic structure and to a common principle of neurogenesis using neuroblasts. Questioning the developmental and evolutionary mechanisms beyond, we aim to characterise neuroblasts that contribute to the brain of the beetle *Tribolium castaneum*. Type II neuroblasts show, unlike type I neuroblasts, a larger amount of progeny by generating intermediate progenitor cells. Neuroblasts with increased offspring have been described in central complex development of the hemimetabolan *Schistocerca gregaria*, and type II neuroblasts are active in *Drosophila* at the larval stage, playing a crucial role to the formation of the central complex, which is not functional in the *Drosophila* larva, but gains functionality in the *Tribolium* larva. They have not been molecularly characterised in any insect other than *Drosophila*. It is not known if other holometabola use type II neuroblasts with a same molecular signature to generate brain structures. In *Drosophila* a distinct temporal gene expression pattern of these neuroblasts and their progeny has been outlined: lacking the expression of asense these stem cells are marked by pointed and deadpan. Intermediate progenitor cells express deadpan, asense and fez/earmuff. In the *Tribolium* embryo we found a cluster of 6-8 putative type II neuroblasts identified by coexpression of pointed and deadpan, bordering to fez/earmuff expressing cells, marked with a CRISPR/Cas9 generated enhancer trap. Some of these putative intermediate progenitor cells also express deadpan. We interpret these cells as type II neuroblasts and plan to put a more detailed focus on their molecular character and division pattern in *Tribolium*. Furthermore, we investigate which brain structures these cells give rise to.

Ecology
Poster: Ecol 10

Variation of cuticular hydrocarbon profiles among honeybee workers with different social roles and between different *Apis mellifera* subspecies

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The honeybee (*Apis mellifera*) expresses a remarkable genetic and phenotypic variation that involves several subspecies, which represent an important reservoir of local adaptations and genetic diversity. However, they face a homogenization of their native geographical distribution via the hybridization and replacement of native populations of the different subspecies. This situation may affect valuable local adaptive traits, like the cuticular hydrocarbons (CHC), which prevent desiccation and mediate intra- and interspecific communication.

Our study is the first to compare the CHC profiles of workers with different tasks inside and outside the hive of five different honeybee (*Apis mellifera*) subspecies. The different subspecies' colonies have been raised under the same environmental conditions to focus on the genetic basis of their phenotypic differences. Therefore, we analyzed the CHC profiles of nurses, pollen, and non-pollen foragers.

We show that the CHC profile is strongly influenced by both subspecies and social role. There is a clear differentiation between nurses and foragers. In addition, CHC profiles of workers with different tasks differ among the five subspecies. Intriguingly the workers of different honeybee subspecies varies widely in the CHC profiles, independent of their task, even though they were maintained under the same environmental conditions. These results point towards a trade-off between the communication and desiccation prevention functions of CHC. CHC are considered to respond to the climatic conditions, thus the differences between subspecies might respond to natural selection driven by the local climates in their native distributions. Furthermore, the clear difference in the CHC profiles of nurses and foragers could also respond to the different task-related environment the worker bees experience. However, such a clear pattern of differentiation among the different subspecies might also serve for communication, playing a role in the division of labor, allowing the individual honeybee workers to perceive each other task-performance.

Neurobiology
Poster: NB 17

Dynamic properties of compass neurons in bumblebees

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Bees use the polarization pattern of the sky for spatial orientation. Polarization information is processed in the sky-compass pathway, and provides a reference to compass neurons in the central complex (CX). The tuning of such neurons has traditionally been characterized with respect to simulated skylight cues that rotate at a slow, constant velocity. However, little is known about their dynamic properties in response to naturalistic stimulus dynamics. Flying bumblebees usually make rapid saccadic turns interspersed with segments of translational flight (Boedekker et al., 2015). During saccades, they rotate around their yaw axis at angular velocities of up to 2000 °/s, which leads to a highly dynamic input into the visual system. We asked if CX-neurons are able to reliably code a polarized-light stimulus with naturalistic temporal properties and if the neuronal activity depends on the rotation velocity and direction of the stimulus. We recorded intracellularly from compass neurons in the CX of bumblebees while stimulating with a rotatable polarizer backlit by a UV-LED (365 nm). The polarizer was either rotated reproducing the dynamics of an actual flight or continuously at discrete velocities between 30°/s to 1920 °/s. We found consistent spiking of CX-neurons during repeated presentations of the naturalistic stimulus sequence. Responses to discrete rotation velocities were significantly phase locked to the stimuli. At high rotation velocities, activity was phase-delayed, which is likely a consequence of cumulative time-delays in photoreception and synaptic transmission. At low rotation velocities, we observed phase-advanced firing, which cannot be explained by delays. We designed a model, which suggests that advanced firing could be facilitated by rebound effects after inhibition and excitation. Using our model to fit neuronal responses, we were able to extract the preferred angle of polarization and the delay of the neurons. Supported by DFG Grant PF714/5-1

Ecology
Poster: Ecol 11

Ontogenetic Thermal Tolerance and Acclimation Capacity in the European common frog (*Rana temporaria*)

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Phenotypic plasticity may allow ectotherms with complex life histories such as amphibians to cope with climate-driven changes in their environment. In particular, plasticity in thermal tolerance (i.e. acclimation of thermal limits) has been proposed as a coping mechanism with global warming and extreme thermal events. However, thermal tolerance and, hence, acclimation capacity, is known to vary with life stage. Using the common frog (*Rana temporaria*) as a model species, we measured the capacity to adjust lower (CTmin) and upper (CTmax) critical thermal limits at different acclimation temperatures at seven consecutive ontogenetic stages. We calculated the acclimation response ratio as a metric to assess the stage-specific acclimation capacity at each of seven consecutive ontogenetic stages and tested whether acclimation capacity is determined by ontogenetic stage, body mass, and acclimation duration. We further examined how acclimation temperature, body mass, age, and ontogenetic stage influenced thermal tolerance (i.e., CTmin and CTmax). In the temperate population of *R. temporaria* that we studied, thermal tolerance as well as acclimation capacity were affected by ontogenetic stage. However, acclimation capacity of both thermal limits was well below 100% at throughout ontogeny. The lowest and highest acclimation capacity in thermal limits was observed in young and late larvae, respectively. The relatively low acclimation capacity of young larvae highlights a clear climate risk to amphibian populations. Examining life-stage specific acclimation capacity and evolutionary thermal adaptation across a broader range of taxa will allow general perspectives to be drawn on the risks imposed by global warming to local populations of ectotherms.

Physiology
Poster: Phy 08

Globins in zebrafish development (*Danio rerio*)

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The vertebrate globin family includes Hemoglobin (Hb), Myoglobin (Mb), Neuroglobin (Ngb), Cytoglobin (Cygb), Androglobin, Globin X (GbX), Globin Y (GbY) and Globin E (GbE). Globins are small respiratory iron-heme proteins that bind their ligands reversibly and occur not only in multicellular animals, but also in fungi, plants and bacteria. Many Globins, e.g. Mb and Hb, are involved in O2 supply, but functional diversity of globins is great. Up to date, for some of these globins exact physiological role is still uncertain. In recent years, globin function was mainly studied in adult organisms, e.g. zebrafish, although many globins are already expressed developmentally during embryogenesis. Zebrafish embryonic development demands sufficient levels of oxygen and good protection against toxic reactive oxygen species (ROS/NOS). In addition, a key developmental regulator is NO signaling. Ngb expression is mainly restricted to neuronal tissues, where it might function in O2 supply or in a neuroprotective manner. Ngb mediated ROS and nitrosative stress protection is conceivable. In teleost fish, a whole genome duplication event presumably led to the duplication of the ancestor cygb gene. Therefore, in zebrafish and many other teleost fish, two isoforms of cygb, the cygb1 and cygb2 gene, exist. Cygb1 expression profile is ubiquitously, whereas Cygb2 highly occurs in the brain. In development, cygb1 expression sharply rises during segmentation phase and is consistently higher than levels of cygb2. Based on the ability of globins to regulate NO levels, to detoxicate ROS or nitrosative stressors (NOS) as well as the conceivable function in oxygen provision, we aimed to study the involvement of the three globins during embryogenesis and early larval stages in vivo. Our workgroup generated three CRISPR/Cas9 mediated globin deficient zebrafish lines, ngb-/-, cygb1-/- and cygb2-/-. First, we monitored the development of globin knockout embryos up to 120hpf under normoxic conditions in multiple ways. We analyzed mortality, hatching rates, head trunk angle, embryo length and yolk usage. Then we documented the occurrence of developmental defects, like malformation of larvae. On molecular basis, we observed expression levels of genes associated with oxygen dependent pathways and oxidative stress, or which are related to development. We also measured globin mRNA levels at the end of embryogenesis (72hpf) to discover putative compensatory effects in globin-KOs. To get deeper insight into the effects of globin knockouts on transcriptomics, we generated and analyzed next generation sequencing (NGS) data of pooled 72hpf globin knockout larvae and wild type larvae. We identified differentially expressed genes and conducted over representation tests to elucidate physiological function of these globins during development.

Neurobiology
Poster: NB 18

Identification and characterization of uni- and multimodal visual neurons in the mushroom body output of *Apis mellifera*

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For honeybees, the detection and recognition of suitable food sources is crucial during foraging and directly linked to the ability to percept visual and olfactory plant cues. In the brain, both visual and olfactory cues are sent to the primary processing centers in the periphery before the information subsequently converges on specific neurons that project to the mushroom bodies (MB), the centers for sensory integration and memory formation. The MB are mainly formed by ~170.000 kenyon cells (KC) in honeybees, organized in a layering architecture. Here, the information is separated to modality specific layers, before it is passed on to the MB output region in the vertical lobe (VL). There, the information is converged on to approximately 400 mushroom body output neurons (MBON). The specific processing of modalities in distinct KC layers persists in the layers of the VL, resulting in a modality-specific tuning of the MBON population. Using extracellular, multi-unit recordings and stimulating with both visual and olfactory cues, this study shows for the first time that this tuning is not only specific across modalities but is also suited to encode detailed aspects within a single modality, such as intensity and wavelength information in visual MBONs. We were able to characterize six distinct groups of a total of 90 visual-sensitive neurons in the MBON population in the VL. Their specific response pattern or tuning to certain wavelengths and intensities allows us to gain more insight in their capability and role in complex processes, like multisensory integration und learning and memory formation in the MB.

Behavioral Biology
Poster: Behav 08

Prenatal maternal stress effects on gut bacterial microbiome and HPA axis activity in wild Assamese macaques

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Early adversity can have long lasting effects on offspring phenotype with maternal effects in mammals often being mediated via pre- and postnatal exposure to maternal glucocorticoids. Experimental studies on model organisms have established causal effects of prenatal maternal stress (PREMS) on the functionality of offspring hypothalamic-pituitary-adrenal (HPA) axis and other outcomes. We contribute by adding ecological validity for a long-lived mammal in its natural environment, consider three possible sensitive periods, and extend the range of plastic offspring traits to the gut bacterial microbiome composition. We collected fecal samples for enzyme-immuno-assays quantifying glucocorticoid metabolites (fGCM) as our proxy of early/late prenatal and postnatal maternal as well as offspring physiological stress in 38 offspring from three age classes in three groups of wild Assamese macaques (*Macaca assamensis*) at Phu Khieo Wildlife Sanctuary, Thailand. General linear modelling suggests that early but not late PREMS is associated with increased HPA activity in infant, juvenile, and adult offspring. With generalized linear mixed models, we show how offspring gut microbiome diversity (Faith’s Phylogenetic Diversity) and composition (dyadic weighted UniFraq distances) increase with early PREMS after controlling for postnatal maternal fGCM, concurrent offspring fGCM levels, season, and age class. These results highlight timing effects in developmental plasticity and demonstrate that moderate adversity in reaction to fluctuating resources is associated with increased HPA axis reactivity all the way into adulthood as well as changes in the gut microbial community composition both of which can have severe consequences for individual health and fitness.

Behavioral Biology
Poster: Behav 09

Interspecific differences in host finding traits in *Nasonia* wasps (Hymenoptera: Chalcidoidea: Pteromalidae: Pteromalinae)

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Interspecific differences in behavioural traits have been investigated only in few parasitoid wasp species. Here we show the interspecific phenotypic differences of complex behavioural traits in parasitoid wasps, *Nasonia* spp. The differences reflect local adaptations and might fortify the prezygotic isolation in sympatric populations, i.e., being directly related to speciation. We identified and quantified the interspecific differences of host finding traits in two closely related species, *Nasonia vitripennis* (Walker, 1835) and *Nasonia longicornis* Darling, 1990. Both wasps parasitize fly puparia, are microsympatric and interfertile, but the former is a host and habitat generalist and the latter is a specialist. The behavioural trait in focus is host acceptance time, i.e., the time a female specimens needs from encountering the host to starting the process of oviposition. Both species differ significantly in this trait. Furthermore, the expression of the trait is modified in the more specialist species *N. longicornis*, depending on the previous host experience of the females. We discuss possible explanations for these differences and their consequences on our understanding of parasitoid wasp speciation and diversification. Finally, we will briefly outline the role and potential of host finding traits in parasitoid wasps for studying phenotype-genotype links and identifying the genomic architecture of complex behavioural traits.

Ecology
Poster: Ecol 12

Form and function of *D. atkinsoni*'s inducible defences

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Predator induced defences, a special form of phenotypic plasticity, are well-known to render prey species less susceptible to predators, for example through alterations of shape and behaviour. Especially the morphology of inducible morphological alterations is assumed to be minutely tailored to fulfil their protective potential. Such inducible defences are well-known in many *Daphnia* species. *D. atkinsoni* has been shown to express so-called "crowns of thorns" at the dorsal part of the head capsule in the presence of *Triops cancriformis*, a tadpole shrimp (Notostraca). Despite these alterations are described, their function in how they protect *D. atkinsoni* is still unknown. Therefore, we aimed at more detailed insights into this defence. Crowns of thorns were induced by exposing *D. atkinsoni* to *T. cancriformis*. Once the animals reached sexual maturity, the animals were fixed, stained with kongo red and image stacks were acquired using confocal microscopy. From these image stacks of control and induced animals, we created a 3D-model of predator-exposed and unexposed *D. atkinsoni*. With this we were able to describe the morphological changes in high detail. We then determined swimming velocities, which together with downstream (fluid) biomechanics reveal the streamline properties of predator-exposed vs. unexposed *D. atkinsoni*. Merging the knowledge on the inducible defences in this species therefore allows to draw a holistic picture of the protective mechanisms. As inducible defences incur costs, our analysis further allows a more comprehensive understanding of costs and trade-offs of this defence.

Behavioral Biology
Poster: Behav 10

Do bumblebees vary their flight altitude to return home in clutter?

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Along a foraging journey, flying insects, such as bees, are guided by the current visual sceneries. After exiting the nest for the first time, bees memorize the views surrounding their nest. Learning relevant aspects of these views is critical as they contribute to pinpointing the nest on later returns. During such learning flights, bees gain flight altitude and increase their distance and height to the nest. They may even exceed the height of objects surrounding the nest, such as flowers, grass, or bushes, and they experience views completely different from those at much lower altitudes in the immediate vicinity of the nest. In a cluttered environment like a forest or a meadow, the views around the nest may be ambiguous to the similarly-looking objects and numerous occlusions, whereas the views above the clutter are not due to a unique pattern formed by the object's arrangement on the floor. Do bees return by flying above or within the clutter? We challenged bumblebees, *Bombus terrestris*, in a lab setting to pinpoint their nest entrance surrounded by 40 randomly placed objects. Moreover, we constrained their flight altitude at various stages of learning and homing flights, so that they could use views within or above the clutter. We observed the bees searching for their nest at several locations within the clutter. Although they could fly above the clutter during learning, the bees meandered through the clutter to their perceived nest location. Even if the way through the clutter to the nest was blocked, the bees did not try to search from above. Our experiments could show that bees can pinpoint the nest within a cluttered environment without using views from above.

Neurobiology
Poster: NB 19

Locusts in the sky: responses of compass cells

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The polarization pattern of the sky is used as a navigation cue by many insects. The underling circuits in the brain have been studied most thoroughly in locusts. Laboratory studies indicate a key role for the central complex in sky compass orientation. Main parameters used in this compass are the sky polarization pattern and the azimuth of the sun (Zittrell et al. 2020, PNAS 117:25810ff). We tested extracellularly recorded units inside a hut on the top of the Biology building and, after lifting the animals beyond the roof, exposed them to the natural sky. Inside the dark hut, the animal was mounted on a rotation stage in the middle of a dark arena; a polarization stimulator was mounted directly above. Two arena tests were performed, either the polarizer or the animal were turned. Subsequently, the animal was rotated under the full natural sky during the third test. Sky conditions were monitored through spectroscopy and polarimetry. Recordings lasted for up to three hours with one to three repeats of all experimental parts. All polarization-sensitive units had axial preference angles when tested in the dark arena. However, all except one unit changed to cicular preference angles when exposed to the full sky. Circular preference angles were offset by about 90° relative to the axial angles. The results suggest that compass neurons change their representations based on the most salient stimulus.

Evolutionary Biology
Poster: EvoBio 09

Adaptation of *Aphidius ervi* to a novel host: preference and fitness consequences

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The parasitoid lifestyle evolved multiple times among the insects, giving rise to the most species rich groups among all animals. Parasitoids develop on or in other animal hosts but maintain a free-living adult stage. In each generation, parasitoids must decide which host to attack, with different hosts providing different quantity and quality of resources for the offspring. In general, parasitoids prefer to attack a limited range of hosts, to which they are best adapted. However, host range extensions do occur, with sometimes dramatic consequences for the parasitoids phenotype. Therefore, when a novel host species is attacked, the question arises as to what advantages and consequences this brings and to what extent adaptation to the novel host occurs. To explore this phenomenon, we studied the parasitoid wasp *Aphidius ervi* raised on two different aphid host species, *Acyrthosiphon pisum* and *Aulacorthum solani* as novel host. The adaptation to the substantially smaller *A. solani* is thus investigated, more precisely whether *A. ervi* parasitises the novel host or still prefers to use the native host. In order to do so, we designed an experiment in which *A. ervi* females are exposed to both aphid species and can choose which hosts they attack. In addition, the host species are used in two different developmental stages to investigate which host species is most preferred at which age and which provides the highest fitness. It is expected that *A. ervi* will have the highest fitness in a younger stage of the natal host. In addition, *A. ervi* may have adapted to *A. solani* as a novel host and the wasps from this population should prefer the novel host. The results will help us understand the selection pressures on host usage of this important biocontrol agent.

Neurobiology
Poster: NB 20

Smelling sticks: Multi-unit-recordings of antennal lobe-neurons in stick insects

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For spatial orientation in darkness, a nocturnal animal like the stick insect *Carausius morosus* cannot rely on vision. Instead, its perception must depend on sensory modalities such as olfaction or touch. Several previous studies of our group were concerned with the sense of touch in insects: in particular, we focused on context-dependent movement of the two long antennae, their tactile sampling pattern and the use of antennal contact events for spatially targeted leg movements. Given that insect antennae carry many chemosensory hairs, antennal movement and sampling likely contributes chemosensory information, too. Since very little is known about olfaction in herbivorous stick insects, the main objectives of the present study were to obtain reliable olfactory activity recordings and, in particular, to establish multi-unit recordings in the antennal lobe (AL) of stick insects. As in other insects, the AL is the first olfactory neuropil, where individual neurons are tuned to a range of single-odor components. As a population, AL neurons can encode complex odor plumes, for example of a food source. Here we show that such a population response separates the odor component hexanal from other odor components. Since hexanal is a characteristic odor component of freshly cut leaves, it is likely to be of behavioral relevance for a herbivore. In addition to the AL response we tested the same odor set, in electroantennograms (EAG), i.e., recordings of the antennal nerve bulk activity. In contrast to the AL-recordings, the EAG signal induced by hexanal was significantly weaker compared to that of other odors tested. The difference between the afferent activity measured in the EAG and the AL population response indicates that early olfactory processing in stick insects separates an odor of potential relevance from other odors. Future work will address the question how stick insects may combine olfaction with touch to integrate spatial information from both modalities.

Evolutionary Biology
Poster: EvoBio 10

Unraveling complex chemical profiles and sexual signaling through haploid genetics: Cuticular hydrocarbon genetics in the jewel wasp *Nasonia*

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Cuticular hydrocarbons (CHCs) are long-chained hydrocarbons that occur on the epicuticle of insects. Primarily, CHCs serve as a physical barrier to prevent desiccation, but they also function in chemical signalling, e.g. as species-specific sex pheromones. In the parasitoid jewel wasp *Nasonia* genus (Hymenoptera: Pteromalidae), it has been shown that CHC profiles can serve as female sexual cues triggering male courtship and copulation behavior in most of the species. However, female CHCs of one particular species, *N. giraulti*, are not sufficient as sexual cues to induce mating in the males, while they remain attracted to heterospecific female CHC profiles from the other species. This astonishing evolutionary shift in sexual communication among closely related species has greatly aroused our interest to explore genetically, chemically and behaviorally, particularly how the sexual signaling function could be lost in one species and how it remains encoded in the CHC profiles of the others. In our research, we established experimental female backcrosses between *N. giraulti* and *N. longicornis* (where sexual signaling of female CHCs is still intact) to enable the correlation of haploid genotypes in *Nasonia* males with CHC phenotypes in the diploid backcrossed females. This is done concurrently with the identification of quantitative trait loci (QTL) on a high-density genomic map based on Restriction-site Associated DNA (RAD) sequencing to identify genetic regions associated with CHC variation. Together with mating behavior tests on backcrossed females, we also aim to decipher how female sexual attractiveness is encoded in the CHC profiles. The results from combining these different approaches will substantially advance our understanding of this intriguing evolutionary shift in sexual communication in *Nasonia* and the genetics of CHC biosynthesis and sexual attractiveness in general.

Morphology
Poster: Morph 07

Reconstructing life cycles of the isopodan group Aegidae – immatures of "marine mosquitoes"

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Aegidae is an ingroup of Isopoda, including marine crustaceans with a global distribution. Species from this group temporarily attach to predominantly actinopterygian fish species, feeding on their blood and body tissue using their specialised mouthparts. Therefore, acting as a type of "marine mosquito". Records of such crustaceans attaching to other marine animals such as cartilaginous fishes have also been recorded and might be an indication of their opportunistic, more generalist feeding behaviour. Some individuals have also been reported to attach to and inhabit sponges. To date, around 148 species of Aegidae have been described and accepted. Yet, our knowledge of these species are almost exclusively restricted to adult specimens. From all the known species, only ten have at least one immature stage partly described or have at least a single illustration. In a few other instances, limited morphological characters of immature specimens were provided. Here, a collection of various developmental stages of Aegidae is presented. Specimens were dissected and photographed, to be compared among species and to their better-known adult stages. This study is the first to attempt to provide life cycles of these animals, including well-documented and described immature stages, as well as notes on the feeding behaviour and life habits of these least known developmental stages.

Behavioral Biology
Poster: Behav 11

Collective Construction: Adjustment of underground foraging tunnel in Leaf-cutting ants

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Leaf cutting ants build underground nest chambers where they house symbiotic fungus. These chambers are connected to each other through various tunnels, and also connecting outside the nest – to foraging areas. It is presumed that the underground foraging tunnels must adapt to an ever-growing nest volume and through increased usage by foraging workers. Mechanisms like self-organization through local interactions and stigmeric communication explain the emergence of global structure. However, most studies have focused on nest chamber construction as a whole, whereas very few studies have looked into emergence of tunnels and the related feedback mechanisms. The aim of our study is to investigate how leaf-cutting ants assess space within a tunnel i.e. how to they assess where the tunnel is narrow or wide so as to widen the tunnel in order to have a free traffic flow. We investigated by presenting a two-dimenional digging arena with a tunnel whose width varied between 1 cm (narrow) and 4 cm (wide), along the entire length of the tunnel. The rationale is that there would be high congestion among individuals due to narrow tunnel than when compared to wider parts of the tunnel, which leads to a low traffic flow initially. The high encounter rate among individuals would therefore lead to widening only narrow parts of the tunnel through digging such that the tunnel widens over time, causing traffic flow and speed of the individuals traversing the tunnel to fall back to normalcy. We empirically found that traffic flow was low initially, increases gradually as the tunnel widens and remained constant. We also found a significant positive correlation between traffic flow and width of the tunnel, as well as between speed of the individuals and width of the tunnel. Overall tunnel width remains to be regulated over time such that it does not widen more than needed. These results suggest that there are positive and negative feedbacks at play which controls the overall tunnel width that emerges over time. We also speculate that encounter rate acts as a mechanism for the amplification and regulation of tunnel width.

Evolutionary Biology
Poster: EvoBio 11

Inbreeding affects the condition-dependent expression of ornamental traits in the West African cichlid *Pelvicachromis taeniatus*

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The evolution of elaborate sexual ornamentation can be explained by sexual selection theory, and the expression of secondary sexual traits often depends on individuals' phenotypic condition. Condition-dependent expression of ornamental traits or trade-offs between traits may depend on individual genetic background or genetic diversity. However, the allocation of resources towards ornamentation may also constrain other physiological processes which may lead to dishonest signaling. Reduced genetic diversity within individuals can impair adaptation potential and reduce stress tolerance. Inbreeding is described to affect genetic diversity, often resulting inbreeding depression. The biparental West African cichlid *Pelvicachromis taeniatus* shows active inbreeding which seems to be adaptive because of inclusive fitness benefits and better brood care of related parents. Deleterious effects of inbreeding regarding growth or mortality have not been observed in this species. Here, we address the question whether inbreeding affects the expression of ornaments in adult *P. taeniatus* of both sexes. We analyzed photographs of inbred and outbred individuals regarding their sex-specific ornamentation. In detail, we compared the area / extension and intensity of the ornamentation between in- and outbred fish. Furthermore, the relationship between coloration and physical body condition in both groups was examined. Whereas inbreeding had no direct effect on color expression, the relationship between physical body condition and coloration significantly differed between in- and outbred individuals of both sexes. Inbred individuals seem to maintain coloration at the expense of other physiological processes resulting in a negative relationship between physical condition and color expression, whereas this relationship was positive in the outbred group. Coloration not mirroring phenotypic condition in inbred cichlids, i.e. dishonest signaling, may ultimately affect sexual selection in this species, potentially affecting receivers' fitness.

Evolutionary Biology
Poster: EvoBio 12

Glycogen metabolism influence *Tribolium* segmentation involed in Wnt signalling through GlyS and AGBE

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Embryonic segmentation of arthropods is a dynamic biological process that produces an organism by pattern formation, morphogenesis and specification of corresponding cells. The involved genes are usually identified by their phenotype after knock-down. However, respective systematic searches may have remained incomplete, because interference with some patterning genes cause embryonic death before cuticle formation. Therefore, we screened such "empty egg phenotypes" without any recognizable cuticle structures for defects during embryogenesis. Here, we show that RNAi targeting two genes involved in glucose metabolism GlyS and AGBE lead to segmentation defects ultimately leading to empty egg phenotypes. Both enzymes have a vital role in wide range of cell signalling pathways and metabolism process that take place during cell proliferation, transport, apoptosis, and glucose regulation. We studied the functions of GlyS and AGBE in *Tribolium* segmentation. We found that RNAi embryos initially develop normally but show strong irregular patterning in the posterior abdomen during elongation, suggesting that GlyS and AGBE functions contribute to establish posterior segments. Indeed, RNAi of GlyS and AGBE led to strong defects and irregular stripes of segment polarity genes wg, hh, and en, which are required to maintain the para-segment boundary and indicated potential influence on Wnt and Hh signalling. To identify the effects of Wnt and Hh signalling, we performed double RNAi with key components of these pathways. These epistasis experiments revealed stronger truncation phenotypes in the double RNAi compared to Tc-arrow and Tc-pangolin, revealing that GlyS and AGBE act additive to Wnt signalling. Likewise, a higher percentage of empty egg were observed with Hh double RNAi, which indicates that Hh function may in parallel to GlyS and AGBE. Our findings provide unique evidence that glycogen synthesis enzymes participate in segmentation.

Developmental Biology
Poster: Dev 08

Modeling EGFR mutations in *Drosophila melanogaster*

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Lung cancer is one of the most common and deadly malignant tumors in the world. The key oncogenes in lung cancer are identified and partially well known. The epidermal growth factor receptor (EGFR) is one of the most important drivers of lung cancer. EGFR-tyrosine kinase inhibitors (EGFR-TKI) like Afatinib and Gefitinib, are targeted drugs specifically developed against the abnormal activation of EGFR in tumor cells, which can effectively inhibit sensitive EGFR mutations. This standard EGFR-TKI therapy of primary (sensitive) mutations in this gene is often accompanied by secondary arising mutations, leading to treatment resistance and tumor relapse. We generated fruit flies carrying a fusion of the *Drosophila* and the human EGFR gene. The N-terminal part including the extracellular and the transmembrane domain contributes to *Drosophila* while the cytoplasmic part originates from human EGFR. A set of variants including EGFR wildtype, L858R single mutation, T790M and L858R double mutation was assembled. With these humanized flies it is possible to study the effects on tracheal tumorigenesis and investigate the EGFR/Ras/Raf/MAPK pathway and TKI's therapeutic effect. Additionally, these flies could represent an effective and simple model system for screening new anti-cancer drugs and TKIs.

Developmental Biology
Poster: Dev 09

Gene expression divergence during *Drosophila* head development on single nuclei resolution

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We apply single-nuclei RNA-seq (snRNA-seq) to gain in-depth insights into gene expression and regulation dynamics throughout eye development in *Drosophila* species on single-nucleus resolution. Comparative snRNA-seq is used to identify candidate genes responsible for morphological variation such as size and shape differences in three closely related *Drosophila* species, *D. melanogaster*, *D mauritiana* and *D. simulans*. These species are known to differ in eye size and shape, and by comparing closely related species, we hope to minimize background noise in expression data. We collected eye-antennal imaginal discs, the larval organ precursor tissues of eyes and the head capsule in holometabolous insects, of all three species. The collected samples span late larval development, in which size and shape differences first manifest. We selected five time points covering major developmental events from growth and patterning up to differentiation. Single nuclei sequencing from single nuclei suspensions was performed by Dresden Concept Genome Center. There, these samples were analyzed using the 10x Genomics Chromium system. By applying single nuclei sequencing it is possible to assessing co-expression and, to a degree, spatial localization of gene expression which is not possible by using bulk sequencing methods alone. It furthermore allows comparing changes in relative cell type composition between developmental stages and species. We will attempt perform gene regulatory network analyses to identify regulatory changes in genetic pathways that underlie differences in eye and head morphology.

Neurobiology
Poster: NB 21

Compartmentalization of brain activity during sleep in an avian brain

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Sleep in humans is characterized by the switching between two distinct brain states: slow wave sleep (SWS) and rapid eye movement (REM) sleep. During SWS in humans, the effective connectivity between cortical regions breaks down and is accompanied by a loss of consciousness [1]. Electroencephalography (EEG) recordings in birds also reveal distinct stages of SWS and REM, despite their different brain structure [2, 3]. However, the network connections that exist during different sleep stages remain unexplored in these animals. We recorded EEG during sleep in 7 zebra finches (3 adults, 4 juveniles) and monitored body movement with infrared video recording. We show that functional connectivity reduces during the SWS bouts. Furthermore, by exploring the EEG waves, we demonstrate the existence of 'local waves', the waves traveling through a considerable portion, but surprisingly not all parts, of the brain. We correlate the abundance of these waves with measures of functional connectivity. Then we demonstrate that the brain shows more propensity for local waves during the SWS, therefore reasoning the lower functional connectivity of the avian brain in this stage. We also used graph theory to explore the highly correlated EEG channels. We found that during sleep, small clusters of highly correlated networks exist, and that these clusters are spatially organized into frontal and caudal networks in each hemisphere. These results highlight comparable compartmentalization of brain activity that occurs in both birds and humans during sleep, despite the different neural architectures of the brain. References Massimini, Marcello, et al. "Breakdown of cortical effective connectivity during sleep." Science 309.5744 (2005): 2228-2232. Low, Philip Steven, et al. "Mammalian-like features of sleep structure in zebra finches." Proceedings of the National Academy of Sciences 105.26 (2008): 9081-9086. Vorster, Albrecht P., and Jan Born. "Sleep and memory in mammals, birds and invertebrates." Neuroscience & Biobehavioral Reviews 50 (2015): 103-119.

Morphology
Poster: Morph 08

The morphology of extant and fossil larvae of false flower beetles with prominent terminal ends

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Whether in air, soil or even water, insects come in high numbers. One of the most species rich groups within insects is Coleoptera, the group of beetles. Every fourth animal in the world is a beetle, at least statistically. Yet, there are so many ecomorphotypes still undiscovered, undescribed and not examined. Scraptiidae, the group of false flower beetles, comprises 400 formally described species. The larvae of these beetles can be found in rotting wood, where they apparently contribute to wood decomposition and carbon cycling. Some of the larvae (possibly within the ingroup of Scraptiinae) are characterized by the presence of a prominent terminal end. We present here seven new extant and 12 fossil specimens of false flower beetle larvae with enlarged terminal ends. We demonstrate that these larvae of Scraptiidae with prominent terminal ends are more common in the fossil record than previously thought. While there were already few comparable fossils known in 40-million-years-old Eocene Baltic amber, two of the new fossils come from 100-million-years-old Cretaceous Kachin amber. Hence the new fossils also expanded the border of appearance of this type of larvae by 60 Ma. Morphometrics of the terminal end reveal mostly a differentiation by size. This is a major challenge for comparison since most of the fossils represent early larval stages and we are for the most part familiar with later larval stages in the modern fauna. Still the larvae demonstrate the presence of carbon-cycling beetle larvae already in the Eocene and Cretaceous faunas.

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